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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 14:04:04 ; Search time 6849.01 Seconds
(without alignments)
10625.327 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679

Sequence: 1 gttgttccttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 1.0, Gapext 0.1

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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1: gb_ba.*

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6: gb_pat.*

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41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1679	100.0	1679	6	AX358872 Sequence
2	1679	100.0	1679	6	AX362365 Sequence
3	1679	100.0	1679	6	AX403748 Sequence
4	1679	100.0	1679	6	AX454470 Sequence
5	1679	100.0	1679	6	AX464242 Sequence
6	1679	100.0	1679	6	AX490948 Sequence
7	1679	100.0	1679	9	AX358331 Homo sapi
8	1510.9	90.0	1839	9	AX665342 Sequence
9	1510.9	90.0	1839	9	AF126426 Homo sapi
10	1204.5	71.7	2040	10	U16845 Rattus norv
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ALIGNMENTS

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DEFINITION Sequence 125 from Patent WO0193983.
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc. (US)
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VERSION													
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DEFINITION Sequence 375 from Patent WO0140466.
ACCESSION AX464242
VERSION AX464242.1 GI:21899137
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E., Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 375 07-JUN-2001; Genentech Inc. (US)
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RESULT 6
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LOCUS AX490948
DEFINITION Sequence 55 from Patent WO0200690.
ACCESSION AX490948
VERSION AX490948.1 GI:22323811
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
AUTHORS Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 55 03-JAN-2002;
Genentech, Inc. (US)
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AUTHORS Clark H.F., Garvey A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I. and Godowski P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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REFERENCE 1 (bases 1 to 1839)
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AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Cloning and identification of human neurotrophin full length cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1839)
AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
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Rattus.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
and Salzer,J.L.
TITLE Cloning of neurotrophin defines a new subfamily of differentially
expressed neural cell adhesion molecules
J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
MEDLINE 95198094
PUBMED 7891157
REFERENCE 2 (bases 1 to 2040)
AUTHORS Salzer,J.L.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
Center, 550 First Avenue, New York, NY 10016, USA
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Best Local Similarity 70.9%; Pred. No. 7e-09;
Matches 1435; Conservative 0; Mismatches 196; Indels 392; Gaps 75;
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Db 58 TGGTAGCTGGATTACGCCAGCCAGACGCCCGTGGATACCAAGTGCITA---CTCCT 114
Qy 39 -----TGC-AC-----A---AGCT--TGAGA---GCAAC-- 58
Db 115 GTCCAAAGTGCCATGCTGAACTGCTACGGGGAAGAGCAGCTTCTGAGACCCGACCTG 174
Qy 59 -----ACAATCTAT-----CA-----GG--AAAGAA 78
Db 175 TGGCGCTGCTTGGCTTGGCTTC--TCTCTCTGGCCACCTTCTGCGCCACAGCA 232
Qy 79 GAA---AGAAA-----A-----AAAC-----C-GA-----ACCTGA 100


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McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1615)
Strausberg,R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC) Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowib, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 26986610.

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Best Local Similarity 79.5%; Mismatches 189; Indels 160; Gaps 57;
Matches 1355; Conservative 0;

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2 GGAC--GCGTG-G-GC--CGAGT---TCTGG-----GAAGTTGTG-----G-- 34

96 CTTGACAAAAAGAGAAAGAAAGAAAGAAAGAAATC-ATGAAAAACC--ATCCAGCC-- 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 -CTGTC-----GAGAAATG--GGGG-----TCTGTGGGTACCTGTCTTCGCCCT 74

151 AAAAAATGCACAAATCTTATCTCTTGG---GCAATCT-TCACGGGGCTGGCTCTCTGTGT 205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
75 GGAAGTGC-----CTCGTGGTCTGTG---TCTCTCA-----GGCTGCTAT---T 111

206 CTCTT-----CCA-AGGAGTGCCCGTGCAGCGAGATGCCACTTCCCAAAGCTATGG 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
112 C-CTTCTACCCACAGAGTGCCTGCGTAGCGGAGATGCCACTTCCCAAAGCTATGG 170

261 ACAACGTGACGGTCCGGGAGGGGAGAGCGGCACACCTCAGGTGCACATATTGACACCGGG 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
171 ACAACGTGACGGTCCAGGCGAGGGGAGAGCGGCCACCCCTCAGGTGCACAAATTGACACCGAG 230

321 TCACCCGGGTGGCTGGCTTAAACCGCAGCACCAATCTCTATGCTGGGAATGACAAGTGGT 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
231 TCACCCGGGTGGCTGGCTTAAACCGCAGTACCAATCTCTATGCTGGGAATGACAAGTGGT 290

381 GCCTGGATCCTCGCGTGGTCTTTCTGAGCAACACCCAAACGCGAGTACAGCATCGAGATCC 440
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291 GCCTAGATCCTCGTGGTGGTCTCTCTGAGTAAACACCCAGACCCAGTACAGCATTTGAGATCC 350

441 AGAAGCTGATGTGTATGAGAGGGGCCCTTACACCTGCTCGGTGCGAGACAGACACCCACC 500
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351 AGAATGTGATGTGTACGATGAGGGGCCCTTATACCTGCTCGGTGCGAGACAGACACCCACC 410

501 CAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTCTT 560
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411 CTAAAGACCTCCAGGGTCCACCTCATTTGTACAGTATCTCCCAAAATTTGTAGAGATTCTT 470

561 CAGATATCTCAATTAATGAGGAAACAATATTAGCTCTACCTGCATAGCAACATTTGGTAGAC 620
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
471 CAGATATCTCAATTAATGAGGAAACAATCATCAGCTCTCACTTGCATAGCCACAGGTAGAC 530

621 CAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGGGTGGCTTTGTGAGTGAAG 680
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
531 CGAGAGCTTACAGTAACTGAGACATATTTCTCCCAAGGGCCGTTGGCTTTGTGAGTGAAG 590

681 ACGAATACTTTGAAATTTACGGGCATCACCCGGGAGCAGTACAGGGGACTACAGTGCAGTG 740
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
591 ATGAGTACCTGGAGATCCAGGGCATCACTCGGGAACAGTCAGCGGAGTACAGTGCAGCG 650

741 CTTCCAAATGACGTGGCGGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAATCTATCCAC 800
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651 CTTCCAAAGACGTGGGGGACACCACTGGTGTGACGAAGAGTGAAGGTCAACCGTGAATCTATCCAC 710

801 CATACATTTTCAAGAACCAAGGTACAGGTGTCCCGCTGGGACAAAAGGGGACACTGCAGT 860
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
711 CATACATCTCAGAAGCTAAGGGGACAGGTGTCCCGCTGGGGGAGAGGGGACACTCTCGAGT 770

861 GTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCAGTGGTGAACAAGGATGACAAAAGACTGA 920
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771 GTGAAGCTTCGCGAGTCCCCTTCAAGCAGAAATTTCAATGGTTCAAGGATGACAAAAGACTGG 830

921 TTCAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTCATCTTCT 980
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831 TCGAAGGAAAGAAAGGGAGTCAAAGTGGAAACAGACCTTTCTCTTCAAAACTCACCTTTT 890
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* be preserved.
* 1 26097: contig of 26097 bp in length
* 26098 26197: gap of 100 bp
* 26198 48570: contig of 22373 bp in length
* 48571 48670: gap of 100 bp
* 48671 65250: contig of 16580 bp in length
* 65251 65350: gap of 100 bp
* 65351 78415: contig of 13065 bp in length
* 78416 78515: gap of 100 bp
* 78516 91388: contig of 12873 bp in length
* 91389 91489: gap of 100 bp
* 91489 102970: contig of 11482 bp in length
* 102971 103070: gap of 100 bp
* 103071 112373: contig of 9303 bp in length
* 112374 112473: gap of 100 bp
* 112474 123106: contig of 10633 bp in length
* 123107 123206: gap of 100 bp
* 123207 133003: contig of 9797 bp in length
* 133004 133103: gap of 100 bp
* 133104 142050: contig of 8947 bp in length
* 142051 142150: gap of 100 bp
* 142151 150046: contig of 7896 bp in length
* 150047 150146: gap of 100 bp
* 150147 156216: contig of 6070 bp in length
* 156217 156316: gap of 100 bp
* 156317 161217: contig of 4901 bp in length
* 161218 161317: gap of 100 bp
* 161318 166676: contig of 5359 bp in length
* 166677 166776: gap of 100 bp
* 166777 171521: contig of 4745 bp in length
* 171522 171622: gap of 100 bp
* 171623 175750: contig of 4129 bp in length
* 175751 175850: gap of 100 bp
* 175851 178697: contig of 2847 bp in length
* 178698 178797: gap of 100 bp
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* 183880 183979: gap of 100 bp
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* 186687 186786: gap of 100 bp
* 186787 188509: contig of 1723 bp in length
* 188510 188609: gap of 100 bp
* 188610 191328: contig of 2719 bp in length
* 191329 191428: gap of 100 bp
* 191429 193900: contig of 2472 bp in length
* 193901 194000: gap of 100 bp
* 194001 195695: contig of 1695 bp in length
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* 195796 197775: gap of 100 bp
* 197776 198652: contig of 877 bp in length
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* 198753 199845: contig of 1093 bp in length
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Matches 1533; Conservative 0; Mismatches 101; Indels 1582; Gaps 287;

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QY 27 TTTA-AATCTC-CT---TGC--ACAAGCTTGAGACA-A-CACA---ATCTATCAGG- 71
Db 146087 TTTACAGCTCTCTGTGTGCTTCCAGCATG-GAGCAGATCACAAGAAGACTCTGAGG 146029
QY 72 --AAAGAAAGAAACA--AAAA-----ACC-----GA-A---CCTGACAA--AAAG--- 108
Db 146028 GCCTAGCAAG-GAGACCAACACAGGACCCAGGAGAGCGCTGGCATGCCACAGGCG 145970
QY 109 -A---AGN-----AAA-----A-----GA-----AGA--- 121
Db 145969 CATTGAGATCTGCCACAGGGGGTGTTCGCCGCTCTCAGTGTCTCCGAGCTGCAGAGT 145910
QY 122 ---A-----GAAAAA-----A--AT-----CATG--AA----- 138
Db 145909 CCCAGCCTGGAACACAGGTTTCAGCATTCCTTACATGTTACTACGCCAGGCCCTGCG 145850
QY 139 -----AAC-----CA-----TCCA-----GC 149
Db 145849 TGGGCTGAACACCTGGCTGTGGCATTCCTCCCTGGAGGCTTCCACTGGCAGGTCAGGC 145790
QY 150 --GAA-----AA-----A-TGCA-----CA----- 161
Db 145789 TGCAAGGAGGGAGTTTCAGAGAGAGAGAGAACACCTAGTGCAGGGAAGCGCACTTGT 145730
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QY 162 ATTCTATCTCTT-----GGCAATCTTC-----ACGGG-GC 191
Db 145729 TTTCATCTCTTACCCAGGC-ATCTTCTTAGTCACAGGAGGAGCGGAGACGGAGG 145671
QY 192 TGG-----CTGC-----TGCT-CTCTTC----- 211
Db 145670 TGGGAGTGTGGGGAATTGAACAGAAATGGGTTTCAAGATGTGTGGATGTTCAGGA 145611
QY 212 -----CHAGG-----AGTGC-----GTGC-G-CAGC-----GGAG- 236
Db 145610 GAGCACAAGGATGAAGAGGAGCAGCAGTGTGCTGACAGCTGTGTCCCTGCGGGAGT 145551
QY 237 -----A-----TGC-----CAC-----C-----TTC-CCCA-----AAG 254
Db 145550 TAAGGACTCCAGTGTGAGGACAGCATATGAAATGTGTAGGGTGTGATTCAGCATATGAAG 145491
QY 255 CTA-----TGACA-----AC-----GT-----GAC-----GG-----TCC 275
Db 145490 CTATCTTCATATGAATGTGAACACTCACAGTGTGTGAGGCAAAACATTCGACCTGGCTTCC 145431
QY 276 -----G-----GCAGG-----GGA-----GAGGCCACC-----CTCAG-GT----- 302
Db 145430 ATAAAGCCCTGTCTGGGCCATATGAGACTCAGAACACCCTTGTGTCTTCAGAGTCTTCAGC 145371
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QY 341 -----A-----AC-C-----GCAG-----CAC-----CATC----- 355
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QY 356 -----CTCT-----ATG-----CTG-----GGAATGACA-AGTGGTGC-CT- 384
Db 145259 GGCTTCTCTCTTGTATTCMAAGAAATGTGCTCTGTAG--ATGACAGAT-GAGCATCTA 145203
QY 385 -----GGATC-----CTCGCG-TGGTCTCTCTG-----AG----- 408
Db 145202 CAAAGGGGAAGCTCTGTGTATGT--TTCTGTGGACACATAGTATGTAGATTTAGAG 145145
QY 409 -----CAAC-----ACC-----C-----AAA-C 420
Db 145144 ACACACACAGTTAGTGACCGATCTCTAAATGACAAAGCATTTCTGGGTTGAGATTTAAATCC 145085
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Db 145084 GCAGAGCTTTACAGGAGTGTCTCTGTGTACCTGTATCTTAGCAGAGATCGCTTTGGTT 145025
QY 450 ATGTGT-----ATGACGAGG-----CCCT----- 469
Db 145024 TTGTGTTTCTCTCTTAATG-C-AGGGTAGAGAGAATAAGTATCCCTGGGCTTCTCAGCA 144967
QY 470 -----TACACCTGCT-----CG-----GTG-----CAGACA----- 490
Db 144966 TGGGATCTGCACCT-CTGAGAAGTTCGGGCTTTAGGATCTCTGTGAATCAGACACCAGG 144908
QY 491 GACAAAC-----CACC-----CAA-----A-G-ACCT----- 509
Db 144907 GA-AACATGAGTTGATGACCTATTGCAATTTCAATCTCATGCTACCTATTATGACCAGC 144849
QY 510 -----C-----TAGGG-----TCC-----A-CC-----TCAT-TGTGCA----- 531
Db 144848 CCCCMAATTAGGATTTATCCCAAAGGCCAAGACATAAATATCATATGGGCACTGCCTCC 144789
QY 532 -----AGTATC-----TCCA-A-----AATTGTAGA----- 552
Db 144788 TAGCCAGAGT-TCTAGACTTTGGAATAATCCACATGGAATTTG-AGAGAGCTGTTT 144731
QY 553 -----GATTTCTT-----CAGA-----TATC-----TCCA----- 572
Db 144730 GATTTGATTTGTTTATAGACAAATGTATCCACGCTGACATCCAAAGTCAGCAGGCA 144671
QY 573 -----T-----TAAT-----GAAAGGAACA-----A-TA-TTAGCCTC 598

Db 144670 GGTTCGGCTTTTCTCTTCTTCCCTAATCCAGAG--ACATGGACTTAGTGAGGC-C 144615
QY 599 ACTGC-----ATA-----GCACTG-GTAGACACAGC----- 626
Db 144614 ACCAGCTTTAAATACCTCTATTAAATTCATGCAACAGAGTATGCCAGACAGCGTCCAGT 144555
QY 627 CT-A-----C-GTCTACTTG-G-AG--A-CA-----CAT-----C 649
Db 144554 CTGAGAGGTGGCTGTCTTCTTGTAGTAGTAATTTATCTGCGGCATCCAACTTATGTAC 144495
QY 650 TCTCC-----CAAAGC-----GGT-TGG-----CTTTG-----TGA-GT----- 676
Db 144494 TCTACAGAAATCAAGCTGCTACCTGCTCATGGGTTCCTTGCACCAAGGCGGAGGTAGC 144435
QY 677 --GAAGACG-----AATA-----CT-T--GGAA-----A-----TT-CAG- 700
Db 144434 CAGAAACGTTATGTTTTCAGAAACAATAGGAAGTGTCTGGGGAATCTGTACTCTTCAGT 144375
QY 701 -----G--G-----CATCAC-----CGGAGCAG--TCAGGGGAC-TAC 730
Db 144374 TCTCTGCTCTCTGTGTTGTCTCCATCTCCATACACTGGGCGAGGTTCTG--CATCC 144319
QY 731 GAGTG-----CAGTG-----CC-----TCCA-ATG-AC-----G-----TG 754
Db 144318 CAGTGTCTCTATTGATCTCCAGTTACATCCACATGCACAGGAAGGTTCTGTTCCTTTG 144259
QY 755 ---G-----CCGGCC-CC-GTGG-----TACGG-----AGAGTAAGGTCA-CCGT 789
Db 144258 TTTGACTCACCTC-CATCCATGTGGGTGGCTTTCGCGCTTTCAG-G--CATGTATCCTT 144203
QY 790 GAACT--ATC-----CACCATATTT--CAGAAGCCAAAG-----GGT--A- 824
Db 144202 GAGTGCATCTGTCTTACCCCATCAGATGGGGAAGAGTCAAGTCTCCAGGTGAAC 144143
QY 825 -CAGGTG---TCCCC-----GTG-----GGA-----CAA----- 844
Db 144142 CCAGGTGCCCTGCCCTGAGATAGATGATTGGCAGGATGCCCTCTGTGCCAAGGCAGCA 144083
QY 845 -AAG-----GG--GACAC-----TG-----CAG-----TGTGAAGCTCAG--C-A 874
Db 144082 GAAGCAGCAGCGACACATTTGTTTGTCCAAAGGTTCTTTTCTG-AGCCACAGGCCAA 144024
QY 875 GTCCCTCTCAGC-----AG-AATTC-----CAGTGGT--ACAAG----- 904
Db 144023 G-----CAGCTGGAGGTGGGTGAGTATTTTCAGGAGCAGATGCTCAGAAAGTGATGG 143970
QY 905 -GATGA-----CAAA--AGACTG-----ATTGAAG-----GA 928
Db 143969 TGATGAGGCACTCAGCAGCAGTAGTCTGACTTTTAAAGCTCTGTGTAGGATATTAATGA 143910
QY 929 A-----A-----GAA-----AG-----GG-----G--TGA-A-AG 944
Db 143909 ATCTGCCACCTCTCTCTTGAATTTGAGCCCTGAGCCATGGGCTTTGCATGTATGACACAG 143850
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Db 143849 TAAGGAAGAGGCCAGGACACTTTAAACCTGAGCCTCATGTTCTCTCTTTCAGGGGAAG 143790
QY 971 CT--C--ATCT-----TCTT--CAATGT--CTCT-GAACAT-GACT-----A 1002
Db 143789 GCTTCCGTTATCTAGTGTGTGTCTTGGGGATGTGGGCATAGAACGTTCTACTTCTAA 143730
QY 1003 TG-----GGAAC-----TACACTT-GCGTG--GCCTC-----CAA--CA 1031
Db 143729 TGCTGGGCTGGAAACACCATGTGTTTCACTTTAGAGGATGACTCACACAGGGGAGGCCA 143670
QY 1032 -----AGCTG-----GG-----CCAC-----ACCA-----ATGCCAG--CA-TCA-- 1058
Db 143669 AATGACAGCAGACCGACCAACCCGCGCTTTCTTCCATTTTCTCCAGACCACTCAG 143610
QY 1059 -----TGCTATTT--T-----GFTCCAGGCGCTCAGCAGGTGAGCAACGGCACCTCG 1105

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Db 143430 CAGCAATGGCAACACCGGACAGCAACCAATCAGATATATACAAATGAATTAAGAAGAA 143371
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Db 143310 TTTTAAAAAGAAATGAAATTTGCTTGGCAGATATTTAGGTACAAATGGAGTTTCTTTT 143251
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Db 143250 CCCAACCGGAGAAACACAGCACACCGGCTTGGACCCACTGCAAGCTGCATCGTGAAC 143191
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DEFINITION complete sequence.
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VERSION AP004248.2 GI:19263067
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 191071)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Mar 7, 2002 this sequence version replaced gi:16117845.
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 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 11, clone RP11-29L13

REFERENCE

1 (bases 1 to 184716)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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 Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 7, 2000 this sequence version replaced gi:6649510.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information

Center project name: L1344

Center clone name: 29_L13

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
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 Consensus quality: 178863 bases at least Q30
 Consensus quality: 180884 bases at least Q20
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 Insert size: 183516; sum-of-contigs
 Quality coverage: 4.6 in Q20 bases; agarose-fp
 Quality coverage: 4.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
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 * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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 * 54278 54377: gap of 100 bp
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 * 69400 69499: gap of 100 bp
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AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Schnerch A., Schein J.E., Jones S.J. and Marra M.A.
Generation and initial analysis of more than 15,000 full-length
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 1325)
Strausberg, R.
Direct Submission
Submitted (08-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.,
Homo sapiens 187,203 genomic DNA of 11q24
Published Only in Database (1999)
2 (bases 1 to 187203)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.,
Direct Submission
Submitted (03-DEC-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555,
Japan (E-mail: hattori@gsc.riken.go.jp,
URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,
Fax: 81-42-778-9324)
On May 31, 2000 this sequence version replaced gi:6997666.

COMMENT

----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humbract11
Center clone name: RP11-803P2
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Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 171133 bases at least Q40
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Insert size: 184603; sum-of-contigs
Quality coverage: 4.41x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Db 128069 CCCCCAAATAGGAATTTATCCCAAAGGCCAAGACATAAATATATAGGCACTGCCTC 128128
QY 532 -----AGTATC-----TCCA-A--AAATGTAGA----- 552
Db 128129 CTAGCCAGGAGT-TCTAGACTTGTGAATAATCCCAATGAATG-AGAAAGCTGTTT 128186
QY 553 -----GATTCTT-----CAGA-----TATC-----TCCA----- 572
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Db 128187 TGAATTTGATTTGTTTACGAGAAATGTATCCAAAGCTGAGCATCCAAAGTCAGGAGGC 128246
Qy 573 | | | | | T---TAAAT---GAAGGGAACA---A---TA-TTAGCCT 597
Db 128247 AGGTTCTGGCTTTGTTCTCTGTTCCCTAAATCCAGGAAG---ACATGGACTTAGTGAGGC- 128302
Qy 598 CACCTGC---ATA---GCAACTG-GTAGACACAGAGC--- 626
Db 128303 CACCAAGCTTTAAATACCTCTATTAAATTCATGCAACAGATATGCCAGAGCAGGTCCAG 128362
Qy 627 -CT-A---C-GGTACTTG-G-A-G---A-CA---CAT--- 648
Db 128363 TCTGAGGAGGTGGCTGTTCTCTGAGTAGCTAAATCTATCTGGGCATCCAAATTTATGTA 128422
Qy 649 CTCTCC---CAAAGC---GGT---TGG---CTTTG---TGA-GT--- 676
Db 128423 CTCTACAGAAATCAAAGCTCCACTGGTCTATGGGGTTTCTTGCCCAAGGGCCGAGGTAG 128482
Qy 677 ---GAAGAGC---AATA---CT-T---GGAA---A---TT-CAG 700
Db 128483 CCAGAAACGATATGTTTCAAGAACATAGGAAGCTGCTGGGGAAGTCTGCTGCTTGCAG 128542
Qy 701 ---G---G---CATCACC---CGGAGCAG---T---CAG 722
Db 128543 TTCTCCTGCTCCTGTTGTTGTTCTCTCATCTCCATACACTGGGGCAGGTTCTGTCATCCAG 128602
Qy 723 GG---GA-CTACGAG---TGCA---G--- 738
Db 128603 TGTCCTCATATGATCT-CCAGTTTACATCCACATGCAAGAGGCTTCCTGTTTCTTTGTT 128661
Qy 739 TG---CCTCCA---ATGACG---TGGC---CGCGCC---C---GTG--- 766
Db 128662 TGACTCACTCCATCCATGTTGGCTGCTCG-GCCTTGACGGCATGTGATCCTTGAGCT 128720
Qy 767 ---G---TAC---GGAGAGTAAAGGTCA---CC---GT-GAAGTAT 796
Db 128721 GCATCTGCTCTTACCCCATCCAGATGGGGA---AGAGGTCAAGTGTCTCCAGGTGGAAC--- 128775
Qy 797 CCA---CAATACATTC---AGA-AGCCAG---GGTACAGG-TGTCC-CCGTG--- 838
Db 128776 CCAGTGGCCCTGC---CCTGAGATAG---AGTGAATGG---CAGGATGGCCTCTGTGCCC 128826
Qy 839 ---GGA---CAAAAG---GG---GACAC---TG---CAG---TGTGAAGCC 868
Db 128827 AAGGAGCAGAGAGCAGCAGGAGACATGTTTGTCCACAGGTTCTTTCTG-AGCC 128885
Qy 869 TCAG--C-AGTCCCTCAGC---AGAAAT---C---CAGTGGT-ACAA 903
Db 128886 ACAGGCCAAG---CAGCTGGAGGGTGGGTGAGTATTTTCAGGCAGGAGTGTCTCAGAA 128939
Qy 904 G---GATGA---CAAA-AGACTG---ATTGAAG--- 926
Db 128940 GTGGATGGGTGATGAGGCACTCAGCACAGTAGTCTGACTTTTAAAGCTCTGTGTAGGA 128999
Qy 927 ---GAA---A---GAA---AG---GG---G--- 938
Db 129000 TATTATGAATGTCACCTCTCTTCTTGAATTTGAGCCTGAGCCATGGCCTTTGTCATGTT 129059
Qy 939 -TGA-A-AGT---GGAA-AA---CA-GAC-CTTT---CCT---CTCA--- 967
Db 129060 ATGACACAGTAAGGAAGAAGGCCAGGACACTTAACTTACCTGAGCTCATGTTCTCTCTT 129119
Qy 968 -A---AA---CT---C---ATCT---TCTTC---AATGT---CTCT-GAAC-AT 997
Db 129120 CAGGGAAGGCTTCCCGTTATCTAGTGTGTGTCTTGGGATGTGGGCATAGAACGTT 129179
Qy 998 GACT---ATG---GGAAC---TACACTT-GCGTG---GCCTC--- 1026
Db 129180 CACTTCTAATGCTGGGCTGGAACACCATGTGTTTCACTAGAGGATGACTCACCAGG 129239
Qy 1027 -GAA---CA---AGCTG---GG---CCAC---ACCA---ATGCCAG- 1053
Db 129240 GCAAGGCCAATGACAGACAGACCAGCAACACCACCGGGCTTTCTCTCCATTTTCTCCAGA 129299

Qy 1054 -CA-TCA-----TGCTATTT-----GGTCCAGGCGCGTCCAGCGAGTGTGAGCAACG 1097
Db 129300 CCACTCACGGGAGTGATGTTCTCTCCAGGTCCAGGCGCGCTCAGGAGTGTGAGCAACG 129359
Qy 1098 GCAGCTCGAGAGGCGCAGGCTGCTGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1157
Db 129360 GCAGCTCGAGGAGGCGCAGGCTGCTGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 129419
Qy 1158 TCAAAATTTGATGTAGTGCCCATTTCCCTCCAGCCCGGGGAAAGGCTGCCGCCACCAACCCAC 1217
Db 129420 TCAAAATTTGATGTAGTGCCCATTTCCCTCCAGCCCGGGGAAAGGCTGCCGCCACCAACCCAC 129479
Qy 1218 CAACACACAGCATGSCAACACACAGCAGCAACCAATCAGATATATATACAAATGAAATTTAG 1277
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Qy 1278 AAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAACAAAGAAATCTTTTGGGG 1337
Db 129540 AAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAACAAAGAAATCTTTTGGGG 129599
Qy 1338 GAAAGAGTTTAAAAAGAAATTTGAAATTTGCCCTTGCAGATATTTAGTACATGAGT 1397
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Qy 1398 TTTCTTTTCCAAACGGGGAAGAACACACAGCAGCAACCCCGCTTGCAGCCTCTCTGCCACAGAGTGCAT 1457
Db 129660 TTTCTTTTCCAAACGGGGAAGAACACACAGCAGCAACCCCGCTTGCAGCCTCTCTGCCACAGAGTGCAT 129719
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Db 129720 CGTCAACCTCTTTTGGTCCAGTGTGGCAAGGCTCAGCCTCTCTGCCACAGAGTGCAT 129779
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Db 129900 GCGCTGTCTTTGAAACCTGAAATAAAAAG-----AGCAA-AAAAAGGCGAA 129949

RESULT 18

AX665344
LOCUS AX665344 1068 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 102 from Patent WO03002765.
ACCESSION AX665344
VERSION AX665344.1 GI:29290465
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 102 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES
Location/Qualifiers
1..1068
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ORIGIN

Query Match 58.1%; Score 974.7; DB 6; Length 1068;
Best Local Similarity 92.4%; Pred. No. 1.8e-05;
Matches 1002; Conservative 0; Mismatches 11; Indels 72; Gaps 14;


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Db 1411 TGCTACCTTGACCCCTTCCCTTCCCTGCTCTCTCTCATCATCATCTCCCAACACATC 1470
Qy 1217 ---CCA-ACACACA-----GCAA---TG-GC-----AA 1237
Db 1471 CTCTGCCATACACAAACAAAGTAAGTTTCATTTGGGCAAAATTTGAGCCTCACATAAA 1530
Qy 1238 CACC-----G-ACAGCAA-----CCAAA--T 1254
Db 1531 CACCCTGAAGACACAACTTGACTTATACATAGTGCACAGCAAGAGCTACATCCAGTGT 1590
Qy 1255 C---A---GA-TAT-----AT-ACAA-----ATG-----A---AATT 1275
Db 1591 CTAATTATCTGTGAATTTCTTAAATGACAATGACATATGCCCCCATCATGTTAATT 1650
Qy 1276 A-----GA----- 1278
Db 1651 ATATCTAATTCCATTAGGTTACGCTCTTTCTTTCTGGGACACTATCTACTATATACC 1710
Qy 1279 ---AGA---AA-----CA---C---AGCC-----TC 1292
Db 1711 ATATCTATAGATTTCAATATAGATGATGTGCCATCTTCTGTAGCCCTCCGCTCTACTC 1770
Qy 1293 A-----TGACACAGAAATTTAGG---GAGGG-----GAA---CAA--- 1322
Db 1771 ATTCTCTCCACCATCTG---CAGAGATTTGAAGTTTG-GGGCTATGATGAACCCCAACA 1826
Qy 1323 --AGAACTATTG-----GGGGA---A-----AAG-AG----- 1345
Db 1827 CTA-AAT---TTTGAAGTCAAGTACCAAAAGGGGAGGAGCATTTTGAAGATAGAACC 1883
Qy 1346 ---TTTTAAAA-AGAAATTT-----GAAA---ATTG---CCTTGCGA---TATTTAG 1385
Db 1884 CTAATTTTAAAGAGAAGTCACTCAATACATGATGATGATGATGATGATGATGATGATG 1943
Qy 1386 G-----TAC-C-----AATGG---AGTTTTC---TTTTCCAAA---CGGGA 1416
Db 1944 GTTTTGTCAAGCTATCTATCAAGTAATAGTACAGTATACCCATCTACTCAAAATATCTG 2001
Qy 1417 A-GAACACAGCA-----CACCGGCTTGACC-----C-----A 1444
Db 2002 ATTTATCTCACCAATCAATATCTACCCACCTGCTTT---CCTCTAGCAATCTATTTA 2058
Qy 1445 CTG-----CAAGCTGCATC---G-----TG-C-AAC-CT-CTTTGGTGC----- 1476
Db 2059 CTGTTTATCAATCT-ATCAATGTAATGTCTAACACTCCCTTT---CTATTCTCTCCCT 2112
Qy 1477 -----CAGTGTGGCAGGGCTCAGCC-----TCTGCGCCACAGAGT---GCC 1518
Db 2113 ACTACTCACTAT---CAA---TTATCCGCCATATGAATCTCTAAACATATTGTATCTCT 2166
Qy 1519 CCACGTGGA-----ACA---TTCTGGAG-C---TGGCCATC---CCAAA---TTCA 1556
Db 2167 CCAC-TGATTTATTTATACCATCAGCAGACATTTGG-CATCTTCAAAATATCTTTCA 2224
Qy 1557 A-TCAGT---CAATGAGACGA-----ACAG-----AAT-----G-----A 1583
Db 2225 ACTTCTGTGAAGCCA-----ACGATCTCACAGGTTAAACAAATACAAAGCAATACCT 2279
Qy 1584 -----GAC-CT-----TCCGG-----CCGAG----- 1599
Db 2280 GTGTTGTGACTCTTTTAAATCTTGATATCTTATCCACCCCAAGGGAGACACTAACAGATAG 2339
Qy 1600 ---C---GTGGC---GC---TG---CGGGCACT---TT---GGTAGA---CTGTG---C- 1631
Db 2340 GCCAAGTAGCAAGCTAATGATCATCTACTACTATTCGGGAAGAGCTGTGTTTCTA 2399
Qy 1632 ---CAC-----CA---CGGC-----G---TGTTG----- 1645
Db 2400 AAACACTTTCTTGGGAAGCAGATCAGCCTAGAAAAGTTTGTAGTACTGTGTTTTC 2459
Qy 1646 ---TTG---TGAA---AC---GT-----GAAA-T 1661
Db 2460 TTTTGCACCTTGAAGGACAAAGTGCCAGCCTTTATGCTTCTCTCAACCCCTTCAAGAAAGT 2519
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Qy 1662 A-----AA---A-----AG-AGCAA-AA-----AAAA 1679
Db 2520 ACATGTCAAGAACCTATGGCTGCTTCTTCTTAGCAGCAAGAACTTGAGAGAAAA 2574

RESULT 23
LOCUS RATCALMA 3069 bp mRNA linear ROD 08-MAY-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete CDS.
ACCESSION M88709
VERSION M88709.1 GI:203245
KEYWORDS cell adhesion-like molecule; opioid binding protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
1 (bases 1 to 3069)
Lippman, D.A., Lee N.M. and Loh, H.H.
Opioid-binding cell adhesion molecule (OBAM)-related clones from a
rat brain cDNA library
Gene 117 (2), 249-254 (1992)
JOURNAL PUBMED 92347701
MEDLINE 1339369
COMMENT Original source text: Rattus norvegicus (strain Simonsen ICR)
(library: UZ) brain cDNA to mRNA.
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location/Qualifiers
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TWRHLSVKEGGFVSEDEYLEISDIKRDQGEYECALNDVAAPDVRKVLITNPYP
ISKAKNTGVSVGQKGLSCSAVPMABFQWFKEDTDLATGLDGVRIENKRISTLTF
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FIKP"

ORIGIN
Query Match 50.8%; Score 853; DB 10; Length 3069;
Best Local Similarity 49.2%; Pred. No. 0.014;
Matches 1329; Conservative 0; Mismatches 240; Indels 1130; Gaps 219;

Qy 2 TTGTG-----TCCCTTC-----AGCAAAACAGTGGATTTAAATCTCTTGCACAGCTT--G 50
Db 474 TTCTGCTCTCTCCCTCCCTTGC-AAACATTTGATTTAAACCTGCT--CAGAA--TTGAG 528

Qy 51 ---AGAGCAA-CA--CAATC-----TATCAGGA--AGAA--AGAA--AGAAAAACCGA 94
Db 529 TACAGAGGAAGCAGCC--TCGGTGGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 579

Qy 95 ACCTGACAAAAAGCAAGAAAAG-A--AGAAGAA-----AAAAAT 132
Db 580 ACC-----ACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 630

Qy 133 CAT-GAAA--ACCATCCAGCAAAATGCAAT--TCTATCTCTTGGGCAATCTTCAAC 186
Db 631 CCTCGAGATGTACATCTCCGCC--TACTG---GATGCTCT-TCTC---GGCCA-C--CA- 677

Qy 187 GGGGCTG-GCTGCTCTGTGCTCTTCTTCAAGAGTGCCTGTCGCGAGGAGATGCCACCT 245
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Db 678 ----CTGCCCTGCTCT-----TCATCCAGAGTGCCTGCGCAGCGAGATGCCACCT 728
QY 246 TCCCAAAGCTATGGACAACGTGAACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCA 305
Db 729 TTTCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGTA 788
QY 306 CTATTGACAACCGGCTCACCGGCTGGCTGCTGAATACCGCAGCACCATTCTCTATGCTG 365
Db 789 CCATAGATGACCGGGTCACAGAGTAGCTTGGCTAAACCGCAGCAAACTCTCTAGCTG 848
QY 366 GGAATGACAAGTGGTGCCTGGAATCCCTGCGCTGGTC--CTTCTGAGCAACACCCAAACGCA 423
Db 849 GGAATGACAAGTGGTGCCTGGAATCCCTGCGCTGGTC--TGGTCAACACCGCTTACCCA 906
QY 424 GTACAGATCGAGATCCAGAACGTGATGTGTATGACGAGGGCCCTTACACCTGCTCGGT 483
Db 907 GTACAGATCATGATCCAGAAATGTGATGTTTATGACGAAGTCCCTGACACCTGCTCTGT 966
QY 484 GCAGACAGAACACCCAAAGACCTCTAGGGTCCACCTCATGTGCAAGTATCTCCCAA 543
Db 967 GCAGACAGAACATCACCCAAACCTTCCCGGGTCCACCTCATAGTCAAGTTCCTCCCAA 1026
QY 544 AAT--TGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGC---CTC 598
Db 1027 GATAATG-A-ACATCTCTTCAGA-----CATTTACT--GTGAATGAGATAGCAGTGTG 1075
QY 599 ACC-----TGCAATGACACTGTGATGACAGAGCCTACGGTTHACTTTGGAGACACATCTC- 651
Db 1076 ACCTTGTTATGTCTGCAATTTGGCAGACCCAGAACCAACAGTGCATGCGGACACCTGTCA 1135
QY 652 -TCCCA--AAG--CGGTTGGCTTTCTGAGTGAAGACGAATACCTTCGAAAT--TCAGGGCA 704
Db 1136 GT--CAAGGAGGCCAG--GGCTTTGTGAGTGAAGATGAATACCTGGAATCTCA--GACA 1190
QY 705 TCACCCGGGAGCTCAGGGGACTACGAGTGCAGTGCCTCCATGACGTGGCGCCGCCCG 764
Db 1191 TCAACCGCAGCAATCTGGAGAGTATGAGTGCAGCGCTTGAATGATGCTGCTGCACCC-- 1248
QY 765 TG--GTACCGAGATTAAGTTCACCTGACCTGACATTCACCATACATATTCAGAGCCAGGG 822
Db 1249 TGATGTTGCGAAAGTAAATCACTGTAAACTATCTCTCCCTATATCTCTCAAAAGCGAA--G 1306
QY 823 TACA--GGTGTCCCGTGGGACAAAAGGGGACA--CTGCAG--TGTGAAGCTCAGCAGTC 877
Db 1307 AACACTGGCGTTTCAGTAGGCCAGAGGG--CATCTG--AGCTGTGAAGCTCTGCTGTC 1363
QY 878 CCTCA--GCAGAAATTCAGTGGTACAAGGATGACAAAAG-----ACTG--ATTGAAG 926
Db 1364 CC--CATGGCTGAATTCAGTGGTTCAAGGAAGATACCAGGTTAGCCACTGGGCT---G 1417
QY 927 GAAAGAAAGGGTGA--AAGTG--GAACACAGACC---TTTCTCTCAAACTCATCTCTTT 981
Db 1418 G-----ATGGCGTGAGAAATTTGAACAAGGCGGCATATCCACT--TTGACT---TTCTT 1467
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QY 1098 GCACGTCGAGGGGCA--GGC--TGGCTGCTGGCT-----G-----C--TGCC---TCT 1137
Db 1586 GC-C-CTA-GA--GCACTGGCTGTCTCTGGCTCTCAGGAGCCTTTTGGCCACTTCT 1640
QY 1138 TC-----T--GGTCTT---GCA---CCTGCTTCT----- 1158
Db 1641 TCATCAAGTTTGTATGAAGAACCTTAGTCTCTGAGCATCGGCTGCTTCTTCCATATCAC 1700
QY 1159 -----CAAA-----TTTTG--A----- 1168

Db 1701 AGACTTTAATCTACACTGCGGAGGGGCAACACGATTTGGGCTTCTCTTTGGTTATTTTTT 1760
QY 1169 TG-----TGAGTG-----C-----CA----- 1179
Db 1761 TGTCTCTCTGACTGTTTGTAGTTTTTTGGTTTGTGATTTCTGGGATTTTCAATTTGATTTGT 1820
QY 1180 ---CTT-----CC-----CCACCG-OG 1191
Db 1821 TTTCTTTTTCGTTGAATGGACCGGGTTGGGGTTGGGATGGGAGGGTCTTACACG 1880
QY 1192 ---GGA-AA-----GG-----CTG--CC--GCC- 1206
Db 1881 AGTAGGATAATCAGGTATTGGTGGGCCCCCAAAATGGAATATATTTCTCTGCTACTCTGGCT 1940
QY 1207 ---ACACC-----ACACC---AC-CACCAACACA--ACA----- 1227
Db 1941 TCTTTTCTCTACTTCTCTTCTTCTTCCATTAACCATTAACACACAAACACACAGCAGCCCT 2000
QY 1228 ---GC-----AATG-----GCA-----ACA-----CCGACA-- 1245
Db 2001 AAGATGGCTTAAATAATGTCCCATGACACGCAACCTGGAAGGTACAACTTGGCCCACT 2060
QY 1246 GCA--AC-CAATCAGA--T--ATAFACA-----AA 1268
Db 2061 GCAGTACACAATAAGAGTTGCATCTACATTTCTCTGTTTCTTTGCTCTTAAAGTTTCAA 2120
QY 1269 T-----GA-----GG-----A-----ATTA-- 1276
Db 2121 TAAGACAGTTTAAAGAGCACATCTTATCCCTATGTTTGTATCACCTATCCCAATAAG 2180
QY 1277 --G-----AAGAAAC-----ACAGCTC-ATGGG--ACA-G----- 1301
Db 2181 CTGCACACCTTTCTTAAGAACTTTCTTACTACATCTCAATGTCACACATGTACATTC 2240
QY 1302 ---AATTTGA-----GG----- 1311
Db 2241 TCATAAAATTTTACCATCTCTCTGGCCATCTCTGCTTAATCTGCAATTTCCACTAGCAG 2300
QY 1312 ---G-----AG--G-GAA-----CAAGAATAC--TTT--G----- 1333
Db 2301 TAAGACTTACAGCTTGTATGAATAATACATGATCCAAAG-CTACAAATTTAGAATCAC 2359
QY 1334 GGGGAAA--A--AG--AG--TT--TTAAAA-----AAGAAAT 1360
Db 2360 GAGGGAAGTCTATCAGGGGTAGTACTTCCCTTAAATGCTAATGCAACTATAAAAG 2419
QY 1361 TGA-AAATTCG--CT-----T--GC-----AG-----ATATT-----T--AGGTA- 1388
Db 2420 TGATCAATAGTAGCTTAATATATATCAAGCTATCAAGCAATCATATTTATTTCCAGTTAC 2479
QY 1389 -CAATGGAGTTT--TCT--TTTCC-----CAAGCGGA-----AGAA----- 1420
Db 2480 TCAATTTGA--TTTCTCTCTCCATCTCTTCTCATATAC-CTATCTTCTTATATCTATTG 2537
QY 1421 --CA---CAGC--AC-ACCC-----GGCTTGGACCACTGCA--AGC--TGCACTGTCG- 1462
Db 2538 TTTCAATTTATCACTACTCTTTTCTCTT---CCCACTGCATCTCATTCATC-T-CA 2592
QY 1463 ---AACCTCT-----TTG-----GTGCC-----AGTGTG-----G-----GCAA 1488
Db 2593 TTTAAATCTTAATCATATTTGTGACTGTGGCTTATTTGTCTCTGTGCACTACCACCAA 2652
QY 1489 G---GGCTCAGCTCTC--TGCC--CA-----CAG--A-GT-- 1514
Db 2653 GACATTCG-CA-CCT-TCAAAATTTGCTTAGCAACTTCTTATGTGAAGCCAGTAATGCT 2709
QY 1515 ---GC---C--CCCAGTGGAAACA-TTC-----TGAGC--TGG----- 1542
Db 2710 CGGGCTACTACCCA-GAAGAACATTTCTTATACCATGGATCTTTGGGAATGCACATAAC 2768
QY 1543 CCAAT---CCCAATT-----CA-----ATCAGT 1562
Db 2769 CCATCCACCCAAATTAGGCTTTGTGAACAGATGGACCAAAAGTAGCAATCTATGGATCAGT 2828

QY 1563 C---CATAGAGA-----CGAACAGATG-----AG--ACCTTC-----CG 1592
 Db 2829 CACTCAT---GATTTTCG-AGAGACTGTTCCCTTAGCCACCTTCTCAGAGGCGAGTCA 2884
 QY 1593 GCCC-----AAG-CGTG-----GC-G-----CT-----GCGGCACTTT--GGTA- 1623
 Db 2885 GCCCCGAAGAAGCCTTGATTATGCTGAATTCTCTTTAACAGCTGGAATAATTAAAGGTAC 2944
 QY 1624 -GA--CTGTGC-----CA-CC-----AC--GG-----AC--GG----- 1639
 Db 2945 CAACCTGTGCTTCTCTCAGCCTTTCAAGAAAGTACATGTCAGAACTTTGGAGAAACTT 3004
 QY 1640 ---CGTG--TG-----TTGT-----GA---AACGTGA--AATAAAAGAGCAAAAAAAA 1679
 Db 3005 CTTTCATGCTGGCTTTATTATAGCAGAAAGAACCTGACCAAAAAAACCRAAAAAAAA 3063

RESULT 24

AF271233

LOCUS

DEFINITION Synthetic construct secretory IgCEPUS-GFP fusion protein
 (IgCEPUS-GFP) gene, complete cds.

ACCESSION

AF271233

VERSION

AF271233.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCES

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

ORIGIN

Query Match

Best Local Similarity

Matches 1154; Conservative

QY 134

ATGAAACCACTCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193

50.1%; Score 842; DB 12; Length 1638;

65.2%; Pred. No. 0.0069;

Mismatches 245; Indels 370; Gaps 128;

1154; Conservative

QY 134

ATGAAACCACTCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193

50.1%; Score 842; DB 12; Length 1638;

65.2%; Pred. No. 0.0069;

Mismatches 245; Indels 370; Gaps 128;

1154; Conservative

QY 134

ATGAAACCACTCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193

50.1%; Score 842; DB 12; Length 1638;

65.2%; Pred. No. 0.0069;

Mismatches 245; Indels 370; Gaps 128;

1154; Conservative

QY 134

ATGAAACCACTCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193

50.1%; Score 842; DB 12; Length 1638;

65.2%; Pred. No. 0.0069;

Mismatches 245; Indels 370; Gaps 128;

1154; Conservative

QY 134

ATGAAACCACTCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193

50.1%; Score 842; DB 12; Length 1638;

65.2%; Pred. No. 0.0069;

Mismatches 245; Indels 370; Gaps 128;

1154; Conservative

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 194 GCTGCTCTGTGTTCTTCCAGAGAGTCCCGTCCGAGCGGAGATGCCACCTTCCCAA 253
 55 GCCGCACTCTCTCTTCCAGAGAGTCCCGTCCGAGCGGAGATGCCACCTTCCCAA 114
 254 GCTATGGAACAACGTGACGGTCCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 313
 115 GCTATGGAACAACGTGACGGTCCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 174
 314 AACCGGGTCAACCGGGTGGCTGGCTTAACCGCAGACCAATCTCTATGCTGGGAATGAC 373
 175 AACCGGGTCAACCGGGTGGCTGGCTTAACCGCAGACCAATCTCTATGCTGGGAATGAC 234
 374 AAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCCAAAGCAGTACAGATC 433
 235 AAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCCAAAGCAGTACAGATC 294
 434 GAGATCCAGAACTGGATGTATGAGC-AGGGCCCTTACACCTGTCTGGTGCAGACAGA 492
 295 CAGATCCAGAACTGGATGTATGAGC-AGGGCCCTTACACCTGTCTGGTGCAGACAGA 353
 493 CAACCAACCAAGACCTCTAGGGTCCACCTTATGTGCAAGTATCTCCCAAAATTGTA-- 550
 354 CAATCAACCAAGACCTCTAGGGTCCACCTTATGTGCAAGTATCTCCCAAAATTGTA--TACC 411
 551 GAGATTTCTTTCAGATATCTCCATTAATGAG--GGAACAATATTAGCTTCACTGCATAG 608
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 609 CAATTTGTAGACAGACCTTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCT 668
 470 CCACGGGCGAGCCAGACCCCAATCACTTGGAGACACATCTCGCCAAAGCTGTGGCT 529
 669 TTGTGAGTGAAGACGAATCTTGAATTTCA--GGGATCAACCCGGGAGAGTCAAGGAC 727
 530 TCATACGAGGAGAGAGTACCTGGAGA--TCACAGGATCAACGAGGAGAGTCCGGGAG 588
 728 TAGCAGTGCAGTCTCTCAATGACGTGGCGCGCCCTGTGTACGAGAGTAAAGTCAACC 787
 589 TAGCAGTGCAGTCTCTCAATGACGTGGCGCGCCCTGTGTACGAGAGTAAAGTCAACC 648
 788 GTGAATATCCACATACATTTTCAAGACCAAGGTTACAGGTTCCTCCGTTGGGACAAAAG 847
 649 GTCAACTTACCCACCGTACATCTCGGATGCGAAGAGCACCGGTGTGCGCGTGGGCGAAG 708
 848 GGGACA--CTGCACTGTGAAGCTTACAGTTCCTTCCCTCAGCAGAAATTCAGTGGTACAGG 905
 709 GG--CATCTCTGATGTGTGAAGCTTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766
 906 ATGACAAAGACTGATTGAAGGAAAGAAAGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 965
 767 ACACAGACCGCTGGCTGAGAGACAGAAAGGCTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGT 826
 966 CAAACACTATCTTCTTCAATGTCTCTGAACATGATGAGGAACTACACTTGGTGGCT 1025
 827 CCGGACTGACTTCTTCAAGCTCTCCGAGCAGGAGTACGGGCAACTACACCTTGGTGGCT 886
 1026 CCAACAGCTGGG--CCAC--ACCAAT--GCCAGAT-----CA-----TGCTATT 1065
 887 CCAACAG--GGGATCACCAGCGCGCTGCGCCACCATGTTGAGCAAGGCGAGGAGGAGTGT 944
 1066 -----TGGT--CCAGCGGCC--GTC-AGC--GA--GGTGAAG--AAACGG--CAC--GT 1103
 945 CACCGGGGTGTGGCCCA---TCCTGTGTCAGAGTGCAGCGCA--CGTAAACGGCCCAAGT 1000
 1104 ----CGAG-----GAGGCG-AGGCTGG--T-----CT--GGC--TGCTG--CC-----T 1135
 1001 TCAGCGTGTCCGGCGAGGGGAGG--GCGATGCGCACCTACGGCAAGCTCCCTTGAAGTT 1058
 1136 CTTCTGCTTTCGACCTGCTTCTCAAAATTTTGTGAGTGCACCTTCCCGACC--CGGG 1193

Db 1059 CATCTGCAC-CAACGGC-AAA-GCTGCCGCTGCC-CTGGCCCAACCCCTCGTG 1104
QY 1194 A-----AG-GCT-----GCCGCCACCAACCAC-----CAACA- 1222
Db 1105 ACCACCTGACCTACGGCGTGCAGTGTCTTACGCGCTACCCGACACATGAAGCAGCAC 1164
QY 1223 -----CAA-CAGCAATGGC-AAA-C-AC-CGACAGCA-----ACCAATCAGATAT 1261
Db 1165 GACTTCTTCAAGTCCGCAATGCCGAGGCTAGCTC-CAGAGCGCAC-ATC-T-T 1217
QY 1262 ATACAA-ATGA-----AATTAGAAGAAACACAGCTCATG-GBACAGAAATTTGAGGG- 1312
Db 1218 CTTCAAGGACGACGCACTACAGACCCGC-GCC-----GAGG--TGAAGTTCGAGGGG 1270
QY 1313 --A-----GGGACAAAGAT-A-CTTTGGGGGAAGAGTTTAAABAAAGAA-AAT 1361
Db 1271 ACACCTGTGTGAAC-CGATCGAGC-TGAAGGGCATCGACTT-----CAAGGAGGACG 1321
QY 1362 G-AAAATTGCCCTTCAGATATTTAGGTACAA-TGGAGTTTCTTTTCCCAACGGGAAG 1418
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QY 1419 AAC-ACAGCACAC-CGGGT-----TGACCCAC-TGC--AAG-CTGATC---GTGC 1462
Db 1354 TACAACAGC-CACAAGCTCTATATCATGG-CGACAAAGCAGAGAACGGCATCAAGGTG- 1410
QY 1463 AACCTCTTT---GGT-GCCA-----GTGTG--GGCAAGGC-T-CAGCCTCTCTGCC 1506
Db 1411 AAC---TTCAAGATCCGCCACAAATCGAG-GACGGCA---CGGTGAG-CTCGCCGAC 1461
QY 1507 CA-----CAGAGTCCGCCA-CGTGGA-----ACAATTCTGAGCTGGCC-ATCCCAA- 1551
Db 1462 CACTACCAGCAGACACCCCATCGCGACGGCCCGTGTCT---GCTGCCGA---CAAC 1515
QY 1552 -ATT-----CAATCAGT---CCAT-AG--AGA-CGAAC-AGA-----ATG 1582
Db 1516 CACTACCTGAGCACCCAGTCCGCTGAGCAAAAGACCCCAACGAGAAGCGCGATCATATG 1575
QY 1583 AGACCTTCGGCCCAAG--CGTG-GCGCTG-CGGG--CACT-TTGTGAGACTGTGCCACC 1635
Db 1576 -GTCTGTCTGG---ASTTGTGACCGCCCGGGATCACTCTCGGCA---TG-G----- 1621
QY 1636 AG-GCGTGTGTGTGAAGCGTGAATAA 1663
Db 1622 ACGAGC-----TGT---AC---AAGTAA 1638

RESULT 25
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WPCOMMENT
Sequence split into 5 fragments LOCUS AC110642 Accession AC110642
Fragment Name Begin End
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AC110642.1 100001 210000
AC110642.2 200001 310000
AC110642.3 300001 410000
AC110642.4 400001 476288
Continuation (3 of 5) of AC110642 from base 200001 (AC110642 Rattus norvegicus clone CH2)

Query Match 49.7%; Score 834.5; DB 2; Length 110000;
Best local similarity 45.7%; Pred. No. 17;
Matches 1388; Conservative 0; Mismatches 206; Indels 1440; Gaps 286;

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QY 35 --TCCTTG-----CAC---AAGCTTGAG-AGCA-----ACACAAT---CTA----- 66
Db 62982 GAGCAATTGTCTATACCACTGGATCTCTGAGTAGAGTTGAACAAATGAATTAATGAAGT 62923
QY 67 -----TC-----AGGA--A-AGAA-----AG-----AAAGAAAA- AA----- 90

Db 62922 GTGTTTCCAGACAAAGGACTAGAGAAATGTGAGCTTATGAAGAAAAAAGAAATATGTCTGTGG 62863
QY 91 -----CC-----GA----- 94
Db 62862 AGTGCAGTTTCTCTGCGTGTGCCATGTGTGTGTGTGATGTGCAATGATATGTGTGTGG 62803
QY 95 -----ACCTG-----ACA-A-AAA-AG-----AAGAAA-----AAG 117
Db 62802 GGGGGGTACAATGTGCGCCACATGCTAGTACTGAGAATATTTAAGAAAGCATTTGGAGGAAG 62743
QY 118 A-AG--AA-----GAAAAA-----AATCA-----TGA-----AA-----ACCATC 145
Db 62742 ACAGTCTAAGGTGCGAAATAGTAGGACATCAATTTGTGTGTTGTTCAACGTTCTACCAAG 62683
QY 146 CAGCCAAA-----AA-TG-----CA-----CAATTC-----T----- 166
Db 62682 GAGCCAGACGTTCTTGTAAAGCTGTAGGGCTCAGCTGGAGCAGTCCGGAGGTGTGAAA 62623
QY 167 -AT--CTCT-----TG-----GGCAATCTTTACG----- 187
Db 62622 CATTACTCTGGAATTAGTGTAAAGGATAAATGTGAGATGTCCAGGCNAGC--CATGGCAG 62565
QY 188 -GG--GCTGGCTG--CTCTGTGTCTTTCCAGAGGAGTGCCTGTC-----G-----CA 230
Db 62564 TGGTAGCT-GCTGAACCTCTGTG--ACTTGAAGAGGTGAG--CCATGCAAGTGTCTTTTTC 62509
QY 231 GC-----GGAGA-----TG--CCACC--TTCC--CCAA--AGCT----- 256
Db 62508 GUAGGTGTGGGAGACCTCTTCCCTTGGCCCGCTTATTTCTGTCTAATTCAGCTTTCCCC 62449
QY 257 ATGGCAACG--TGACG-GTCCGGCAGG-GGAG--AGGCCACCCCTCA-----GG 301
Db 62448 ATAGA---GGCTGAAGAGACAGGAGGAGGAGAAAGAG-----T-ATTTGTATGGG 62400
QY 302 T---GCA-----CT--AT-TGACACCGGCTCACCC-----GGGT 330
Db 62399 TGAGCAGTGGGTAGGTGGATATATAAC-----TCAGCCTTGAATPAAGAACAGCAGGAA 62344
QY 331 GGCCTGGCTAA-----ACCGCAGCACCATCC-TCT-----ATGCTGGGAATG-----AC 373
Db 62343 GGCCTTGTGAATTTACCG-AG-ACATCTCTTTTAAAGAAAGGTG--ANGTATTCAC 62289
QY 374 AAG-----TG--GTGC-----CTGG-----ATCTGCG-----GTG 397
Db 62288 AGGCCCTGTTCTTCTTCTGTGTAGTGCACTCACTGGCTTAGGAGCTATCC--CTACAGAT 62232
QY 398 GTCC---TTC-----TGAGCA--ACACC-CAA-----AC-GCA-----GT- 425
Db 62231 GTCTGTGTTCCCAACAT-AGCATTAACCAACCAAGTCTGAGGACTGCACCAATGTAGGTA 62173
QY 426 -AC--AGCATC--GAG-ATCCAGAA--CG-TG--GATGT-----GTATG--AC 460
Db 62172 AACAGAGCATCAGGGAGCACCAGCAGAGCCGTTSCACAGAGTTTCAGGT-TGGACAC 62114
QY 461 GAGG-G--C--CCTTA-----CA-----C-CTGC--- 478
Db 62113 AAGGTCTTCATCTATATATGTCATTTTGTGGCAGGCTGGCAGGGCTCTCTGT 62054
QY 479 --TC-----GG-----TG-----CAG--AC-----AGAC 493
Db 62053 ATTCTGTTGGCTTATGACTTCTACCCCTCAGTTACGTAAAGAGGAATGAAGAA 61994
QY 494 A-----ACCA-----CCCAAGA-----CCTCTAGGCTCC----- 518
Db 61993 AAGAGAGCACCAAGTGTGTCTCAGAGAACTAGCAATTTCTCT-GGG-CCATGSCAGGTAG 61936
QY 519 ---AC-----C-----TCATTG-----TG--C-----AAGT---ATC 537
Db 61935 CTAGACAGAGGGGTGAGGTAGGCTGAGGTTCAATGAGGAATGCACTTTAAAGTTGAATC 61876
QY 538 -----TC---C-CAAA-----ATTGTAG-----CA-----TT 556
Db 61875 CTTGAGTATTCAGACAGCAAAAGAGATAGAGAAATAATAGAGCCCTGTGTACAGTT 61816

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QY 557 T-----CT-----TCAG-----A-TA-----TCTCCATT-----574
Db 61815 TGTGCTGTAGACTCAGCGGTTAAGTACACAGGACACATTTTCAATTGTGTGGACA 61756
QY 575 -----AA-----TGAAGGGAACA---ATATTA-----G 594
Db 61755 AGGTACATGGAGAAGATTGAATGGACCACTCATTTTACCAGGAAGAAATGGAACCTGG 61696
QY 595 C-CTCAC---CTGCATA-----GC---AACCAG---615
Db 61695 CTCTCAGACAGCTGCATATATAGTCTCAATGACAAATCAGGACAAATGGCCAAAGTGAAA 61636
QY 616 ---TAGACCAG---AGCCT-AC---GGT-TA-C-TTGGAGACACATCTCTCC-----654
Db 61635 GAATAGAACAGTCCAGACTCACTCAAAAGTAGCAATGTA---ACCTCTTCCAGGGGCC 61579
QY 655 ---CAAGCGTTGGC-----TT-TGTGA-----GTGAA---GAC---GA 684
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QY 685 ---ATACTTGGAA---ATTC---AG-GGCA-----TC---ACCCGG---712
Db 61520 GTGCTTAC-AGGAAGGGCGCTTAGTCGAAAGCTAGCAGTTAGATTCTAGAA---GGTG 61465
QY 713 -GAGCAGTCAAGGACTACG---AGTG-----CA-----GT---G-CCTC-----744
Db 61464 TGAGCAGT-AGGTGACTAAGCTAAGTACAAACCAATTGAAAGGTAAAGTCTCAGGGTTT 61406
QY 745 CA-----ATG-----AC---GTGGCGCG---GC---CGGTG---GT-----768
Db 61405 TCATGATCATGTGTTTCAATTACATGTGTCTGCAAAATGCTTTCCATGTCTATGTGCTT 61346
QY 769 -----AC-----GG---AGAGTA---AAGGTCACG---GTGAACTATC-CACCAT 803
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QY 804 -----ACATTC---AGAAGCAAGGGTA-----CAGGTGTCCC-----C-----835
Db 61288 GATGCTTAAATTCGCAAGAAGC---TGATGAATCTTGACCCCAAGCTAACATAAA 61233
QY 836 GTGGGACA-----AAGGG---GACACTG---CA---GTGT-GAAGC-----867
Db 61232 GTTGGACAGTGTGACTTCAAGGGGCAAGA-AATGGAATTCATGGGTAGTAGTAGA 61174
QY 868 -----CT---CAG---CAGTCCCC-----TC-----AGCA-----GAAT 890
Db 61173 TCCAAAATTTTCAGGACTGGACAGGNCAG-CCCATGTGCAATCAAGAGCATGTTGAT 61115
QY 891 TCCAGTGGT-----ACAGGA-TGACA-AAAGACTGA-T-TGA-AGG-----927
Db 61114 ---GTGGTGTGATTTAACCAAGAGTGACACCAATCTGAGCTCTCAGTAGGGCGATCG 61059
QY 928 -----A-----AAGAAAGGG-GTGAAAGTGA-----AAACAGAC 956
Db 61058 GGTTTTGGCAGTGTTCAGGTGAGACAGAGGAGGGAATATGGACACCATGTTCTAAATAGCC 60999
QY 957 CT-----TTCTCT-----C---TCAAA--A---CTCAT-----CTT---C---979
Db 60998 CTGAAAATTTCAATTGACAGAGCAGATCAGAGAGGTCTAATCAGAGGCCTTATCCCTG 60939
QY 980 TTCA--ATGCTCTGAA--CA-----TGAC--TATGGGAC-----TA-----C 1012
Db 60938 TTCAATATTCTCT-AATGCAATCTGATTTCTGACTTTAT--GTACCATCCCAATAATCACC 60882
QY 1013 A-----CTTGGGTGG---CCT-----CCAA-----C-----1030
Db 60881 ACTTCTCTTTCATGGAAGTCTTAGACCCCAAAAGCCAAATAGCCCAAGAGTTTGTATG 60822
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QY 1086 AGGTAGCAACCGCACGTTCAGGAGGCGAGCGTGTGCTGTGCTCTCTTCTGTGTCT 1145
Db 60701 AGGTCAACAATGGGACGTCAAGGAGGCGAGCGTGCATTTTGGCTCTCTCTCTGTGTCT 60642
QY 1146 TGACACTGTCTCTCAAAATTTTGTATGTAGTGCCACTTCCCCACCCCGGGAAGGCTGCCGC 1205
Db 60641 TACACTGTCTCTCAAAATTTTGTATGTAGTGCCCTCTCTCTGCGGGGAGA-GCTGTGTC 60583
QY 1206 CACCACCACCAACACACACAGCAATGGCAACACCCAGCAGCAACCAATCAGATATATAC 1265
Db 60582 CACC-GCATC-TCAATTTCAACAGCACT-GCAACA-TGA-AGCAACAAGTCAGA---AT-C 60532
QY 1266 AATGAAATTTAGAAAGAACACAGCCTCATGGACAGAAATTTGAGGAGGGAACAAGA 1325
Db 60531 AATGAAATTTCCGAGATATCACGCC-AATGAGACAGAAATTCGAGGGAGGGAACAAGC 60473
QY 1326 ATACTTTGG---GGGG---AAAAAGATTTTAAAAAA-GAAA-TTGAAAAATTTGCTTGCAG 1377
Db 60472 ATACTGTGTTAAGGGGAAAAAAGCTTAAAAAAGAAATTTGAAATTTGCTTGCAG 60413
QY 1378 ATATTAGGTACAAATGGAGT---TTCTTTTCCCAACGGGAAGAACACAGCACACCCG 1433
Db 60412 ACATTTCCGTACCACTGAGTTTCTTTTCTTTCCAAATGGGAAGAA---GGCGCACCTA 60356
QY 1434 GCTTGACCCCA-CTGCAAGCTGCATCGTCAACCTCTTTGTCGCCAGTGTGGCAGAGGC 1492
Db 60355 GCTTGACCCCAACCCACAAAGCTGCATGTGTGACCTCTCTGTTGCCAGGTGGGCAAGGC 60296
QY 1493 TCAGCCTCTCTGCCCCAC-AGAGTGCCCC--CCAGTGGAAACATTTCTGGAGCTGGCCATCCC 1549
Db 60295 TCAGCCACTCTGCCCACTAAAGTGCCCCCA-TCGAAACATTTCTGGAGTGGCCATCCC 60238
QY 1550 AATTCATCAGTCCATAGAGAC-GAACAGATGAGACCTTCG---GGCCC--AAGCGT 1602
Db 60237 AAATTTTCATCGTCCATAGACACAAGCACAGAGTGA---AACAGGGGCCCAAGAA--GT 60183
QY 1603 GCGCTGCGGCACTTTTGGTAGACTGTGCCACACGCGGTGTGT-----TGTGAAA--1653
Db 60182 GCCACGAGGGCCCTTTTGGTGGCTGCGCATGATGCGGTGTGTGATGAAGTGTGAATC 60123
QY 1654 C---GT-GAAATAAA---AAGAGCAAAAAA-AA 1679
Db 60122 CGAAGTAAAAAANAACAAAGAAATAAAAAAGAA 60089
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RESULT 26

AF271618

LOCUS

DEFINITION

AF271618

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

AP271618 2935 bp DNA linear SYN 21-MAY-2001
Synthetic construct secretory IgCEPUS-GFP fusion protein
(IgCEPUS-GFP) gene, complete cds.
AF271618 GI:14161270
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 2935)
Kim, D.-S. and Moss, D.J.
Neuronal-specific secretory IgCEPUS-GFP fusion protein expression
in transfected cells
Unpublished
2 (bases 1 to 2935)
Kim, D.-S. and Moss, D.J.
Direct Submission
Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea Location/Qualifiers


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1. .575
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ORIGIN
Query Match 49.3%; Score 828.5; DB 12; Length 2935;
Best Local Similarity 47.3%; Pred. No. 0.033;
Matches 1283; Conservative 0; Mismatches 249; Indels 1181; Gaps 187;

QY 1 GTTG----T----GTCT--TC-----A-GCAAAA-----C----- 20
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Db 354 GTTGCTTTTCGAGGCGCTTTGTCTGAAGGATGCAAAATCTACGGATGCTAGCGAGGGGG 413
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QY 21 --AGTG-----GATT-----TA-AATCTC-CTTGCAACAGCTTGAGAGCAACACAATC 64
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Db 414 GAAGGGGGGAGAGATTACCTCATACCATGTCGCTTGACCA-----ATCACCA--TC 464
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QY 65 -----TATCAGAAAGA--AAG-----AA-AGAAAAAACCC--G--- 93
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Db 465 CTGTCGCGGCTCTCTCGGCAGACGAGGGGCTCTGGACCAACAGAAAAAGGCTTGGCCC 524
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QY 94 AACC-----TGAC-----AAAAAGAG--A-----AA-----A--AGA 118
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Db 525 ATCCCCATGGTACCGAGCTGTATATAGAGAGCGCTTCGCCCAAGTCGCGTACCGGA 584
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QY 119 ---AGA-----AGAAAA-----AAAT-----A-----CA- 134
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Db 585 CTCAGATCTCGAGCTCAAGCTTGGAAATTCGACGTGACGTACCGGGCGCCCTGGCAG 644
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QY 135 TGA-----AA-----AC-CA--TCC--A---G---CCA-----AAATGCACA 161
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QY 222 CCGTGGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAACGTACCGTCCGGCAGG 281
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Db 765 CCGTGGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAACGTACGTCCGGCAGG 824
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QY 282 GCGAGAGGCCACCTCAGGTGCACTATTGACAACCGGGTCACCGGGTGCCTGGGTAA 341
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Db 825 GGGAGATGCCACGTCAGGTGCTCCGTGGACAACCGCGTCACCGGTGCGCTTGGCTGA 884
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QY 342 ACCGAGACCATCTCTATCTCGGGAATGACAAGTGGTGGCTGGATCTCTCGGTGTC 401
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Db 885 ACCGAGCAGCATCTCTATCGCGCAATGACAAGTGGTGTCTTGACCCGAGGATGGTGC 944
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 2179)
AUTHORS Lipman,D.A., Lee,N.M. and Loh,H.H.
TITLE Opioid-binding cell adhesion molecule (ORCAM)-related clones from a
rat brain cDNA library (1992)
JOURNAL Gene 117 (2), 249-254 (1992)
MEDLINE 92347701
PUBMED 1339369
COMMENT Original source text: Rattus norvegicus (strain Simonsen ICR) brain
cDNA to mRNA.

FEATURES

source

Location/Qualifiers

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238..1335

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ORIGIN

Query Match 48.8%; Score 819.5; DB 10; Length 2179;
Best Local Similarity 53.6%; Pred. No. 0.028;
Matches 1242; Conservative 0; Mismatches 260; Indels 815; Gaps 185;

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QY 45 A-GCT-----TGAGAGCA-----ACAC--AACTCTAT-----CAGGAA---AG-AA-- 77
DB 62 ATGTTAAACAGTGGAGCAGGGCTGTCTGACTCTGTGTCCTGCGCGCAGTGAGCAATG 121
QY 78 -----AGAAAGA---A-AAAAACCG---AACCTG-----A----- 100
DB 122 GTCTTAG-AAGACTTATTAGCTCCGAGAGCGCTGGACTCAGCCTTGCCTTCTCCGCTC 180
QY 101 -CA-----CA-----TATCT-----CT-----TGGGCA--T--CTTCAG 187
DB 181 CCAGCTCTGGTTGTCTCTGTGTGCTTTCGTCCTCAACATTCGGCTATTCTGAGAG 240
QY 111 GAAAAAGAGAGAAAAAATCATGAAACCAATCCAGC--CAA-----AAAT-- 156
DB 241 G-----GCAGGGA-----CA--AGGACCGTGCAGCTGCAAGAGTTCTAGGAAAGTTG 285
QY 157 --GC-----ACAAAT-----TC-----TATCT-----CT-----TGGGCA--T--CTTCAG 187
DB 286 TGGCTCTCGAGAAATGGGGTCTGTGGGTACCTGTCTCGCCCTGG--AAGTGCCT---CG 340
QY 188 GGG-----CT--GGCTCTCTGTGTCTCTT-----CCA--AGGAGTGGCCGTGGCGAGC 232
DB 341 TGGTGTGTCTCTGAGGCTG--CTGT--TC--CTTGATCCACAGAGGTGCGGTGGCGAGC 396
QY 233 GGAGATGCCACCTTCCCAAGCTATGGACAACGTCGTCGCGGACGGGGAGAGCGCC 292
DB 397 GGAGATGCCACCTTCCCAAGCTATGGACAACGTCGTCGCGGACGGGGAGAGAGCGCC 456
QY 293 ACCCTCAGGTGCACCTATTGACACCGGGTCAACCGGGTGGCTTAAACCGCAGGACC 352
DB 457 ACCCTCAGGTGCACCTATTGACACCGGGTCAACCGGGTGGCTTAAACCGCAGGACC 516

QY 353 ATCTCTATCTGCGGAATGACAAGTGTGCTGCTGGATCCTCGGTGTC--CTTCTGAGCA 410
DB 517 ATCTCTATGCTGCGGAATGACAAGTGTGCTGCTGGATCCTCGGTGTC--CTTCTGAGCA 574
QY 411 ACACCCAAACGAGTACAGCATCGAGATCCAGAACGCTGTGATGTATGACGAGGCGCTT 470
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DB 695 AAGTCTCTCCCAAGATATG-A-ACATCTCTCAGA-----CATTACT--GTGATGA 743
QY 589 TATTAGC---CTCACC-----TGATAGCAACTGGTAGACAGACCTTACGGTTACTTG 639
DB 744 GATAAGCAGTGTGACCTTGTATGTCTGCAATTTGGCAGACCAACCAAGTGCATG 803
QY 640 GAGACATCTCTC--CCA--AAG--CGTTGGCTTTGTGAGTGAAGACGATATCTTGG 892
DB 804 GCGCAC--CTGTAGTCAAGGAAGGCCAG--GGCTTTGTGAGTGAAGATGAATACCTGG 859
QY 693 AAAT--TCAGGGCATCAACCGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTCCCAATGAC 751
DB 860 AAATCTCA--GACATCAAGCGACCAATCTGAGAGTATGAGTGCAGCGCTTGAATGAT 918
QY 752 GTGGCGCGCCCGTG--GTAACGAGAGTAAAGGTCAACCGTGAACATATCAACATCATTT 809
DB 919 GTCGCTGCACC--TGATGTCGAAAGTAAATACTCACTGTAATACTATCTCCCTATATCT 976
QY 810 CAGAGCCCAAGGTTACA--GGTGTCCCGTGGGACAAAGGGGACA--CTGCAG--TGTCGA 864
DB 977 CAAAAGCGAA--GAACACATGGCGTTTCAGTAGCCAGAAAGGG--CATCTG--AGCTGTGA 1031
QY 865 AGCTCAGCAGTCCCTCA--GCAGAAATTCAGTGTGTACAAGGATGACAAAAG----- 915
DB 1032 AGCTCTGTGTCTCC--CATGGCTGATTCAGTGTGTTCAAGGAAGATACCAAGTTAGCC 1089
QY 916 ACTG--ATTGAAGGAAGAAAGGGTGA--AGTG--GAAACAGACC---TTTCTCTCAA 968
DB 1090 ACTGGCT-----GG-----ATGGCGTGAGATTGAGAAACAAAGCGCGCATATCACT-TT 1139
QY 969 AACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACACTACCTCTGGCGCTCCA 1028
DB 1140 GACT-----TCTTCAATGTCTCAGAGAGGATTTAGGAACATATCTCTGTGGCCACA 1195
QY 1029 ACAAGCTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCAGCGA-G 1087
DB 1196 ACAAGCTTGGGAACCAATGCCAGCATCACTGTATGGCGCTGGAGCAGTCATTGATG 1255
QY 1088 GTG-AGCAA--CGGACAGTGGAGGGGA--GGC--TGGCTCTGGCTGTCT--GCCTCT 1137
DB 1256 GTGTA--AACTCGGC-C-TCTA-GA--GCATGGCTGTGTCTCTGGCT-CTCAGGAGC-CT 1306
QY 1138 TCTGTCTTGGAC-CTGCTTC--TCRAATTTTGTATGTAGTGCCA--CTTCCCCACCCGGG 1193
DB 1307 TCT-----TTGCCACTTCTTCAAGTTTGTATGAAGA-----AACCTT----- 1346
QY 1194 AAAGG-----CTG--C--CGCCACCAACCAACCAACACA-ACAGCAATGGCAACAC--C- 1241
DB 1347 --AGGTCTCTGAGCATGCGCTTCTCCA-TATCAGAGACTTTAAT--CTACACTGG 1401
QY 1242 GA-----CAGCAACCA-----ATC-----AGATATAT-----ACAAATG 1270
DB 1402 GAGGGGCA--AAACAGTTTGGGCTTCTTTTGTATTTTGTCTTCTTGGAC---TG 1456
QY 1271 AAATTAG-----AAGAAACACAGCTCATGGGA---CAGAAATTTGA----- 1309
DB 1457 --TTTGTCTTGTGGTTGA-----TTTC--TGGGATTTTC---AATTGATTTGTTTT 1503
QY 1310 -----G-----GGA--GGGGAACAAAGATATCTTTGGG-----GGA--AAAGA 1344

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Db 1504 TCITTTTTCGTTGAATGGACCGGG-----TTGGGGTTGGATGGGCAGG 1550
Qy 1345 GTTTTA-----AAAA--AGAAATTG-----AAATTTGCCTTGCGATAT 1381
Db 1551 GTTCTACACGAGTAGGATAATCAGGTATTGGTGGGCCCCAAA--TG----GAATATAT 1604
Qy 1382 T--TAGGTACAAATGGAGTT-----TTCTTTTCC----- 1407
Db 1605 TCCT-GCTACCTTGGCCTTCCTTTTCTACTCTCTCTCTACCCATTAAACACAAA 1663
Qy 1408 ----CAA--ACG-----AAGAA--CACA-G-CA--CACCC-----GG 1434
Db 1664 CACACAGCACACCCCTAAGATGGCCTAATAAATGTCCCATGACACGCCCTGAGG 1723
Qy 1435 ----CTTGGACCCAC--TGCA-----AGCTGATCTGTGA--ACC-----TC 1468
Db 1724 TACAACTTGG-CCACACAGTGCAGTACACAATAAGAGTTGCATC-TACATTTCTCTGTTTC 1781
Qy 1469 TTTG-----GT-----GCCAGTGTGGCA--AGGGCTCAGCCT----- 1499
Db 1782 TTTGCTTTAAGTTTCAATAAGACAGTTT-----AAAAGAGCACATCCTTATCCCTAT 1837
Qy 1500 -----CT-----CTGCCAC-----AGA----- 1512
Db 1838 GTTTGTATCACCTATCCCATTAAGCTGCACACCTTTTCTAAGAAACTTTCTTACTACATC 1897
Qy 1513 -----GTGCCCCCAGTGGNACATTCGGAGC-----TGGCCATC-----CC 1549
Db 1898 CTCAATGTGCACACATGT--ACATTCT--CATAAAATTTTACCATCTTCTCTGGCC 1950
Qy 1550 AAATTC-----AATCAG-----TCCA-TAG--AGACGAACAG-----AATGAG 1584
Db 1951 --ATTCTGTTAATCTGCATTTTCCACTAGCAGTAAGACTTACAGGCTTGATGAAT-AT 2007
Qy 1585 ACCTTCGG--CCCAAGC-----GTGGCGCTGGGGCA--CTTT-----GG 1621
Db 2008 ACAT-----GTATCCAAAGCTACAAATTTAGAAGT--CAC-GAGGGAAGTCTATCTAGGGG 2060
Qy 1622 TAG-AC-----TG-----TGCCAC-CACGGCGTGTGTTGT-GAAACGTGA--AAT 1661
Db 2061 TAGTACTTCCCTTAAATGTGAATGCAACTCA-----TAAAAAAGTGATCAAT 2108
Qy 1662 A-----AA-----AAG--AGCAAA--AA--AAA 1678
Db 2109 AGCTAGCTAATTATATCAGCTATCAAGCAATCATATA 2145
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Search completed: May 28, 2004, 18:56:48
Job time : 6950.01 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:09:09 ; Search time 743.61 Seconds
(without alignments)
9592.021 Million cell updates/sec

Title: US-10-017-084a-522

Perfect score: 1679

Sequence: 1 gttgtcttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 1.0 , Gapext 0.1

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1679	100.0	1679	3	Aac78590 Human PRO
3	1679	100.0	1679	4	Aac87037 Nucleotid
4	1679	100.0	1679	4	Aas21431 Human CDN
5	1679	100.0	1679	6	Abk33598 cDNA enco
6	1679	100.0	1679	6	Abk188099 Human PRO
7	1679	100.0	1679	6	Abk195588 Human ang
8	1679	100.0	1679	7	Acd24040 Novel hum
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15	1679	100.0	1679	7	Aca03790 cDNA enco
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18	1679	100.0	1679	7	Abx89328 DNA encod
19	1679	100.0	1679	7	Abx92696 cDNA enco
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ALIGNMENTS

RESULT 1
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ID AAZ34324 standard; cDNA; 1679 BP.
XX
AC AAZ34324;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO337 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
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PR 10-MAR-1998; 98US-0077450P.
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PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI, 1999-551358/46.

XX P-PSDB; AAY41773.

XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.

XX Claim 2; Fig 221; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
XX AAY41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match		100.0%;	Score 1679;	DB 2;	Length 1679;	
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QY	61	AATCTATCGGAAGAAAGAAAGAAACCGAAGCTGACAAAAGAGAAAGAAAGAG	120			
DB	61	AATCTATCGGAAGAAAGAAAGAAACCGAAGCTGACAAAAGAGAAAGAAAGAG	120			
QY	121	AAGAAAAAATCATGAAACCATCAGACCAAAATGCAAAATCTATCTCTTGGCAAT	180			
DB	121	AAGAAAAAATCATGAAACCATCAGACCAAAATGCAAAATCTATCTCTTGGCAAT	180			
QY	181	CTTACGGGGCTGGCTGTCTGTGTCTCTTCCAAAGAGTGCCCGTGCAGCGGAGATGC	240			
DB	181	CTTACGGGGCTGGCTGTCTGTGTCTCTTCCAAAGAGTGCCCGTGCAGCGGAGATGC	240			
QY	241	CACCTTCCCAAGCTATGACAAAGCTGACGGTCCGCGAGGGGGAGCGCCACCTCAG	300			
DB	241	CACCTTCCCAAGCTATGACAAAGCTGACGGTCCGCGAGGGGGAGCGCCACCTCAG	300			
QY	301	GTGCACTATTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTA	360			
DB	301	GTGCACTATTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTA	360			
QY	361	TGCTGGGAATGCAAGTGTGCTTGATCTCTCGGTGTCTCTTCTGAGCAACCCAAAC	420			
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QY	601	CTGCATAGCAACTGTGTAGACAGAGCTACGGTACTTGGAGACATCTCTCCAAAGC	660			
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QY	1501	TCCTGCCACAGAGTGGCCCACTGTGGAACATTTCTGGAGCTGGCCATCCCAAAATTTCA	1560			
DB	1501	TCCTGCCACAGAGTGGCCCACTGTGGAACATTTCTGGAGCTGGCCATCCCAAAATTTCA	1560			
QY	1561	GTCCATAGAGACGAACAGAAATGAGACCTTCCGCGCCCAAGCGTGGCGCTCGGSCA	1620			
DB	1561	GTCCATAGAGACGAACAGAAATGAGACCTTCCGCGCCCAAGCGTGGCGCTCGGSCA	1620			
QY	1621	GTAGACTGTGCCACCAAGCGGCTGTGTGTGAACCTGTGTGAACCTGTGTGAACCT	1679			
DB	1621	GTAGACTGTGCCACCAAGCGGCTGTGTGTGAACCTGTGTGTGAACCTGTGTGAACCT	1679			
RESULT 2						
AAC78590						
ID	AAC78590 standard; cDNA; 1679 BP.					
XX	AAC78590;					
XX	08-FEB-2001 (first entry)					
DE	Human PRO337 nucleotide sequence SEQ ID NO:522.					
XX	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;					
KW	expressed sequence tag; detection; cancer; ss.					
OS	Homo sapiens.					
XX	WO200053756-A2.					
PD	14-SEP-2000.					
XX	18-FEB-2000; 2000WO-US0004341.					
PR	08-MAR-1999; 99WO-US005028.					
PR	12-MAR-1999; 99US-0123957P.					
PR	29-MAR-1999; 99US-0126773P.					
PR	21-APR-1999; 99US-0130232P.					
PR	28-APR-1999; 99US-0131445P.					
PR	14-MAY-1999; 99US-0134287P.					
PR	23-JUN-1999; 99US-0141037P.					
PR	26-JUL-1999; 99US-0145698P.					

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PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 2000WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
PI Kijavini IU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2000-611443/58.
DR P-PSDB; AAB44329.
DR
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
XX Claim 2; Fig 221; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytosolic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1679; DB 3; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTTTCAGCAAAACAGTGGATTAAATCTCTTGTGCAAGCTTGAGAGCAAC 60
DB 1 GTTGTGCTTTCAGCAAAACAGTGGATTAAATCTCTTGTGCAAGCTTGAGAGCAAC 60
QY 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTGGGCAAT 180
DB 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTGGGCAAT 180
QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCCAGAGTGGCCGTCGCGAGGATGC 240
DB 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCCAGAGTGGCCGTCGCGAGGATGC 240
QY 241 CACCTTCCCAAGCTATGGAACAGTGCAGTCCGCGAGGGGAGAGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGGAACAGTGCAGTCCGCGAGGGGAGAGCCACCTCAG 300
QY 301 GTCGCTATTGTAACAACCGGGTCAACCGGGTGGCTGGCTTAACCGCAGCACCCTCTA 360
DB 301 GTCGCTATTGTAACAACCGGGTCAACCGGGTGGCTGGCTTAACCGCAGCACCCTCTA 360
QY 361 TGCTGGGATGACAGTGGTGGCTGGATCCCTGCTGCTCTTCTGAGCAACACCCAAAC 420
DB 361 TGCTGGGATGACAGTGGTGGCTGGATCCCTGCTGCTCTTCTGAGCAACACCCAAAC 420
```

```
QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
QY 481 GGTGACAGACAGCAACCAACCAACCAACCAACCTCTAGGGTCCACCTCATTTGTCAGATATCTCC 540
DB 481 GGTGACAGACAGCAACCAACCAACCAACCAACCTCTAGGGTCCACCTCATTTGTCAGATATCTCC 540
QY 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
DB 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCACTGGTATAGACAGAGCCCTACGGTTACTTGGAGACACATCTCTCCAAAGC 660
DB 601 CTGCATAGCACTGGTATAGACAGAGCCCTACGGTTACTTGGAGACACATCTCTCCAAAGC 660
QY 661 GGTGGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
DB 661 GGTGGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTAGCAGTGCAGTGCCTCCAATGACGTGGCCGCCCTGTGTPACGAGAGTAA 780
DB 721 AGGGGACTAGCAGTGCAGTGCCTCCAATGACGTGGCCGCCCTGTGTPACGAGAGTAA 780
QY 781 GGTCAACGCTGAATCTCCACATATCTCAGAACCAAGGTTACAGTGTCCCGCTGG 840
DB 781 GGTCAACGCTGAATCTCCACATATCTCAGAACCAAGGTTACAGTGTCCCGCTGG 840
QY 841 ACAAAGGGGACACTGCGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 900
DB 841 ACAAAGGGGACACTGCGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 900
QY 901 CAAAGATGACAAAAGACTGATTTGAAGGAAAGAAAGGGTGAAGTGAAGAAACAGACCTTT 960
DB 901 CAAAGATGACAAAAGACTGATTTGAAGGAAAGAAAGGGTGAAGTGAAGAAACAGACCTTT 960
QY 961 CCTCTCAAACTCATCTTCTTCAATGCTCTGAAATGACATGATATGGAACATACCTTGGT 1020
DB 961 CCTCTCAAACTCATCTTCTTCAATGCTCTGAAATGACATGATATGGAACATACCTTGGT 1020
QY 1021 GGCTTCCAACAGCTGGGCGCACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGT 1080
DB 1021 GGCTTCCAACAGCTGGGCGCACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGCGAGTGAAGCAACCGCAGCTCAGAGGGAGGCTGGTCTGGCTGCTGCTCTTCT 1140
DB 1081 CAGCGAGTGAAGCAACCGCAGCTCAGAGGGAGGCTGGTCTGGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTAGTGCACCTTCCCGCCCGGGAAGGCT 1200
DB 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTAGTGCACCTTCCCGCCCGGGAAGGCT 1200
QY 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
DB 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
QY 1261 TATCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1320
DB 1261 TATCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1320
QY 1321 AAGAATACCTTTGGGGGAAAGATTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
DB 1321 AAGAATACCTTTGGGGGAAAGATTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
QY 1381 TTTAGGTACAAATGAGATTTTCTTTTCCAAACCGGGAAGAAACACAGCAACACCCGCTTGA 1440
DB 1381 TTTAGGTACAAATGAGATTTTCTTTTCCAAACCGGGAAGAAACACAGCAACACCCGCTTGA 1440
QY 1441 CCCACTGCAAGCTGCATCGTGCACCTCTTTTGGTGGCAGTGTGGGCAAGGCTCAGCCTC 1500
DB 1441 CCCACTGCAAGCTGCATCGTGCACCTCTTTTGGTGGCAGTGTGGGCAAGGCTCAGCCTC 1500
```


XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
XX breast, prostate, cervical.

Claim 3; Fig 375; 813pp; English.

XX AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
XX polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 4; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTTCGCAACAGCTTGAGCAACAC 60
DB 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTTCGCAACAGCTTGAGCAACAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAAATCATGAAACCATCAGGCAAAATGCAATTCATCTCTTGGGCAAT 180
DB 121 AAGAAAAAAATCATGAAACCATCAGGCAAAATGCAATTCATCTCTTGGGCAAT 180
QY 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCAGAGAGTCCCGTGGCAGCGGAGATGC 240
DB 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCAGAGAGTCCCGTGGCAGCGGAGATGC 240
QY 241 CACCTTCCCAAGCTATGCAACAGTGAAGTCCGGCAGGGGGGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGCAACAGTGAAGTCCGGCAGGGGGGAGCGCCACCTCAG 300
QY 301 GTGCACTATTGCAACCCGGGTCAACCGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GTGCACTATTGCAACCCGGGTCAACCGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 TCGTGGGATGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
DB 361 TCGTGGGATGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
QY 421 GCAGTACAGCATCGAGATCCAGAACCGTGGATGTGATGACGAGGGGCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACCGTGGATGTGATGACGAGGGGCTTACACCTGCTC 480
QY 481 GTGCAAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB 481 GTGCAAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
QY 541 CAAATTTGTAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCAC 600
DB 541 CAAATTTGTAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCAC 600

DB 541 CAAATTTGTAGATTTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCAC 600
QY 601 CTGCAATAGCAACTGTAGACAGAGCCTACGTTACTTTGGAGACACATCTCTCCCAAGC 660
DB 601 CTGCAATAGCAACTGTAGACAGAGCCTACGTTACTTTGGAGACACATCTCTCCCAAGC 660
QY 661 GGTTCGCTTTGTAGTGAAGACGAATATCTTGAAATTCAGGGCATCACCCGGGAGCAGTC 720
DB 661 GGTTCGCTTTGTAGTGAAGACGAATATCTTGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTACGAGTGCAGTCCCAATGACGTGGCCGCCCGTGGTACGAGAGTAAA 780
DB 721 AGGGGACTACGAGTGCAGTCCCAATGACGTGGCCGCCCGTGGTACGAGAGTAAA 780
QY 781 GGTTCGCTTTGTAGTGAAGACGAATATCTTGAAATTCAGGGCATCACCCGGGAGCAGTC 840
DB 781 GGTTCGCTTTGTAGTGAAGACGAATATCTTGAAATTCAGGGCATCACCCGGGAGCAGTC 840
QY 841 ACAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
DB 841 ACAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
QY 901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGTGAAGTGAAGAAACAGACCTTT 960
DB 901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGTGAAGTGAAGAAACAGACCTTT 960
QY 961 CTTCTCAAACTCATCTTCTCAATGTCTCTGAAATGATGATGGGAACTACACTTGGCT 1020
DB 961 CTTCTCAAACTCATCTTCTCAATGTCTCTGAAATGATGATGGGAACTACACTTGGCT 1020
QY 1021 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTGTGTCAGGGGCGCT 1080
DB 1021 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTGTGTCAGGGGCGCT 1080
QY 1081 CAGCAGGTGAGCAACGGCACTGAGGAGGCGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1140
DB 1081 CAGCAGGTGAGCAACGGCACTGAGGAGGCGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1140
QY 1141 GGTCTTGACCTGCTTCTCAATTTTGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 1200
DB 1141 GGTCTTGACCTGCTTCTCAATTTTGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 1200
QY 1201 GCGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
DB 1201 GCGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
QY 1261 TATACAAATGAAATTTAGAAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAC 1320
DB 1261 TATACAAATGAAATTTAGAAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAC 1320
QY 1321 AAAAGAAATCTTTGGGGGAAAGAGTTTTTAAAAAGAAATTCAAAAATTCGCTTGCAGATA 1380
DB 1321 AAAAGAAATCTTTGGGGGAAAGAGTTTTTAAAAAGAAATTCAAAAATTCGCTTGCAGATA 1380
QY 1381 TTTAGGTAACAATGGAGTTTTCTTTTCCAAAACGGGAAGAACACAGCACACCCGGCTTGA 1440
DB 1381 TTTAGGTAACAATGGAGTTTTCTTTTCCAAAACGGGAAGAACACAGCACACCCGGCTTGA 1440
QY 1441 CCCACTGCAAGTGCATCGTGCAACCTCTTTGGTGGCAGTGTGGGCAAGGGCTCAGCCTC 1500
DB 1441 CCCACTGCAAGTGCATCGTGCAACCTCTTTGGTGGCAGTGTGGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCGCACAGAGTGCCTCCCACTTCTGGAGCTGGCCATCCCAAAATTCAAATCA 1560
DB 1501 TCTGCGCACAGAGTGCCTCCCACTTCTGGAGCTGGCCATCCCAAAATTCAAATCA 1560
QY 1561 GTTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCTTCGGGGCACTTTG 1620
DB 1561 GTTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCTTCGGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCAACCGCGTGTGTGTGAAACCTGAAATTAAGAGCAAAAAA 1679
DB 1621 GTAGACTGTGCCACCAACCGCGTGTGTGTGAAACCTGAAATTAAGAGCAAAAAA 1679

RESULT 5

ABK33598

ID ABK33598 standard; cDNA; 1679 BP.

XX AC ABK33598;

XX DT 08-MAY-2002 (first entry)

XX DE cDNA encoding human PRO protein, Seq ID No 125.

XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

XX KW breast cancer; prostate tumour; rectal tumour; liver tumour;

XX KW pericyte cell proliferation; chondrocyte cell proliferation;

XX KW tumour necrosis factor-alpha; gene; ss.

XX OS Homo sapiens.

XX FN WO200208288-A2.

XX PD 31-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US021066.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220585P.

XX PR 25-JUL-2000; 2000US-0220605P.

XX PR 25-JUL-2000; 2000US-0220607P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 25-JUL-2000; 2000US-0220638P.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 25-JUL-2000; 2000US-0220666P.

XX PR 26-JUL-2000; 2000US-0220893P.

XX PR 28-JUL-2000; 2000WO-US020710.

XX PR 01-AUG-2000; 2000US-0222425P.

XX PR 22-AUG-2000; 2000US-0227133P.

XX PR 23-AUG-2000; 2000WO-US023522.

XX PR 24-AUG-2000; 2000WO-US023328.

XX PR 10-NOV-2000; 2000WO-US030873.

XX PR 28-NOV-2000; 2000US-0253467P.

XX PR 01-DEC-2000; 2000WO-US032678.

XX PR 20-DEC-2000; 2000US-0074725P.

XX PR 20-DEC-2000; 2000WO-US034956.

XX PR 28-FEB-2001; 2001WO-US006520.

XX PR 01-MAR-2001; 2001WO-US006666.

XX PR 22-MAR-2001; 2001US-00816744.

XX PR 10-MAY-2001; 2001US-00854208.

XX PR 25-MAY-2001; 2001WO-US017092.

XX FA (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski RJ;

XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX DR WPI; 2002-172001/22.

XX DR P-PSDB; AAU83654.

XX PT One hundred and twenty two nucleic acids encoding PRO polypeptides.

XX PT useful for treating a PRO related disorder and for diagnosing tumors such

XX PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor

XX PT or liver tumor.

XX PS Claim 2; Fig 125; 359pp; English.

XX CC The invention relates to one hundred and twenty two nucleic acids

XX CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides

XX CC encode human secreted proteins. The PRO nucleic acids, polypeptides,

XX CC agonists and antagonists are useful for treating a PRO related disorder.

XX CC The PRO polypeptides are useful for diagnosing tumours, especially lung

XX CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or

XX CC liver tumour. The PRO polypeptides are useful for stimulating the

CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK33596-ABK33657 represent human PRO
 CC protein coding sequences of the invention

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 6; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGACCAAC 60

DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGACCAAC 60

QY 61 AATCTATCAGGAAGAAGAAAGAAAAACCGAACCTGCACAAAAAGAAAAAGAAAG 120

DB 61 AATCTATCAGGAAGAAGAAAGAAAAACCGAACCTGCACAAAAAGAAAAAGAAAG 120

QY 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATCTTATCTTTGGGCAAT 180

DB 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATCTTATCTTTGGGCAAT 180

QY 181 CTTACGGGGTGGCTCTCTGTGTCTTTTCAAGAGTGCCTGTGCGCAGCGGAGATGC 240

DB 181 CTTACGGGGTGGCTCTCTGTGTCTTTTCAAGAGTGCCTGTGCGCAGCGGAGATGC 240

QY 241 CACCTTCCCAAAAGTATGACAAACGTGACGGTCCGCGAGGGGAGCGCCACCTCAG 300

DB 241 CACCTTCCCAAAAGTATGACAAACGTGACGGTCCGCGAGGGGAGCGCCACCTCAG 300

QY 301 GTGCACATTTGACAAACCGGGTCAACCGGGTGGCTTAAACCGCAGCAACCACTCTTA 360

DB 301 GTGCACATTTGACAAACCGGGTCAACCGGGTGGCTTAAACCGCAGCAACCACTCTTA 360

QY 361 TGCTGGGAATGACAAAGTGGTGGTCTCGGTGGTCTCTTCTGAGCAACCCGAAAC 420

DB 361 TGCTGGGAATGACAAAGTGGTGGTCTCGGTGGTCTCTTCTGAGCAACCCGAAAC 420

QY 421 GCAGTACAGCATCCAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

DB 421 GCAGTACAGCATCCAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

QY 481 GGTGCAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540

DB 481 GGTGCAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540

QY 541 CAAAATGTAGAGATTCTTCAGATATCTCCATTAATGAAGGGAACAATAATTAGCCTCAC 600

DB 541 CAAAATGTAGAGATTCTTCAGATATCTCCATTAATGAAGGGAACAATAATTAGCCTCAC 600

QY 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660

DB 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTGAGTGAAGACAGAACTTTGAAAATTCAGGGCATACCCGGGAGCAGTC 720

DB 661 GGTGGCTTTGTGAGTGAAGACAGAACTTTGAAAATTCAGGGCATACCCGGGAGCAGTC 720

QY 721 AGGGGACTACAGTGCAGTGCCTCCATGACGTGGCGCGCCCGTGTAGGAGATGAAA 780

DB 721 AGGGGACTACAGTGCAGTGCCTCCATGACGTGGCGCGCCCGTGTAGGAGATGAAA 780

QY 781 GGTCAACCGTGAATCTATCCACATACATTTTCAAGAGCCAGGTCACAGGTGTCCCGGTGGG 840

DB 781 GGTCAACCGTGAATCTATCCACATACATTTTCAAGAGCCAGGTCACAGGTGTCCCGGTGGG 840

QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900

25-JUL-2000; 2000US-0220624P.
 25-JUL-2000; 2000US-0220664P.
 28-JUL-2000; 2000WQ-US020710.
 02-AUG-2000; 2000US-0222595P.
 17-AUG-2000; 2000US-00643657.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 07-SEP-2000; 2000US-0230978P.
 18-SEP-2000; 2000US-00664510.
 18-SEP-2000; 2000US-00665350.
 24-OCT-2000; 2000US-0242922P.
 08-NOV-2000; 2000US-00709238.
 08-NOV-2000; 2000WO-US030952.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000WO-US034956.
 22-JAN-2001; 2001US-00767609.
 28-FEB-2001; 2001US-00796498.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 05-MAR-2001; 2001US-00802706.
 14-MAR-2001; 2001US-00808689.
 22-MAR-2001; 2001US-00816744.
 05-APR-2001; 2001US-00828366.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00854280.
 25-MAY-2001; 2001US-00860028.
 25-MAY-2001; 2001US-00860034.
 25-MAY-2001; 2001WO-US017092.
 30-MAY-2001; 2001US-00870574.
 01-JUN-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 (GETH) GENENTECH INC.
 (BAKE/) BAKER K P.
 (FERR/) FERRARA N.
 (GERB/) GERBER H.
 (GERB/) GERBETSEN M E.
 (GODD/) GODDARD A.
 (GODO/) GODOWSKI P J.
 (HILL/) HILLAN K J.
 (GURN/) GURNEY A L.
 (MARS/) MARSTERS S A.
 (PANJ/) PAN J.
 (PAON/) PAONI N F.
 (STEP/) STEPHAN J F.
 (WATA/) WATANABE C K.
 (WILL/) WILLIAMS P M.
 (WOOD/) WOOD W I.
 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 WPI; 2002-171939/22.
 P-PSDB; ABB95450.
 One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 infarction), endothelial or angiogenic disorders in a mammal.
 Claim 1; Fig 55; 567pp; English.
 The present invention provides the protein and coding sequences of human
 PRO proteins. These are useful for treating or diagnosing a
 cardiovascular, endothelial or angiogenic disorder, including cardiac
 hypertrophy, trauma, cancer, age-related macular degeneration,
 atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 healing. The present sequence is a coding sequence of the invention

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1679; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60
 DB 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60
 QY 61 AATCTATCAGGAAAGAAAGAGAAAAAACCAGACTGCACAAAAAGAGAAAAAGAG 120
 DB 61 AATCTATCAGGAAAGAAAGAGAAAAAACCAGACTGCACAAAAAGAGAAAAAGAG 120
 QY 121 AGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAATTCCTCTTTGGGCAAT 180
 DB 121 AGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAATTCCTCTTTGGGCAAT 180
 QY 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCCAAGAGTGCCCGTGGCAGCGGAGATGC 240
 DB 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCCAAGAGTGCCCGTGGCAGCGGAGATGC 240
 QY 241 CACCTTCCCAAAAGCTATGCAAAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAG 300
 DB 241 CACCTTCCCAAAAGCTATGCAAAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAG 300
 QY 301 GTGCACATATTGACAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGACCATCTCTA 360
 DB 301 GTGCACATATTGACAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGACCATCTCTA 360
 QY 361 TGCTGGGAATGACAAGTGTGCTGCTGCTCTTCTGAGCAACCAATTCCTCTTCTGAGCAAC 420
 DB 361 TGCTGGGAATGACAAGTGTGCTGCTGCTCTTCTGAGCAACCAATTCCTCTTCTGAGCAAC 420
 QY 421 GCAGTACAGCATCGAGATCCAGAAACGTGGATGTGTATGACGAGGGGCCCTTTACACCTGCTC 480
 DB 421 GCAGTACAGCATCGAGATCCAGAAACGTGGATGTGTATGACGAGGGGCCCTTTACACCTGCTC 480
 QY 481 GGTGCAGACAGACCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
 DB 481 GGTGCAGACAGACCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
 QY 541 CAAAATTGTAGAGATTTCTTTCAGATATCTCCATATGAAAGGAAACAATATTAGCCCTAC 600
 DB 541 CAAAATTGTAGAGATTTCTTTCAGATATCTCCATATGAAAGGAAACAATATTAGCCCTAC 600
 QY 601 CTGCATAGCAACTGGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
 QY 661 GGTGGCTTTGTGAGTGAAGAGCAATACCTTGGAAATTCAGGGCATCACCGGGAGCAGTC 720
 DB 661 GGTGGCTTTGTGAGTGAAGAGCAATACCTTGGAAATTCAGGGCATCACCGGGAGCAGTC 720
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 DB 721 AGGGGACTACGAGTGCAGTCCCTCCAAACGTCGGCCGCCCTGCTGTTACGGAGAGTAA 780
 QY 781 GGTCAACCGTGAATATCCACCATATCTTCAAGCAATGATGAGGGTACAGGTGTCCCGTGG 840
 DB 781 GGTCAACCGTGAATATCCACCATATCTTCAAGCAATGATGAGGGTACAGGTGTCCCGTGG 840
 QY 841 ACARAGGGGACATGTCAGTGTGAAGCTTCAGAGTCCCTCAGCAGATTCCTCAGTGGTA 900
 DB 841 ACARAGGGGACATGTCAGTGTGAAGCTTCAGAGTCCCTCAGCAGATTCCTCAGTGGTA 900
 QY 901 CAAGGATGACAAAAGACTCATTTGAAAGAAAGAAAGGGGTGAAAGTGAAGAAACAGACTTT 960
 DB 901 CAAGGATGACAAAAGACTCATTTGAAAGAAAGAAAGGGGTGAAAGTGAAGAAACAGACTTT 960
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 DB 961 CCTCTCAAACTCATCTCTTCAATGTCTCTGAAACATGATCTATGGGAACATACACTTGGT 1020

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QY 1081 CAGCGAGTGAGCAACGGCAGCTGAGGAGGGCAGGCTCGCTCTGGCTGCTGCTCTTCT 1140
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Db 1141 GGTCTTGCACTGCTTCTCAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
QY 1201 GCCGCCACACACACCAACCAACACCAATGGCAACAGCAAGCAAGCAAGCAAGCAAGCA 1260
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QY 1261 TATCAAAATGAATTTAGAAGAAACACAGCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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QY 1321 AAGGAATACTTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
Db 1321 AAGGAATACTTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
QY 1381 TTTAGGTACAATGGAGTTTCTTTTCCCAACGGGAAGCAACACAGCAACCCCGCTTGGGA 1440
Db 1381 TTTAGGTACAATGGAGTTTCTTTTCCCAACGGGAAGCAACACAGCAACCCCGCTTGGGA 1440
QY 1441 CCCACTGCAAGTGCATGCGCACTTTTGGTGCCAGTGTGGGCAAGGCTCAGGCTC 1500
Db 1441 CCCACTGCAAGTGCATGCGCACTTTTGGTGCCAGTGTGGGCAAGGCTCAGGCTC 1500
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Db 1501 TCTGCCACAGAGTCCCCCGGACATCTTGGAGCTGGCCATCCCAATTTCAATCA 1560
QY 1561 GTCCATAGAGACGACAGAAATGAGACCTTCGCGCCCGGCTGGCGGCACTTTG 1620
Db 1561 GTCCATAGAGACGACAGAAATGAGACCTTCGCGCCCGGCTGGCGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACCGGCTGTGTGTAACCTGTAATTAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACCGGCTGTGTGTAACCTGTAATTAAGAGCAAAAAA 1679

RESULT 8
ACD24040
ID ACD24040 standard; cDNA; 1679 BP.
XX
AC ACD24040;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PR0337 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.

06-MAY-2002; 2002US-00140474.
31-MAR-1997; 97WO-US005230.
12-JUN-1998; 98WO-US012456.
14-JUL-1998; 98WO-US014552.
28-AUG-1998; 98WO-US017888.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98WO-US019093.
14-SEP-1998; 98WO-US019094.
14-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
29-OCT-1998; 98WO-US022991.
29-OCT-1998; 98WO-US022992.
20-NOV-1998; 98WO-US024855.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
10-MAR-1999; 99WO-US005190.
20-APR-1999; 99WO-US008615.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
01-SEP-1999; 99WO-US020111.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
30-NOV-1999; 99WO-US028409.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
22-DEC-1999; 99WO-US030720.
30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005746.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US013705.
17-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
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PR	20-DEC-2000; 2000WO-US034956.	QY	1	GTGTGTCCTT	GTGTGTCCTT
PR	28-FEB-2001; 2001US-00796498.	DB	1	GTGTGTCCTT	GTGTGTCCTT
PR	01-MAR-2001; 2001WO-US006520.	QY	61	AATCTATCAGG	AATCTATCAGG
PR	09-MAR-2001; 2001US-00802706.	DB	61	AATCTATCAGG	AATCTATCAGG
PR	14-MAR-2001; 2001US-00808689.	QY	121	AAGAAAAAAT	AAGAAAAAAT
PR	22-MAR-2001; 2001US-00816744.	DB	121	AAGAAAAAAT	AAGAAAAAAT
PR	05-APR-2001; 2001US-00828366.	QY	181	CTTCACGGGG	CTTCACGGGG
PR	10-MAY-2001; 2001US-00854208.	DB	181	CTTCACGGGG	CTTCACGGGG
PR	18-MAY-2001; 2001US-00860216.	QY	241	CACCTTCCCA	CACCTTCCCA
PR	25-MAY-2001; 2001US-00866028.	DB	241	CACCTTCCCA	CACCTTCCCA
PR	25-MAY-2001; 2001US-00866034.	QY	301	GTGCACTAT	GTGCACTAT
PR	25-MAY-2001; 2001WO-US017092.	DB	301	GTGCACTAT	GTGCACTAT
PR	01-JUN-2001; 2001US-00872035.	QY	361	TGCTGGGAAT	TGCTGGGAAT
PR	01-JUN-2001; 2001WO-US017800.	DB	361	TGCTGGGAAT	TGCTGGGAAT
PR	05-JUN-2001; 2001US-00874503.	QY	421	GCAGTACAG	GCAGTACAG
PR	14-JUN-2001; 2001US-00882636.	DB	421	GCAGTACAG	GCAGTACAG
PR	19-JUN-2001; 2001US-00886342.	QY	481	GGTGAGAG	GGTGAGAG
PR	20-JUN-2001; 2001WO-US019692.	DB	481	GGTGAGAG	GGTGAGAG
PR	21-JUN-2001; 2001US-00887879.	QY	541	CAAAATTTG	CAAAATTTG
PR	22-JUN-2001; 2001WO-US020116.	DB	541	CAAAATTTG	CAAAATTTG
PR	29-JUN-2001; 2001WO-US021066.	QY	601	CTGCATAG	CTGCATAG
PR	09-JUL-2001; 2001WO-US021735.	DB	601	CTGCATAG	CTGCATAG
PR	18-JUL-2001; 2001US-00908827.	QY	661	GGTTGGCTT	GGTTGGCTT
PR	06-AUG-2001; 2001US-00924419.	DB	661	GGTTGGCTT	GGTTGGCTT
PR	09-AUG-2001; 2001US-00927796.	QY	721	AGGGGACT	AGGGGACT
PR	16-AUG-2001; 2001US-00931836.	DB	721	AGGGGACT	AGGGGACT
PR	19-DEC-2001; 2001US-00028072.	QY	781	GGTCACTG	GGTCACTG
XX		DB	781	GGTCACTG	GGTCACTG
PA	(GETH) GENENTECH INC.	QY	841	ACAAAAGG	ACAAAAGG
XX		DB	841	ACAAAAGG	ACAAAAGG
XX	Baker KP, Betesini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	QY	901	CAAGGATC	CAAGGATC
PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	DB	901	CAAGGATC	CAAGGATC
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	QY	961	CCTCTCAA	CCTCTCAA
XX	WPI; 2003-341980/32.	DB	961	CCTCTCAA	CCTCTCAA
DR	P-PSDB; ABO17803.	QY	1021	GGCTTCAA	GGCTTCAA
XX		DB	1021	GGCTTCAA	GGCTTCAA
PT	New secreted and transmembrane PRO nucleic acids, for treating	QY	1021	GGCTTCAA	GGCTTCAA
PT	inflammation, organ failure, atherosclerosis, cardiac injury,	DB	1021	GGCTTCAA	GGCTTCAA
PT	infertility, birth defects, premature aging, acquired immunodeficiency	QY	1021	GGCTTCAA	GGCTTCAA
PT	syndrome (AIDS), or cancer.	DB	1021	GGCTTCAA	GGCTTCAA
XX	Claim 2; Fig 375; 660pp; English.				
PS					
PS					
CC	The invention describes an isolated nucleic acid (I) comprising, or which				
CC	has 80 % sequence identity to, or the full-length coding sequence of, one				
CC	of 275 nucleotide sequences, and which encodes a corresponding				
CC	polypeptide selected from 275 amino acid sequences, where all sequences				
CC	are given in the specification. The polypeptide encoded by (I) is used to				
CC	detect PRO polypeptides, link a bioactive molecule to a cell expressing a				
CC	PRO polypeptide, modulate a biological activity of a cell, stimulate the				
CC	release of tumour necrosis factor (TNF)-alpha from human blood, modulate				
CC	the uptake of glucose or free fatty acid by cells, stimulate or inhibit				
CC	the proliferation or differentiation of cells or gene expression,				
CC	stimulate the release of proteoglycans, inhibit the binding of cytokine				
CC	from peripheral blood mononuclear cells, stimulate the release of cytokine				
CC	to factor VIIA, or detect the presence of tumour in a mammal. The nucleic				
CC	acid and polypeptide encoded by it, are useful for treating inflammatory				
CC	diseases, organ failure, atherosclerosis, cardiac injury, infertility,				
CC	birth defects, premature aging, acquired immunodeficiency syndrome				
CC	(AIDS), cancer, or diabetic complications. The nucleic acid is useful as				
CC	hybridisation probes, in chromosome and gene mapping, and in generating				
CC	antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,				
CC	diagnostics, biosensors or bioreactors. Both are useful in tissue typing.				
CC	This sequence encodes a novel human secreted and transmembrane PRO				
XX	polypeptide				
XX					
XX	Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;				
XX					
XX	Query Match 100.0%; Score 1679; DB 7; Length 1679;				
XX	Best Local Similarity 100.0%; Pred. No. 1.5e-15;				

QY 661 GGTTCGCTTTGAGTGAAGACGATATCTTGAAATTCAGGGCATCACCCGGGACGTC 720
Db |||||
QY 661 GGTTCGCTTTGAGTGAAGACGATATCTTGAAATTCAGGGCATCACCCGGGACGTC 720
Db |||||
QY 721 AGGGGACTACGAGTGCAGTCCCTCAATGACGTGCGCCCGCGTGTACGGAGAGTAAA 780
Db |||||
QY 721 AGGGGACTACGAGTGCAGTCCCTCAATGACGTGCGCCCGCGTGTACGGAGAGTAAA 780
Db |||||
QY 781 GGTCCCGTGAATCTATCCACATATATTCAGAAGCCAAAGGTACAGGTGTCCTCCGTGGG 840
Db |||||
QY 781 GGTCCCGTGAATCTATCCACATATATTCAGAAGCCAAAGGTACAGGTGTCCTCCGTGGG 840
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QY 841 ACAAAGGGGACATGTCAGTGTGAAGCTTCAGAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||||
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QY 901 CAAGGATGACAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
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QY 901 CAAGGATGACAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
Db |||||
QY 961 CCTCTCAAACTCATCTTCTCAATGCTCTGAAATGACTATGGGAATCACTTGGT 1020
Db |||||
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Db |||||
QY 1021 GGCCTCCAAAGCTGGGCGCACACCAATGCCAGCATCATGCTATTGGTCCAGGGCGCGT 1080
Db |||||
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Db |||||
QY 1081 CAGCGAGGTGAGCAACGGCACTCGAGGAGGGCAGGCTCGTCTGCTCTCTCTCT 1140
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QY 1201 GCCGCCACCCACCAACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db |||||
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QY 1441 CCCACTGCAAGTGCATCTGTCAACCTCTTTGTCAGTGTGGGCAAGGGCTCAGCCTC 1500
Db |||||
QY 1501 TCTGCCACAGAGTGCCTCCACAGTGAACATTTCTGAGTGGCCATCCCAATTCATCA 1560
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Db |||||
QY 1561 GTCCATAGAGACGAAACAGATGAGACTTCCGCGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db |||||
QY 1561 GTCCATAGAGACGAAACAGATGAGACTTCCGCGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db |||||
QY 1621 GTAGACTGTGCCACACGCGGTGTGTTGAAACGTGAATTAAGAGCAAAAAA 1679
Db |||||
QY 1621 GTAGACTGTGCCACACGCGGTGTGTTGAAACGTGAATTAAGAGCAAAAAA 1679
Db |||||

RESULT 10

ACD42387

ID ACD42387 standard; cDNA; 1679 BP.

XX

AC ACD42387;
XX
DT 05-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antidiabetic;
KW ophthalmological; cytotatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
OS
XX Homo sapiens.
XX
PN US2003040014-A1.
XX
PD 27-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066269.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 24-SEP-1998; 98WO-US019437.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149366P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.

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PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Denoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AJ, Kljavin IJ, Mather JP, Napier MA, Pan J,
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
PI Wood WI, Zhang Z;
XX
XX MPI; 2003-503396/47.
DR P-PSDB; ABO25175.
DR
XX
XX New secreted and transmembrane PRO polypeptides, useful for treating
XX diabetes, retinal disorders and stimulating an immune response.
XX
XX Claim 2; Fig 51; 254pp; English.
XX
XX The invention describes an isolated polypeptide (I) having at least 80 %
XX amino acid sequence identity to 30 secreted and transmembrane
XX polypeptides. PRO polypeptides are also useful for stimulating
XX hypertrophy of adult heart, for inhibiting vascular endothelial growth
XX factor stimulated proliferation of endothelial cells, stimulating
XX proliferation of stimulated T-lymphocytes and for inducing proliferation
XX of PDB12 pancreatic ductal cells and are thus useful in the treatment of
XX disorders which involve protein secretion by the pancreas, including
XX diabetes. PRO polypeptides are useful for inducing vascular permeability
XX and in enhancing survival of retinal neurons cells and are thus useful
XX for the treatment of retinal disorders. PRO polypeptides are also useful
XX for stimulating an immune response and inducing inflammation by inducing
XX mononuclear cell and eosinophil infiltration at the site of infection of
XX an animal. The PRO polypeptides are further useful for inducing apoptosis
XX in endothelial cells for inhibiting neoplastic growth. This sequence
XX encodes a novel human secreted and transmembrane PRO polypeptide
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1679; DB 7; Length 1679;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-15;
XX Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCCTTGACAAAGCTTGAGACCAAC 60
XX
XX 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCCTTGACAAAGCTTGAGACCAAC 60
XX
XX 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX
XX 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX
XX 121 AAGAAAAAATATGAAAAACCATCCAGCCAAAAATGCAAAATCTATCTCTTGGGCAAT 180
XX
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Db 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
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Db 1321 AAAGAATACTTTGGGGGGAAGAGATTTTAAAAAGAAATTCGAAATTTGCCCTTGAGATA 1380
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Db 1381 TTTAGGTCAATGGAGTTTCTTTTCCCAACGGGAAGAACACACACACCCCGGCTTGGGA 1440
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Db 1441 CCCACTGCAAGCTGCATCGTGCACCTCTTTGGTGCAGTGTCGCGGCTCAGCCTC 1500
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Db 1561 GTCCATAGAGACGAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGCACCTTTG 1620
QY 1621 GTAGACTGTGCCACACGCGCTGTGTGTAACCTGTAATATAAAGACCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACGCGCTGTGTGTAACCTGTAATATAAAGACCAAAAAA 1679

RESULT 11
ACD42857
ID ACD42857 standard; cDNA; 1679 BP.
XX AC ACD42857;
XX DT 09-SEP-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
XX KW cell death; growth induction cascade; blood coagulation cascade;
XX KW viral infection; gene; ss.
XX OS Homo sapiens.
XX PN US2003050239-A1.
XX PD 13-MAR-2003.
XX PF 15-OCT-2001; 2001US-00978191.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 03-NOV-1997; 97US-0064249P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 21-NOV-1997; 97US-0066364P.
XX PR 10-MAR-1998; 98US-0077450P.
XX PR 11-MAR-1998; 98US-0077632P.
XX PR 11-MAR-1998; 98US-0077641P.
XX PR 11-MAR-1998; 98US-0077649P.
XX PR 12-MAR-1998; 98US-0077791P.
XX PR 13-MAR-1998; 98US-0078004P.
XX PR 17-MAR-1998; 98US-00040220.
XX PR 20-MAR-1998; 98US-0078886P.
XX PR 20-MAR-1998; 98US-0078910P.
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XX PR 20-MAR-1998; 98US-0078939P.
XX PR 25-MAR-1998; 98US-0079294P.
XX PR 26-MAR-1998; 98US-0079656P.
XX PR 27-MAR-1998; 98US-0079663P.
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XX PR 27-MAR-1998; 98US-0079689P.
XX PR 27-MAR-1998; 98US-0079728P.
XX PR 27-MAR-1998; 98US-0079786P.
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XX PR 30-MAR-1998; 98US-0079923P.
XX PR 31-MAR-1998; 98US-0080105P.
XX PR 31-MAR-1998; 98US-0080107P.
XX PR 31-MAR-1998; 98US-0080165P.
XX PR 31-MAR-1998; 98US-0080194P.
XX PR 01-APR-1998; 98US-0080327P.
XX PR 01-APR-1998; 98US-0080328P.
XX PR 01-APR-1998; 98US-0080333P.
XX PR 01-APR-1998; 98US-0080344P.
XX PR 08-APR-1998; 98US-0081049P.
XX PR 08-APR-1998; 98US-0081070P.
XX PR 08-APR-1998; 98US-0081071P.
XX PR 09-APR-1998; 98US-0081195P.
XX PR 09-APR-1998; 98US-0081203P.
XX PR 09-APR-1998; 98US-0081229P.
XX PR 15-APR-1998; 98US-0081817P.
XX PR 15-APR-1998; 98US-0081819P.
XX PR 15-APR-1998; 98US-0081838P.
XX PR 15-APR-1998; 98US-0081952P.
XX PR 15-APR-1998; 98US-0081955P.
XX PR 21-APR-1998; 98US-0082568P.
XX PR 21-APR-1998; 98US-0082569P.
XX PR 22-APR-1998; 98US-0082700P.
XX PR 22-APR-1998; 98US-0082704P.
XX PR 22-APR-1998; 98US-0082797P.
XX PR 22-APR-1998; 98US-0082804P.
XX PR 23-APR-1998; 98US-0082796P.
XX PR 27-APR-1998; 98US-0083336P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 29-APR-1998; 98US-0083392P.
XX PR 29-APR-1998; 98US-0083495P.
XX PR 29-APR-1998; 98US-0083496P.
XX PR 29-APR-1998; 98US-0083499P.
XX PR 29-APR-1998; 98US-0083500P.
XX PR 29-APR-1998; 98US-0083545P.
XX PR 29-APR-1998; 98US-0083554P.
XX PR 29-APR-1998; 98US-0083558P.
XX PR 29-APR-1998; 98US-0083559P.
XX PR 30-APR-1998; 98US-0083742P.
XX PR 05-MAY-1998; 98US-0084366P.
XX PR 06-MAY-1998; 98US-0084414P.
XX PR 06-MAY-1998; 98US-0084441P.
XX PR 07-MAY-1998; 98US-0084598P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 07-MAY-1998; 98US-0084627P.
XX PR 07-MAY-1998; 98US-0084637P.
XX PR 07-MAY-1998; 98US-0084639P.
XX PR 07-MAY-1998; 98US-0084640P.
XX PR 07-MAY-1998; 98US-0084643P.
XX PR 13-MAY-1998; 98US-0085323P.
XX PR 13-MAY-1998; 98US-0085338P.
XX PR 13-MAY-1998; 98US-0085339P.
XX PR 15-MAY-1998; 98US-0085573P.
XX PR 15-MAY-1998; 98US-0085579P.
XX PR 15-MAY-1998; 98US-0085580P.
XX PR 15-MAY-1998; 98US-0085582P.
XX PR 15-MAY-1998; 98US-0085689P.
XX PR 15-MAY-1998; 98US-0085697P.
XX PR 15-MAY-1998; 98US-0085700P.
XX PR 15-MAY-1998; 98US-0085704P.
XX PR 18-MAY-1998; 98US-0086021P.
XX PR 22-MAY-1998; 98US-0086392P.
XX PR 22-MAY-1998; 98US-0086414P.
XX PR 22-MAY-1998; 98US-0086430P.
XX PR 22-MAY-1998; 98US-0086486P.
XX PR 28-MAY-1998; 98US-0087098P.
XX PR 28-MAY-1998; 98US-0087106P.
XX PR 28-MAY-1998; 98US-0087208P.
XX PR 26-JUN-1998; 98US-00105413.
XX PR 26-JUN-1998; 98US-0090863P.
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Db 781 GGTCAACCGTGAATATATCCACCACATATTTTCAGAAAGGCTACAGGTGTCCCGTGGG 840
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QY 1441 CCCACTGCAAGCTGCATCGTCAACCTTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db 1561 GTCCATAGAGACGAAAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCAAGCGGTGTGTGAAACGTGAAATTAATAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAAGCGGTGTGTGAAACGTGAAATTAATAAAGAGCAAAAAA 1679

RESULT 12

ACD68655
ID ACD68655 standard; cDNA; 1679 BP.

XX AC ACD68655;

XX AC ACD68655;

DT 17-SEP-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane protein; PRO; cytosolic;

XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;

XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;

XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;

colon tumour; breast tumour; prostate tumour; rectal tumour;
liver tumour; bone disorder; cartilage disorder; sports injury;
arthritis; wound; gene; ss.

Homo sapiens.

US2003045687-A1.

06-MAR-2003.

12-AUG-2002; 2002US-00218631.

01-JUN-2001; 2001WO-US017800.

29-JUN-2001; 2001WO-US021066.

09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

WPI; 2003-512315/48.

P-PSDB; ABO33767.

New genes, and its encoded secreted and transmembrane polypeptides,

useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or

pericyte proliferation, especially for treating lung tumors, arthritis or

wounds in a mammal.

Claim 2; Fig 125; 314pp; English.

The invention describes an isolated nucleic acid molecule comprising a

sequence with at least 80% identity to: (a) a nucleotide encoding any of

122 PRO (secreted and transmembrane) polypeptides whose sequences are

fully defined in the specification; or (b) any of 122 nucleotide

sequences having e.g. 4834, 2504 or 1759 bp fully defined in the

specification; or the full length coding sequence of any these 122

nucleotide sequences. The PRO polypeptides or polynucleotides are useful

as pharmaceuticals, diagnostics, biosensors or bioreactors. These are

particularly useful for detecting tumours (e.g. lung tumour, colon

tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)

in a mammal, for stimulating the release of TNF-alpha from human blood,

for stimulating the proliferation or differentiation of chondrocyte

cells, for stimulating proliferation of pericyte cells, or for modulating

normal human dermal fibroblast proliferation. The PRO nucleic acid or

polypeptide is also useful for treating tumours or various bone and/or

cartilage disorders (e.g. sports injuries or arthritis), or wounds. The

PRO polypeptides are useful in drug screening, particularly as targets

for therapeutic intervention in these diseases, and in the diagnostic

determination of the presence of these diseases. The PRO polypeptides are

also useful as molecular weight markers, or for chromosome

identification. The PRO genes are useful as hybridisation probes, or for

screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may

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PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 28-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 27-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-352836/33.
XX P-PSDB; ABU81057.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
XX Claim 2; Fig 375; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
CC the human PRO polypeptides of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from the USPTO web
CC site at seqdata.uspto.gov/patseq/entry.html
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTTGAGAGCAAC 60
DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTTGAGAGCAAC 60
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DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
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DB 121 AAGAAAAAAATCATGAAAAACCATCCAGCAAAATTCACAATTTCTTTGGGCAAT 180
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DB 181 CTTACGGGGCTGGGTGCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGC 240
QY 241 CACCTTCCCAAGCTATGGACAAGCTGCGGTGCGGCGAGGGGAGCGCCACCTCAG 300
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DB 301 GTGCACCTATTGACAAACCGGGTCAACCGGGTGGCTTAAACCGGAGCACCCTCTA 360
QY 361 TGCTGGGAATGACAAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAAC 420
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Db 421 CGAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGAGGCCCTTACACTGCTC 480
Qy 481 GGTGAGACAGACCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
Db 481 GGTGAGACAGACCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
Qy 541 CAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Db 541 CAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Qy 601 CTGATAGCAACTGTGATAGACAGACCTTACGTTACTTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGATAGCAACTGTGATAGACAGACCTTACGTTACTTTGGAGACACATCTCTCCCAAGC 660
Qy 661 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Qy 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCCCGCCGCTGGTACGAGAGTAA 780
Db 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCCCGCCGCTGGTACGAGAGTAA 780
Qy 781 GGTCAACGTGAATCTCCACCATCATTTTCAAGAGCCAAAGGTACAGGTGCCCGTGG 840
Db 781 GGTCAACGTGAATCTCCACCATCATTTTCAAGAGCCAAAGGTACAGGTGCCCGTGG 840
Qy 841 ACAAAGGGGACATGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db 841 ACAAAGGGGACATGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Qy 901 CAAGGATGACAAAGACTGATTTGAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGGATGACAAAGACTGATTTGAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
Qy 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACTTGGT 1020
Db 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACTTGGT 1020
Qy 1021 GGCTTCAACAAAGTGGGCCACACAAATGCGAGCATCATGTATTTGGTCCAGCGCGGT 1080
Db 1021 GGCTTCAACAAAGTGGGCCACACAAATGCGAGCATCATGTATTTGGTCCAGCGCGGT 1080
Qy 1081 CAGCGAGTGAACAGCGCAGTGGAGGAGGCGTGGTCTGGTCTGGTCTGGTCTTCT 1140
Db 1081 CAGCGAGTGAACAGCGCAGTGGAGGAGGCGTGGTCTGGTCTGGTCTGGTCTTCT 1140
Qy 1141 GGTCTTGACCTGCTTCTCAAAATTTTGAATGTGAGTGCACATTCCTCCACCCGGGAAAGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAAAATTTTGAATGTGAGTGCACATTCCTCCACCCGGGAAAGCT 1200
Qy 1201 GCGGCCACACACACACACACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
Db 1201 GCGGCCACACACACACACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
Qy 1261 TATCAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGGGGGAAC 1320
Db 1261 TATCAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGGGGGAAC 1320
Qy 1321 AAAGAATACTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCCTTCAGATA 1380
Db 1321 AAAGAATACTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCCTTCAGATA 1380
Qy 1381 TTTAGTACATGAGATTTCTTTTCCAAACGGGAGAAACACAGCACACCCGGCTTGA 1440
Db 1381 TTTAGTACATGAGATTTCTTTTCCAAACGGGAGAAACACAGCACACCCGGCTTGA 1440
Qy 1441 CCCACTGCAAGCTGATCGTCAACCTCTTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGCTGATCGTCAACCTCTTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy 1501 TCTGCCACAGAGTGGCCCACTGGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGGCCCACTGGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Qy 1561 GTCCATAGAGACCAACACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGTGGGGCACTTTG 1620
Db 1561 GTCCATAGAGACCAACACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGTGGGGCACTTTG 1620
Qy 1621 GTAGACTGTGCCACCGCGGTGTGTGTGAACGTGAATATAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCGCGGTGTGTGTGAACGTGAATATAAAGAGCAAAAAAAA 1679

RESULT 14
ACA63892
ID ACA63892 standard; cDNA; 1679 BP.
XX
AC ACA63892;
AC
XX
DT 16-JUN-2003 (first entry)
XX
Novel human secreted and transmembrane protein PRO337 cDNA.
DE Human; secreted and transmembrane protein; PRO; antiinflammatory;
XX antiarteriosclerotic; cardiast; anti-infertility; anti-HIV; cytostatic;
XX antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
EN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0004020P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 30-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.

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PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US007532.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US009439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-328860/31.
XX P-PSDB; ABU72281.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
XX as PRO, useful for treating inflammation, organ failure, atherosclerosis,
XX cardiac injury, infertility, birth defects, premature aging, AIDS, or
XX cancer.
XX
XX Claim 2; Fig 221; 453pp; English.
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XX
CC The invention describes an isolated nucleic acid (1) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGAGCAACAC 60
DB |||||
DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGAGCAACAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB |||||
DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCAGCCAAATTCATCTCTTTGGCAAT 180
DB |||||
DB 121 AAGAAAAAATCATGAAACCATCAGCCAAATTCATCTCTTTGGCAAT 180
QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGC 240
DB |||||
DB 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGC 240
QY 241 CACCTTCCCAAGCTATGGAACAAGTACGGTCCGGAGGGGGAGAGCGCCCTCAG 300
DB |||||
DB 241 CACCTTCCCAAGCTATGGAACAAGTACGGTCCGGAGGGGGAGAGCGCCCTCAG 300
QY 301 GTGCATATTGCAACCCGGGTCAACCGGGTGCCTGGCTTAAACCGCAGCACCCTCTTA 360
DB |||||
DB 301 GTGCATATTGCAACCCGGGTCAACCGGGTGCCTGGCTTAAACCGCAGCACCCTCTTA 360
QY 361 TCGTGGGATGACAGTGGTGCCTGGATCCTCGGTGGTCTCTTCTGAGCAACACCAAC 420
DB |||||
DB 361 TCGTGGGATGACAGTGGTGCCTGGATCCTCGGTGGTCTCTTCTGAGCAACACCAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACTGTGATGTATGACGAGGGGCCCTTACACCTGCTC 480
DB |||||
DB 421 GCAGTACAGCATCGAGATCCAGAACTGTGATGTATGACGAGGGGCCCTTACACCTGCTC 480
QY 481 GGTGCAGACAGCAACCCAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB |||||
DB 481 GGTGCAGACAGCAACCCAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
QY 541 CAAATTTGTAGAGATTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCAC 600
DB |||||
DB 541 CAAATTTGTAGAGATTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
DB |||||
DB 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
QY 661 GGTGGCTTTGTGAGTGAAGACGAATCTTGAATTCAGGGCATCACCCGGGAGCAGTC 720
DB |||||
DB 661 GGTGGCTTTGTGAGTGAAGACGAATCTTGAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTACGAGTGCAGTGCCTCAATGACCTGCGCGCGCGTGGTACGAGAGTAA 780
DB |||||
DB 721 AGGGGACTACGAGTGCAGTGCCTCAATGACCTGCGCGCGCGTGGTACGAGAGTAA 780
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QY 781 GGTACCGTGAAGTACTTCCACCATATTTTCAAGCCCAAGGTACAGGTGTCCTCCGCTGGG 840
Db 781 GGTACCGTGAAGTACTTCCACCATATTTTCAAGCCCAAGGTACAGGTGTCCTCCGCTGGG 840
QY 841 ACAAAAGGGGACACTGCGAGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGTGA 900
Db 841 ACAAAAGGGGACACTGCGAGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGTGA 900
QY 901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
Db 901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
QY 961 CTTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAATTCACCTTGGT 1020
Db 961 CTTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAATTCACCTTGGT 1020
QY 1021 GGCCTCCACAGCTGGGCCACCAATGCCAGCATCATCTATTTGTCAGAGGCGCT 1080
Db 1021 GGCCTCCACAGCTGGGCCACCAATGCCAGCATCATCTATTTGTCAGAGGCGCT 1080
QY 1081 CAGCAGGTGAGCAACGGGCACTCGAGGAGGCGCTGCGTCTGCTGCTGCTGCTCTTCT 1140
Db 1081 CAGCAGGTGAGCAACGGGCACTCGAGGAGGCGCTGCGTCTGCTGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGACCTGCTTCTCAATTTTGAATGTGAGTGCCACTTCCCAACCCGGGAAAGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAATTTTGAATGTGAGTGCCACTTCCCAACCCGGGAAAGCT 1200
QY 1201 GCGGCCACACACACACACACACACATGGCAACACGACAGCAACCAATCAGATA 1260
Db 1201 GCGGCCACACACACACACACACACATGGCAACACGACAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAATTTAGAGAAACACAGCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
Db 1261 TATACAAATGAATTTAGAGAAACACAGCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
QY 1321 AAAGAAATCTTTGGGGGAAAGAGTGTAAAAAGAAATTTGAAATTTGCCTTGCAGATA 1380
Db 1321 AAAGAAATCTTTGGGGGAAAGAGTGTAAAAAGAAATTTGAAATTTGCCTTGCAGATA 1380
QY 1381 TTTAGTACATGAGTGTCTTTTCCCAACGGGAAAGACACAGCAGCAGCCGCTTGA 1440
Db 1381 TTTAGTACATGAGTGTCTTTTCCCAACGGGAAAGACACAGCAGCAGCCGCTTGA 1440
QY 1441 CCACTGCAAGTGCATGTCGCAACCTCTTTGGTCCAGTGTGGCAAGGCTCAGCCTC 1500
Db 1441 CCACTGCAAGTGCATGTCGCAACCTCTTTGGTCCAGTGTGGCAAGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTCCCGCCAGTGGAAACATTTGGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCACAGAGTCCCGCCAGTGGAAACATTTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGACAGCAAGATGAGACCTTTCGCGCCCAAGCTGGCGTGGCGGCACTTTG 1620
Db 1561 GTCCATAGACAGCAAGATGAGACCTTTCGCGCCCAAGCTGGCGTGGCGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACCGCGTGTGTGTGAACCTGAAATTAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACCGCGTGTGTGTGAACCTGAAATTAAGAGCAAAAAA 1679

RESULT 15

ACR03790

ID ACR03790 standard; cDNA; 1679 BP.

XX AC

XX ACR03790;

XX AC

DT 23-MAY-2003 (first entry)

XX cDNA encoding human PRO polypeptide #188.

XX DE

XX Human; PRO polypeptide; secreted and transmembrane protein;

XX KW

XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

XX KW

KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW ss.
XX
OS Homo sapiens.
XX US2003036180-A1.
XX 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-00143114.
XX
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 16-SEP-1998; 98WO-US019177.
XX 17-SEP-1998; 98WO-US019330.
XX 07-OCT-1998; 98WO-US019437.
XX 29-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 20-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 22-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005746.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006319.
XX 20-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000WO-US007377.
XX 30-MAR-2000; 2000WO-US007532.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.


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QY 1021 GGCCTCCACAGCTGGGCCACACCAATGCCAGCATCTGCTATTGCTCAGGGCGCGT 1080
Db |||||
QY 1081 CAGCGAGTGGAGCAACGCGACGTCAGAGAGGCGCTGCTGCTGCTGCTGCTTCT 1140
Db |||||
QY 1081 CAGCGAGTGGAGCAACGCGACGTCAGAGAGGCGCTGCTGCTGCTGCTGCTTCT 1140
QY 1141 GGTCTTGACACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
Db |||||
QY 1141 GGTCTTGACACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
QY 1201 GCGGCCACACACACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
Db |||||
QY 1201 GCGGCCACACACACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
QY 1261 TATCAAAATGAAATTAGAAGAAACACAGCCCTCATGGGACAGAAATTTGAGGAGGGGAAAC 1320
Db |||||
QY 1321 AAAGAATACTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
Db |||||
QY 1381 TTTAGGTACAAATGAGTTTCTTTTCCCAACGGGAAGAACACAGCACACCCGCGCTTGA 1440
Db |||||
QY 1441 CCCACTGCAAGCTGCATCGTGCACCTCTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC 1500
Db |||||
QY 1501 TCTGCCACAGAGTGCCTCCCGCCAGTGGAACTTCTGGAGCTGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGACAGCAAGACAGAACTGAGACCTTCGGGCCAAGCGTGGCGTGGCGGCACTTTG 1620
Db |||||
QY 1621 GTAGACTGTGCCACACCGCGCTGTGTGTAACGTGAAATTTAAAGAGCAAAAAA 1679
Db |||||
RESULT 16
ID ACA04996 standard; cDNA; 1679 BP.
AC ACA04996;
XX
XX
XX 28-MAY-2003 (first entry)
XX
XX
XX Novel human secreted and transmembrane protein PRO337 cDNA.
XX
XX Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
XX PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
XX PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
XX fibroblast growth factor receptor; cell death; chromosome mapping;
XX gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
XX obesity; diabetes; insulinemia; vascular permeability;
XX cardiac insufficiency disorder; immune response; hearing loss;
XX auditory hair cell regeneration; bone disorder; cartilage disorder;
XX sports injury; arthritis; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003032063-A1.
XX
XX
XX 13-FEB-2003.
XX
XX 01-FEB-2002; 2002US-00066494.
XX
XX
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PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059283P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 14-SEP-1998; 98US-0099812P.
PR 16-SEP-1998; 98WO-US019093.
PR 17-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98WO-US019437.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030399.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 01-MAR-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005601.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUL-2001; 2001WO-US021066.
PR 15-NOV-2001; 2001US-00002796.
```


XX (GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Kijavlin IJ, Mather JP, Napier MA, Pan J;

PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;

XX Wood WI, Zhang Z;

DR WPI; 2003-341964/32.

DR P-PSDB; ABU67293.

XX Thirty seven nucleic acids encoding novel secreted and transmembrane PRO

PT polypeptides, useful for modulating biological activity of cell

PT expressing the polypeptide, and in chromosome and gene mapping.

XX Claim 2; Fig 51; 255pp; English.

XX The invention describes an isolated, secreted and transmembrane

CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting

CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,

CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth

CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for

CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a

CC cell expressing the polypeptides. The bioactive molecule causes cell

CC death. (II) Is useful as hybridisation probes, in chromosome and gene

CC mapping, in generation of antisense RNA and DNA, in the preparation of

CC PRO polypeptide, for generating transgenic animals or knockout animals

CC which in turn are useful in the development and screening of

CC therapeutically useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chromosome

CC identification. (I) Or Ab is useful for the preparation of medicament for

CC treating conditions which are responsive to the PRO polypeptide or anti-

CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes

CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for

CC inhibiting tumour growth, enhances vascular permeability and immune

CC response, for inducing regeneration of auditory hair cells and for

CC treating hearing loss in mammals, and for treating bone and/or cartilage

CC disorders such as sports injuries and arthritis. This sequence encodes a

CC novel human secreted and transmembrane polypeptide associated

XX oligonucleotide

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTCTCAGCAAAAACAGTGGATTAAATCTCTTTCGCAAGCTTGAGAGCAACAC 60

DB 1 GTTGTGCTCTCAGCAAAAACAGTGGATTAAATCTCTTTCGCAAGCTTGAGAGCAACAC 60

QY 61 AATCTATCAGGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

DB 61 AATCTATCAGGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AAGAAAAAATCATGAAAAACCATCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT 180

DB 121 AAGAAAAAATCATGAAAAACCATCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT 180

QY 181 CTTACGGGGCTGGTGTCTGTGTCTCTTCAAGAGAGTCCCGTGCAGCGGAGATGC 240

DB 181 CTTACGGGGCTGGTGTCTGTGTCTCTTCAAGAGAGTCCCGTGCAGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGCAACAGTGAGCGTCCGGAGGGGAGAGCGCCACCCCTCAG 300

DB 241 CACCTTCCCAAGCTATGCAACAGTGAGCGTCCGGAGGGGAGAGCGCCACCCCTCAG 300

QY 301 GTGCACTATTGACAAACCGGGTACCCTGGCTTAAACCGCAGCACCATCTCTTA 360

DB 301 GTGCACTATTGACAAACCGGGTACCCTGGCTTAAACCGCAGCACCATCTCTTA 360

QY 361 TGCTGGGAATGAAAGTGGTGGATCTCTCGCGTGGTCTCTTCTGAGCAACACCCAAAC 420

DB 361 TGCTGGGAATGAAAGTGGTGGATCTCTCGCGTGGTCTCTTCTGAGCAACACCCAAAC 420

QY 421 GCAGTACAGCATCGAGATCCAGAACTGTATGTATGAGAGGGGCCCTTACACCTGTCTC 480

DB 421 GCAGTACAGCATCGAGATCCAGAACTGTATGTATGAGAGGGGCCCTTACACCTGTCTC 480

QY 481 GGTGCAGACAGAACCCAAAGACCTCTAGGGTCCAACCTCATTTGTGCAAGTATCTCC 540

DB 481 GGTGCAGACAGAACCCAAAGACCTCTAGGGTCCAACCTCATTTGTGCAAGTATCTCC 540

QY 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCCTC 600

DB 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCCTC 600

QY 601 CTGCATAGCAACTGGTAGACCCAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGC 660

DB 601 CTGCATAGCAACTGGTAGACCCAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGC 660

QY 661 GGTGGCTTTGTAGTGAAGACGAATACTTTGGAATTTAGGGGATCACCCGGAGAGCTC 720

DB 661 GGTGGCTTTGTAGTGAAGACGAATACTTTGGAATTTAGGGGATCACCCGGAGAGCTC 720

QY 721 AGCGGACTACGAGTGCAGTGCCTCCAACTGACGTGCGCGCCCGTGGTACGAGAGTAA 780

DB 721 AGCGGACTACGAGTGCAGTGCCTCCAACTGACGTGCGCGCCCGTGGTACGAGAGTAA 780

QY 781 GGTCAACCGTGAATATCCACCATATATTTTCAAGCAAGGGTACAGGTGTCTCCCGTGG 840

DB 781 GGTCAACCGTGAATATCCACCATATATTTTCAAGCAAGGGTACAGGTGTCTCCCGTGG 840

QY 841 ACAAAGGGGACACTGCGAGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900

DB 841 ACAAAGGGGACACTGCGAGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900

QY 901 CAAAGATCAAAAAGACTGATTGAAGAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTT 960

DB 901 CAAAGATCAAAAAGACTGATTGAAGAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTT 960

QY 961 CTTCTCAAAATCATCTTTTCAATGTCTCTGAAATGACTATGGGAACTACACTTGGT 1020

DB 961 CTTCTCAAAATCATCTTTTCAATGTCTCTGAAATGACTATGGGAACTACACTTGGT 1020

QY 1021 GGCCTCCACAGCTGGGCGCACCAATGCCAGCATCATGCTATTTGTTCCAGGCGCGT 1080

DB 1021 GGCCTCCACAGCTGGGCGCACCAATGCCAGCATCATGCTATTTGTTCCAGGCGCGT 1080

QY 1081 CAGCGAGGTGAGCAACGGCAGCTCGAGGAGGCGAGCTGCGTCTGCTGCTGCTCTTCT 1140

DB 1081 CAGCGAGGTGAGCAACGGCAGCTCGAGGAGGCGAGCTGCGTCTGCTGCTGCTCTTCT 1140

QY 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTTCCCAACCCCGGAAAGGT 1200

DB 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTTCCCAACCCCGGAAAGGT 1200

QY 1201 GCGGCCACCCACCAACCAACAGCAACGCAATGGGCAACCCGACAGCAGCAATCAGATA 1260

DB 1201 GCGGCCACCCACCAACCAACAGCAACGCAATGGGCAACCCGACAGCAGCAATCAGATA 1260

QY 1261 TATACAAATGAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320

DB 1261 TATACAAATGAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320

QY 1321 AAGAAATCTTTGGGGGAAAGAGTTTTTAAAAAAGAAATTTGAAATTTGAAATTTGAGATA 1380

DB 1321 AAGAAATCTTTGGGGGAAAGAGTTTTTAAAAAAGAAATTTGAAATTTGAAATTTGAGATA 1380

QY 1381 TTTAGGTAATGAGTGTCTTTTCCCAACCGGAGAAACACAGCAACCCCGGCTTGA 1440

DB 1381 TTTAGGTAATGAGTGTCTTTTCCCAACCGGAGAAACACAGCAACCCCGGCTTGA 1440

QY 1441 CCCACTGCAAGCTGATCGTGCACCTCTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC 1500

XX	Claim 2; SEQ ID NO 522; 55pp; English.		
PS	The invention relates to an isolated secreted and transmembrane		
XX	polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful		
CC	in PRO polypeptide detection methods. The PRO polypeptide is useful for		
CC	linking a bioactive molecule to a cell. The PRO polypeptide or an		
CC	antibody against it is useful for modulating a biological activity of a		
CC	cell. The PRO polypeptide is useful in industrial applications including		
CC	pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO		
CC	polypeptide is also useful as a thrombolytic agent, interferon,		
CC	interleukin, erythropoietin, colony stimulating factor and other		
CC	cytokines. The PRO polypeptide is useful for treating disease such as		
CC	cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,		
CC	amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,		
CC	atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,		
CC	Parkinson's disease; cardiovascular disease e.g. hypertension and		
CC	myocardial ischaemia; kidney disease e.g. renal failure and		
CC	glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial		
CC	asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory		
CC	bowel disease; reproductive disorders e.g. premature labour and		
CC	preclampsia; carcinogenesis. The present sequence represents a cDNA		
CC	encoding a PRO polypeptide of the invention. Note: The sequence data for		
CC	this patent did not form part of the printed specification but was		
CC	obtained in electronic format directly from USPTO at		
CC	seqdata.uspto.gov/sequence.html?DocID=20020177553		
XX	Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;		
SQ			
Query Match	100.0%; Score 1679; DB 7; Length 1679;		
Best Local Similarity	100.0%; Pred. No. 1.5e-15;		
Matches 1679; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 GTTGTGCTCTCAGCAAAACAGTGGATTAAATCTCTTTCGACAACTTGAGCGACAC 60		
DB	1 GTTGTGCTCTCAGCAAAACAGTGGATTAAATCTCTTTCGACAACTTGAGCGACAC 60		
QY	61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120		
DB	61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120		
QY	121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180		
DB	121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180		
QY	181 CTTACGGGGCTGGCTGTGTCTCTTCAAGAGAGTCCCGTCCGAGCGGAGATGC 240		
DB	181 CTTACGGGGCTGGCTGTGTCTCTTCAAGAGAGTCCCGTCCGAGCGGAGATGC 240		
QY	241 CACTTCCCAAGCTATGGAACAACGTGACGCTCCGCGAGGGGAGCGCCACCTCAG 300		
DB	241 CACTTCCCAAGCTATGGAACAACGTGACGCTCCGCGAGGGGAGCGCCACCTCAG 300		
QY	301 GTGCACTATTGACACCGGGTACCCGGGTGGCTGGCTGATTAACCGGAGCAATCTCTA 360		
DB	301 GTGCACTATTGACACCGGGTACCCGGGTGGCTGGCTGATTAACCGGAGCAATCTCTA 360		
QY	361 TGTGGAATGACAGTGTGCTGTGATCTCTGCGTGGTCTTCTGAGCAACACCCAAAC 420		
DB	361 TGTGGAATGACAGTGTGCTGTGATCTCTGCGTGGTCTTCTGAGCAACACCCAAAC 420		
QY	421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480		
DB	421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480		
QY	481 GGTGACAGACAGCAACCCAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540		
DB	481 GGTGACAGACAGCAACCCAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540		
QY	541 CAAATTTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAC 600		
DB	541 CAAATTTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAC 600		
QY	601 CTGCTAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660		
DB	601 CTGCTAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660		
QY	661 GGTGGCTTTGTGAGTGAAGACGAATATCTTGAATTTAGGGCATCACCCGGGAGCAGTC 720		
DB	661 GGTGGCTTTGTGAGTGAAGACGAATATCTTGAATTTAGGGCATCACCCGGGAGCAGTC 720		
QY	721 AGGGACTACGAGTGCAGTCCATACGCTGGCCGCCCGCTGGTACGGAGAGATAA 780		
DB	721 AGGGACTACGAGTGCAGTCCATACGCTGGCCGCCCGCTGGTACGGAGAGATAA 780		
QY	781 GGTCAACGCTGAACTATCCACCATATATTTCAGAGCAAGGGTACAGGTGTCCTGGG 840		
DB	781 GGTCAACGCTGAACTATCCACCATATATTTCAGAGCAAGGGTACAGGTGTCCTGGG 840		
QY	841 ACAAAGGGGACACTGCACTGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900		
DB	841 ACAAAGGGGACACTGCACTGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900		
QY	901 CAAGATGACAAAGCACTGATTGAAGGAAAGAAAGGGTGAAGTGGAAACAGACCTTT 960		
DB	901 CAAGATGACAAAGCACTGATTGAAGGAAAGAAAGGGTGAAGTGGAAACAGACCTTT 960		
QY	961 CCTCTCAAACTCATCTCTTCAATGTCTCTCAATGATGATGGAACTACACTTGGCT 1020		
DB	961 CCTCTCAAACTCATCTCTTCAATGTCTCTCAATGATGATGGAACTACACTTGGCT 1020		
QY	1021 GGCCTCCAAAGCTGGGCGCACCAATGTCAGAGCATATGTTTGGTCCAGGGCCCT 1080		
DB	1021 GGCCTCCAAAGCTGGGCGCACCAATGTCAGAGCATATGTTTGGTCCAGGGCCCT 1080		
QY	1081 CAGCGAGGTGACCAAGCGCAGCTCGAGGAGGCGAGCTGGCTGGCTGGCTCTTCT 1140		
DB	1081 CAGCGAGGTGACCAAGCGCAGCTCGAGGAGGCGAGCTGGCTGGCTGGCTCTTCT 1140		
QY	1141 GGTCTTGACCTGCTCTCAAAATTTTGATGTGAGTGGCGAGCTGGCTGGCTGGCT 1200		
DB	1141 GGTCTTGACCTGCTCTCAAAATTTTGATGTGAGTGGCGAGCTGGCTGGCTGGCT 1200		
QY	1201 GCGGCGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260		
DB	1201 GCGGCGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260		
QY	1261 TATACAAATGAAATTTAGAGAAACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAAC 1320		
DB	1261 TATACAAATGAAATTTAGAGAAACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAAC 1320		
QY	1321 AAAAGAAATCTTTGGGGGAAAGAGTCTTAAAGAAAGAAATTTGAAATTTGCGCTTGCAGATA 1380		
DB	1321 AAAAGAAATCTTTGGGGGAAAGAGTCTTAAAGAAAGAAATTTGAAATTTGCGCTTGCAGATA 1380		
QY	1381 TTTAGGTAACATGAGTCTTTCTTTTCCAAACGGGAGAAACACAGCAACCCCGGCTTGA 1440		
DB	1381 TTTAGGTAACATGAGTCTTTCTTTTCCAAACGGGAGAAACACAGCAACCCCGGCTTGA 1440		
QY	1441 CCCACTGCAAGCTGCATGTCGCAACCTCTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC 1500		
DB	1441 CCCACTGCAAGCTGCATGTCGCAACCTCTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC 1500		
QY	1501 TCTGCCACAGAGTCCCGGCAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560		
DB	1501 TCTGCCACAGAGTCCCGGCAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560		
QY	1561 GTCCATAGAGAGCAACAGATGAGACCTTCCGGCCCAAGCGTGGCTGGCGGCACTTTG 1620		
DB	1561 GTCCATAGAGAGCAACAGATGAGACCTTCCGGCCCAAGCGTGGCTGGCGGCACTTTG 1620		
QY	1621 GTAGACTGTGCCACCGCGCTGTGTGTGAACCTGTGAACCTGTGAACCTGTGAACCTGTGA 1679		
DB	1621 GTAGACTGTGCCACCGCGCTGTGTGTGAACCTGTGAACCTGTGAACCTGTGAACCTGTGA 1679		

RESULT 18
ABX89328
ID ABX89328 standard; cDNA; 1679 BP.
XX
AC ABX89328;
XX
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO337.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008415.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001US-00802706.
PR 09-MAR-2001; 2001US-00808689.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
XX P-PSDB; ABUS9838.
XX
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
XX useful for treating pericyte-associated tumors, diabetes and various bone
XX and/or cartilage disorders, e.g. arthritis.
XX
XX Claim 2; Fig 375; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX CC

CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein
XX
SQ

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
DB	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
QY	121	AAGAAAAAATCATGAAACCATCCAGCCCAAAATGCAATCTCTTTGGGCAAT	180
DB	121	AAGAAAAAATCATGAAACCATCCAGCCCAAAATGCAATCTCTTTGGGCAAT	180
QY	181	CTTCAGGGGCTGGCTCTGTGTCTCTTCCAGGAGTCCCGTGGCAGCGAGATGC	240
DB	181	CTTCAGGGGCTGGCTCTGTGTCTCTTCCAGGAGTCCCGTGGCAGCGAGATGC	240
QY	241	CACCTTCCCAAAGCTATGGAACACGTGACGGTCCGGCAGGGGAGCGCCCTCAG	300
DB	241	CACCTTCCCAAAGCTATGGAACACGTGACGGTCCGGCAGGGGAGCGCCCTCAG	300
QY	301	GTSCACTATTGACACCGGTGACCCGGTGGCTGGCTTAACCGCAGACCATCTCTA	360
DB	301	GTSCACTATTGACACCGGTGACCCGGTGGCTGGCTTAACCGCAGACCATCTCTA	360
QY	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTCCGCTGGTCTCTGAGCAACCCAAAC	420
DB	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTCCGCTGGTCTCTGAGCAACCCAAAC	420
QY	421	GCAGTACAGATCAGATCCAGAACCTGGATGTGTATGACGAGGGCCCTTACACCTGTC	480
DB	421	GCAGTACAGATCAGATCCAGAACCTGGATGTGTATGACGAGGGCCCTTACACCTGTC	480
QY	481	GGTGACAGACAGAAACACCCAAAGACCTTAGGTGATGATGACGAGGGCCCTTACACCTGTC	540
DB	481	GGTGACAGACAGAAACACCCAAAGACCTTAGGTGATGATGACGAGGGCCCTTACACCTGTC	540
QY	541	CAAAATTTAGAGATTCTTCAGATATCTCCATTAATGAGGGGAAACAAATATTAGCCTC	600
DB	541	CAAAATTTAGAGATTCTTCAGATATCTCCATTAATGAGGGGAAACAAATATTAGCCTC	600

QY	601	CTGCATAGCAACTGTGTAGACGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660
DB	601	CTGCATAGCAACTGTGTAGACGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660
QY	661	GGTTGGCTTTGTGAGTGAAGAGCAATACATTGGAAATTCAGGGGCATCACCCGGGAGCAGTC	720
DB	661	GGTTGGCTTTGTGAGTGAAGAGCAATACATTGGAAATTCAGGGGCATCACCCGGGAGCAGTC	720
QY	721	AGGGGACTAGAGTGCAGTCCCTCAATGACGTGGCGCGCCGTGGTACGAGAGTAA	780
DB	721	AGGGGACTAGAGTGCAGTCCCTCAATGACGTGGCGCGCCGTGGTACGAGAGTAA	780
QY	781	GGTCCACCGTGAATCTCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCTCCCGTGG	840
DB	781	GGTCCACCGTGAATCTCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCTCCCGTGG	840
QY	841	ACAAAAGGGGACATCGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
DB	841	ACAAAAGGGGACATCGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
QY	901	CAAGGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAAAAGACCTTT	960
DB	901	CAAGGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAAAAGACCTTT	960
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DB	1021	GGCTCCAAACAGCTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT	1080
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QY	1141	GGTCTTGACCTGCTTCTCAAAATTTGATGTGATGCTCCCTCCACCCCGGAAAGGCT	1200
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DB	1201	GGCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	1260
QY	1261	TATACAAATGAAATAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGGAGGAC	1320
DB	1261	TATACAAATGAAATAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGGAGGAC	1320
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DB	1321	AAAGAAATACCTTTGGGGGAAAAAGAGTTTAAAAAAGAAATTTGAAATTCCTTGCAGATA	1380
QY	1381	TTTAGGTACATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGACACCCCGCTTGA	1440
DB	1381	TTTAGGTACATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGACACCCCGCTTGA	1440
QY	1441	CCCACTGCAAGCTGCATCGTCAACCTCTTTGTGTCAGTGTGGGCAAGGGCTCAGCCTC	1500
DB	1441	CCCACTGCAAGCTGCATCGTCAACCTCTTTGTGTCAGTGTGGGCAAGGGCTCAGCCTC	1500
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DB	1501	TCTGCCCAACAGAGTGCCTCCACAGTGTGAAACATTTCTGGAGCTGGCCATTCCTCAATCA	1560
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DB	1561	GTCCATAGAGAGAACAGAAATGAGACTTCCCGGCCCAAGCGTGGCGCTCGGGGCACTTTG	1620
QY	1621	GTAGACTGTGCCACACCGCGGTGTGTGAAACCTGTGAAATAAAAAGACAAAAA	1679
DB	1621	GTAGACTGTGCCACACCGCGGTGTGTGAAACCTGTGAAATAAAAAGACAAAAA	1679

RESULT 19
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 ID ABX92696 standard; cDNA; 1679 BP.
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 AC ABX92696;
 XX
 DT
 XX
 DE
 XX
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 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytostatic; antidiabetic; anti-inflammatory;
 KW antiarthritic; anti-tumour; vulnary; antianaemic; dermatological;
 KW cardiant; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002169284-A1.
 XX
 PD 14-NOV-2002.
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 PF 16-OCT-2001; 2001US-00378697.
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 XX 26-MAY-1981; 81US-00267213.
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 PR 25-AUG-1999; 99US-00380138.
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 PR 30-DEC-1999; 99US-0031243.
 PR 30-DEC-1999; 99US-0031274.
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 PR 06-JAN-2000; 2000US-0000376.
 PR 11-FEB-2000; 2000US-0003565.
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 PR 24-FEB-2000; 2000US-0005004.
 PR 02-MAR-2000; 2000US-0005841.
 PR 10-MAR-2000; 2000US-0006319.
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 PR 17-MAY-2000; 2000US-0013705.
 PR 22-MAY-2000; 2000US-0014042.
 PR 30-MAY-2000; 2000US-0014941.
 PR 02-JUN-2000; 2000US-0015264.
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 PR 08-NOV-2000; 2000US-00709238.
 PR 27-NOV-2000; 2000US-00723749.
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 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000US-0034956.
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 PR 22-MAR-2001; 2001US-00816920.
 PR 22-MAR-2001; 2001US-00909552.
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 PR 29-JUN-2001; 2001US-0021066.
 PR 09-JUL-2001; 2001US-0021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-288163/28.
 DR P-PSDB; ABU61159.
 DR
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies.
 XX
 PS Claim 2; Fig 221; 459pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The bioactive molecule maybe a
 CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
 CC The PRO polypeptides are useful for treating immune disorders, diabetes
 CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
 CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
 CC tumours, and wound healing. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and gene

CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. The present sequence encodes a human PRO polypeptide
CC of the invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipSIDentry.html

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTGTGCTCTCAGCAACACAGTGTAAATCTCTTGTGCAACAGCTTGAGAGCAAC 60
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QY |||
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DB |||
QY |||
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RESULT 20

ACD41982
ID ACD41982 standard; cDNA; 1679 BP.

XX ACD41982;

XX AC ACD41982;

XX DT 05-SEP-2003 (first entry)

XX XX Human secreted/transmembrane protein (PRO) cDNA #188.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour;
XX cystostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
XX proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
XX BMC; Glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
XX chondrocyte cell proliferation; chondrocyte cell differentiation;
XX pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
XX endothelial cell; A-peptide; factor VIIa.
OS Homo sapiens.

XX PN US2003036179-A1.
 XX PD 20-FEB-2003.
 XX PF 10-MAY-2002; 2002US-00142431.
 XX XX 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
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 PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
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 PR 22-MAR-2001; 2001US-00816744.
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 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 03-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 23-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX XX (GETH) GENENTECH INC.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Deanoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-466355/44.
 P-PSDB; ABO25028.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 375; 659pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences, given in the specification; or (c) comprising the full-length coding sequence of the nucleotide sequences given in the specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a PRO polypeptide, the isolated PRO polypeptides detailed above, a chimaeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, modulating at least one biological activity of a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, stimulating the proliferation or differentiation of chondrocyte cells (or proliferation of or gene expression in pericyte cells), stimulating the proliferation of inner ear utricular supporting

CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
 CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
 CC cells, detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences given
 CC in the specification. The polynucleotide is useful in molecular biology,
 CC including uses as hybridisation probes, in chromosome and gene mapping,
 CC in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide may also be used in preparing PRO polypeptides by
 CC recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The PRO polypeptide or the
 CC antibody is used in preparing a medicament for treating a condition
 CC responsive to the polypeptide or antibody, such as tumours, and in
 CC various diagnostic assays. The present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTTCGCAAGCTTTCAGAGCAAC 60
 DB 1 GTTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTTCGCAAGCTTTCAGAGCAAC 60

QY 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGCACAAAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGCACAAAAAGAAAGAAAG 120

QY 121 AAGAAAAAATCATGAAACCATCAGCCGCAAAATGCGCAATTCATCTTTGGGCAAT 180
 DB 121 AAGAAAAAATCATGAAACCATCAGCCGCAAAATGCGCAATTCATCTTTGGGCAAT 180

QY 181 CTTTCAGGGCTGGCTGCTCTGTGCTCTCTCAAGAGTGCCTGCGCAGCGGAGATGC 240
 DB 181 CTTTCAGGGCTGGCTGCTCTGTGCTCTCTCAAGAGTGCCTGCGCAGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGACAACTGACGGTCCGCGAGGGGAGCGCCACCTCTCAG 300
 DB 241 CACCTTCCCAAGCTATGACAACTGACGGTCCGCGAGGGGAGCGCCACCTCTCAG 300

QY 301 GTGCACTATGCAACCGGGTCAACCGGTGGCTGGCTGCTTAACCGCAGACCATCTCTTA 360
 DB 301 GTGCACTATGCAACCGGGTCAACCGGTGGCTGGCTGCTTAACCGCAGACCATCTCTTA 360

QY 361 TGTGGAATGCAAGTGTGCTGTGATCCTCGCTGGTCTCTTCAGCAACACCCCAAC 420
 DB 361 TGTGGAATGCAAGTGTGCTGTGATCCTCGCTGGTCTCTTCAGCAACACCCCAAC 420

QY 421 GCAGTACAGATCGAGATCCAGAACTGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 GCAGTACAGATCGAGATCCAGAACTGATGATGATGATGATGATGATGATGATGATGAT 480

QY 481 GTGCAAGACAGCAACACCCCAAGACCTTAGGTCCACCTCATTTGTCAGATATCTCC 540
 DB 481 GTGCAAGACAGCAACACCCCAAGACCTTAGGTCCACCTCATTTGTCAGATATCTCC 540

QY 541 CAAAATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTC 600
 DB 541 CAAAATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTC 600

QY 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTGAGTGAGAGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
 DB 661 GGTGGCTTTGTGAGTGAGAGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

QY 721 AGGGGACTACGAGTGCAGTCCCAATGACGTGGCGCGCGCTGGTACGAGAGTAA 780
 DB 721 AGGGGACTACGAGTGCAGTCCCAATGACGTGGCGCGCGCTGGTACGAGAGTAA 780

RESULT 21

ACA60526

ID ACA60526 standard; cDNA; 1679 BP.

XX ACA60526;

XX 11-JUN-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane polypeptide; PRO;

KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;

KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
 KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tissue typing; gene; ss.

XX Homo sapiens.

XX OS

XX US2002177165-A1.

XX PD 28-NOV-2002.

XX PF 01-FEB-2002; 2002US-00066500.

XX PR 26-AUG-1997; 97US-0056974P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 19-SEP-1997; 97US-0059588P.

XX PR 17-OCT-1997; 97US-0062285P.

XX PR 24-OCT-1997; 97US-0062816P.

XX PR 27-OCT-1997; 97US-0063082P.

XX PR 27-OCT-1997; 97US-0063329P.

XX PR 29-OCT-1997; 97US-0063733P.

XX PR 21-NOV-1997; 97US-0066364P.

XX PR 25-NOV-1997; 97US-0066840P.

XX PR 16-DEC-1997; 97US-0069694P.

XX PR 09-FEB-1998; 98US-0074086P.

XX PR 09-FEB-1998; 98US-0074092P.

XX PR 25-MAR-1998; 98US-0079294P.

XX PR 08-APR-1998; 98US-0081049P.

XX PR 14-JUL-1998; 98WO-US014552.

XX PR 10-AUG-1998; 98US-0095988P.

XX PR 18-AUG-1998; 98US-0097000P.

XX PR 09-SEP-1998; 98US-0099601P.

XX PR 10-SEP-1998; 98US-0099803P.

XX PR 10-SEP-1998; 98US-0099811P.

XX PR 10-SEP-1998; 98US-0099812P.

XX PR 14-SEP-1998; 98WO-US019093.

XX PR 16-SEP-1998; 98WO-US019330.

XX PR 17-SEP-1998; 98US-0100858P.

XX PR 17-SEP-1998; 98WO-US019437.

XX PR 24-SEP-1998; 98US-0101922P.

XX PR 28-OCT-1998; 98US-0106032P.

XX PR 20-NOV-1998; 98US-0109304P.

XX PR 20-NOV-1998; 98WO-US024855.

XX PR 25-NOV-1998; 98WO-US025190.

XX PR 01-DEC-1998; 98WO-US025108.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 23-MAR-1999; 99US-0125778P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 15-JUN-1999; 99US-0139695P.

XX PR 20-JUL-1999; 99US-0145070P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 17-AUG-1999; 99US-0149396P.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 08-SEP-1999; 99WO-US020594.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 15-SEP-1999; 99WO-US021547.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1999; 99WO-US028301.

XX PR 02-DEC-1999; 99WO-US028565.

XX PR 07-DEC-1999; 99US-0169495P.

XX PR 20-DEC-1999; 99WO-US030999.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 18-FEB-2000; 2000WO-US004342.

XX PR 22-FEB-2000; 2000WO-US004414.

XX PR 01-MAR-2000; 2000WO-US005601.

XX PR 02-MAR-2000; 2000WO-US005841.

XX PR 09-MAR-2000; 2000WO-US006471.

XX PR 20-MAR-2000; 2000WO-US007377.

XX PR 30-MAR-2000; 2000WO-US008439.

PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 XX (GETH) GENENTECH INC.

XX PA

XX PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Baton DL;

XX PI Ferrara N, Fong S, Gao W, Geiber H, Gerritsen ME, Goddard A;

XX PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;

XX PI Praoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;

XX PI Wood WI, Zhang Z;

XX WPI; 2003-328482/31.

XX P-PSDB; ABU72061.

XX Novel secreted and transmembrane polypeptide for modulating biological

XX activity of cell expressing the polypeptide, for identifying agonists or

XX antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 51; 254pp; English.

XX The invention describes an isolated, secreted and transmembrane

XX polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP

XX (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,

XX PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor

XX (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or

XX PRO951 polypeptide, and for linking a bioactive molecule to a cell

XX expressing the above polypeptides. The bioactive molecule, a toxin,

XX radiolabel or an antibody, causes cell death. PRO is useful in assays to

XX identify other proteins or molecules involved in binding interaction. The

XX polynucleotide (II) encoding (I) is useful in chromosome and gene

XX mapping, in generation of antisense RNA and DNA, for generating

XX transgenic animals or knockout animals which in turn are useful in the

XX development and screening of therapeutically useful reagents, to

XX construct hybridisation probes for mapping the gene which encodes the PRO

XX and for the genetic analysis of individuals with genetic disorders, in

XX gene therapy, for chromosome identification and as a chromosome marker.

XX (I) and (II) are useful for tissue typing. This sequence encodes a novel

XX human secreted and transmembrane PRO polypeptide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGCTCTCAGCAAAACAGTGGATTAAATCTCTTGCACAAGCTTGAGAGCAAC 60

Db 1 GTTGTGCTCTCAGCAAAACAGTGGATTAAATCTCTTGCACAAGCTTGAGAGCAAC 60

Qy 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

Db 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

Qy 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAATTCCTCTCTGGGCAAT 180

Db 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAATTCCTCTCTGGGCAAT 180

Qy 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCCAGGAGTGCCCGTGGCAGCGAGATGC 240

PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100859P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025190.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 98US-0125778P.
 PR 02-JUN-1999; 98WO-US012252.
 PR 15-JUN-1999; 98US-0139695P.
 PR 20-JUL-1999; 98US-0145070P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 17-AUG-1999; 98US-0149396P.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 30-NOV-1999; 98WO-US028313.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028555.
 PR 07-DEC-1999; 98US-0169493P.
 PR 20-DEC-1999; 98WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001WO-US0002795.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski FJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WJ, Zhang Z;
 XX WPI; 2003-341963/32.
 DR P-PSDB; ABU67162.
 XX
 PT New secreted and transmembrane polypeptide for modulating biological
 PT activity of a cell expressing the polypeptide, identifying agonists or
 PT antagonists of the polypeptide, and as molecular weight markers.
 XX
 PS Claim 2; Fig 51; 254pp; English.

XX The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) Is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This sequence encodes a
 CC novel human secreted and transmembrane polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1679; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCAAGCTTGAGACCAAC 60
 DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCAAGCTTGAGACCAAC 60
 QY 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 QY 121 AAGAAAAAATATGAAACCCATCCAGCCAAATGCAATCTCTCTCTGGGCAAT 180
 DB 121 AAGAAAAAATATGAAACCCATCCAGCCAAATGCAATCTCTCTCTGGGCAAT 180
 QY 181 CTTACCGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCTGCGCAGCGGAGATGC 240
 DB 181 CTTACCGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCTGCGCAGCGGAGATGC 240
 QY 241 CACCTTCCCAAGACTATGACAACTGACAACTGACAACTGACAACTGACAACTGAC 300
 DB 241 CACCTTCCCAAGACTATGACAACTGACAACTGACAACTGACAACTGACAACTGAC 300
 QY 301 GTGCACCTATTGACAACTGACAACTGACAACTGACAACTGACAACTGACAACTGAC 360
 DB 301 GTGCACCTATTGACAACTGACAACTGACAACTGACAACTGACAACTGACAACTGAC 360
 QY 361 TGTGGGAATGACAACTGACAACTGACAACTGACAACTGACAACTGACAACTGACAACT 420
 DB 361 TGTGGGAATGACAACTGACAACTGACAACTGACAACTGACAACTGACAACTGACAACT 420
 QY 421 GCAGTACAGCATCGAGATCCAGACGAGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 GCAGTACAGCATCGAGATCCAGACGAGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 481 GGTGACAGACAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 540
 DB 481 GGTGACAGACAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 540
 QY 541 CAAAATTGTAGAGATTTCCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
 DB 541 CAAAATTGTAGAGATTTCCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
 QY 601 CTGCATAGCACTGGTAGACAGACCTAGGTTACTTTGGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCACTGGTAGACAGACCTAGGTTACTTTGGAGACACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTGAGTGAAGAGCAATACCTTGGAAATTCAGGCGCATCACCCGGAGCAGTC 720
Db |||
QY 661 GGTGGCTTTGTGAGTGAAGAGCAATACCTTGGAAATTCAGGCGCATCACCCGGAGCAGTC 720
Db |||
QY 721 AGGGGACTACGAGTGCAGTGCCTCCCAATGACGTGGCGCCCGTGGTACGGAGAGTAA 780
Db |||
QY 721 AGGGGACTACGAGTGCAGTGCCTCCCAATGACGTGGCGCCCGTGGTACGGAGAGTAA 780
Db |||
QY 781 GGTCCAGCTGAATATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCCGTGGG 840
Db |||
QY 781 GGTCCAGCTGAATATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCCGTGGG 840
Db |||
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||
QY 901 CAAGGATGACAAAGACTGATTTGAAGGAAAGGGGTGAAAGTGGAAACAGACCTTT 960
Db |||
QY 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAAATGATGATATGGAACTACATTTGGT 1020
Db |||
QY 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAAATGATGATATGGAACTACATTTGGT 1020
Db |||
QY 1021 GGCCTCCAAAGCTGGGCGCACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCGCGT 1080
Db |||
QY 1021 GGCCTCCAAAGCTGGGCGCACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCGCGT 1080
Db |||
QY 1081 CAGCGAGTGAAGCAACCGGACGTCGAGAGGGGAGGCTGGCTGCTGCTCTCTCTTCT 1140
Db |||
QY 1081 CAGCGAGTGAAGCAACCGGACGTCGAGAGGGGAGGCTGGCTGCTGCTCTCTCTTCT 1140
Db |||
QY 1141 GGTCTTGCACCTGCTTCTCAATTTTGTGATGTCAGTGCCTCTCCACCGGGGAAGGCT 1200
Db |||
QY 1141 GGTCTTGCACCTGCTTCTCAATTTTGTGATGTCAGTGCCTCTCCACCGGGGAAGGCT 1200
Db |||
QY 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
Db |||
QY 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
Db |||
QY 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAC 1320
Db |||
QY 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAC 1320
Db |||
QY 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAATTTGAAATTCGCTTGCAGATA 1380
Db |||
QY 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAATTTGAAATTCGCTTGCAGATA 1380
Db |||
QY 1381 TTTAGGTACAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCGGCTTGA 1440
Db |||
QY 1381 TTTAGGTACAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCGGCTTGA 1440
Db |||
QY 1441 CCCACTGCAAGTGCATCTGTCAACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCCTC 1500
Db |||
QY 1441 CCCACTGCAAGTGCATCTGTCAACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCCTC 1500
Db |||
QY 1501 TCTGCCACACAGAGTGGCCCACTGTGGAACATTTCTGGAGTGGCCATCCCAATTCATCA 1560
Db |||
QY 1501 TCTGCCACACAGAGTGGCCCACTGTGGAACATTTCTGGAGTGGCCATCCCAATTCATCA 1560
Db |||
QY 1561 GTCCATAGAGACGAAACAGAAATGAGACCTTCCGCGCCCAAGCGTGGCGCTCGGGGCACTTTG 1620
Db |||
QY 1561 GTCCATAGAGACGAAACAGAAATGAGACCTTCCGCGCCCAAGCGTGGCGCTCGGGGCACTTTG 1620
Db |||
QY 1621 GTAGACTGTGCCACCGGCGTGTGTGAAACGTGAAATTAAGAGAGCAAAAAA 1679
Db |||
QY 1621 GTAGACTGTGCCACCGGCGTGTGTGAAACGTGAAATTAAGAGAGCAAAAAA 1679
Db |||

RESULT 23

ACA66437

ID ACA66437 standard; cDNA; 1679 BP.

XX AC ACA66437;
XX DT 24-JUN-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane protein PRO337.
XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW leukemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW infertility; premature aging; psoriasis; inflammatory disease;
KW renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW hepatitis; multiple sclerosis; gene therapy.
XX OS Homo sapiens.
XX PN US2003004102-A1.
XX PD 02-JAN-2003.
XX PF 15-OCT-2001; 2001US-00978189.
XX PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078888P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.

05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US000365.
18-FEB-2000; 2000WO-US000434.
24-FEB-2000; 2000WO-US000504.
01-MAR-2000; 2000WO-US000560.
02-MAR-2000; 2000WO-US000584.
10-MAR-2000; 2000WO-US000631.
21-MAR-2000; 2000WO-US000753.
30-MAR-2000; 2000WO-US000843.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US030873.
27-NOV-2000; 2000US-00723749.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US0006520.
22-MAR-2001; 2001US-00816744.
22-MAR-2001; 2001US-00816920.
22-MAR-2001; 2001WO-US009552.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001WO-US021855.
(GETH) GENENTECH INC.
PA
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
DR WPI; 2003-341189/32.
DR P-PSDB; ABU80428.
XX
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
XX
PS Claim 2; Fig 221; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence encodes a PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60
DB 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60
QY 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCACAAATCTCTTCTGGGCAAT 180
DB 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCACAAATCTCTTCTGGGCAAT 180
QY 181 CTTCAAGGGCTGGCTCTCTGTCTCTTCTTCCAGGAGTGCCTGCGGCGAGGATGC 240
DB 181 CTTCAAGGGCTGGCTCTCTGTCTCTTCTTCCAGGAGTGCCTGCGGCGAGGATGC 240
QY 241 CACCTTCCCAAGCTATGACAAACGTGACGCTCCGGAGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGACAAACGTGACGCTCCGGAGGGGAGAGCGCCACCTCAG 300
QY 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTTAAACCGCAGACCATCTCTTA 360
DB 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTTAAACCGCAGACCATCTCTTA 360
QY 361 TGTGGGAATGACAAAGTGGTGGTCTTGGATCTCTGGGTGGTCTTCTTGAGCAACCCCAAC 420
DB 361 TGTGGGAATGACAAAGTGGTGGTCTTGGATCTCTGGGTGGTCTTCTTGAGCAACCCCAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTC 480
QY 481 GGTGACAGACAGCAACCAACCAACCAACCAACCTTAGGGTCCACTTGTGCAAGTATCTCC 540
DB 481 GGTGACAGACAGCAACCAACCAACCAACCAACCTTAGGGTCCACTTGTGCAAGTATCTCC 540
QY 541 CAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTTCAC 600
DB 541 CAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTTCAC 600
QY 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTACTTGGAGACATCTCTCCCAAGC 660
DB 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTACTTGGAGACATCTCTCTCCCAAGC 660
QY 661 GGTGGCTTTGTGAGTGAAGCAAGAAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
DB 661 GGTGGCTTTGTGAGTGAAGCAAGAAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTAGAGTGCAGTGCTCTCCAAATGACGTGGCGCGCCCGTGTGAGGAGATGAA 780
DB 721 AGGGGACTAGAGTGCAGTGCTCTCCAAATGACGTGGCGCGCCCGTGTGAGGAGATGAA 780

Db 721 AGGGGACTACGAGTGCAGTCCCAATGACGTGGCGCCGCTGGTACGAGAGTAA 780
QY 781 GGTACCGTGAATCTCACCATACATTTTCAGAAAGCAAGGTGACAGGTGTCCCGTGGG 840
Db 781 GGTACCGTGAATCTCACCATACATTTTCAGAAAGCAAGGTGACAGGTGTCCCGTGGG 840
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db 841 ACAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
QY 901 CAAAGATGACAAAGAACTGATTTCAAGGAAAGAAAGGGGTGAAAGTGAAGAAAGACCTTT 960
Db 901 CAAAGATGACAAAGAACTGATTTCAAGGAAAGAAAGGGGTGAAAGTGAAGAAAGACCTTT 960
QY 961 CTTCTCAAACTCATCTTCTTCAATGCTCTGAACATGACTATGGAACCTACACTTGGCT 1020
Db 961 CTTCTCAAACTCATCTTCTTCAATGCTCTGAACATGACTATGGAACCTACACTTGGCT 1020
QY 1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGCGAGGTGAGCAACGCGCAGCTCGAGGAGGGCAGGCTGCTGCTGCTCTTCT 1140
Db 1081 CAGCGAGGTGAGCAACGCGCAGCTCGAGGAGGGCAGGCTGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGACCTGCTTCTCAAAATTTTGTATGATGCTGATGCTCCACCGGGAAAGGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAAAATTTTGTATGATGCTGATGCTCCACCGGGAAAGGCT 1200
QY 1201 GCGGCCACCAACCAACCAACCAAGCAATGGCAACCGCAGCAACCAATCAGATA 1260
Db 1201 GCGGCCACCAACCAACCAACCAAGCAATGGCAACCGCAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAAC 1320
Db 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAAC 1320
QY 1321 AAAGATATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTCGAAATTCGCTTGCAGATA 1380
Db 1321 AAAGATATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTCGAAATTCGCTTGCAGATA 1380
QY 1381 TTTAGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCGCGCTTGA 1440
Db 1381 TTTAGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCGCGCTTGA 1440
QY 1441 CCCACTGCAAGTGCATCTGCAACCTCTTTGGTGCAGTGTGGCAAGGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGTGCATCTGCAACCTCTTTGGTGCAGTGTGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCCCAAGTGCCTCCCACTGCAATCTTGGAGCTGGCCATCCCAAAATTCATCA 1560
Db 1501 TCTGCCCAAGTGCCTCCCACTGCAATCTTGGAGCTGGCCATCCCAAAATTCATCA 1560
QY 1561 GTCCATAGAGACGAACAGAAATGAGACTTCCCGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACAGAAATGAGACTTCCCGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACCGCGTGTGTGAAACGTGAAATATAAGAGACCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACCGCGTGTGTGAAACGTGAAATATAAGAGACCAAAAAA 1679

RESULT 24

ID ACA68559 standard; cDNA; 1679 BP.

XX AC ACA68559;

XX 25-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

Human; secreted and transmembrane protein; PRO; cardiant; cytotstatic; antiangiogenic; hypotensive; vulnery; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.

US2003088063-A1.

XX 08-MAY-2003.

XX 12-AUG-2002; 2002US-00219003.

XX 25-JUL-2000; 2000US-0220664P.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX P-PSDB; ABU82110.

DR WPI; 2003-393229/37.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 2; Fig 125; 314pp; English.

XX The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACAGCTTGAGCAACAC 60

Db 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACAGCTTGAGCAACAC 60

QY 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

Db 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT 180

Db 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT 180

QY 181 CTTTCACGGGGCTGGCTGCTGTGTCTTCCAGAGTGCCTGCGGCGGAGATGC 240

Db 181 CTTTCACGGGGCTGGCTGCTGTGTCTTCCAGAGTGCCTGCGGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGGACACAGTCCGTCGGGAGGGGAGAGCGCCACCTCAG 300

PR 05-OCT-1999; 99WO-US0231089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-0074259.
 PR 28-FEB-2001; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.

XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2003-331925/31.
 DR P-PSDB; AB067033.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX
 PS Claim 2; Fig 375; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
 CC comprises the full-length coding sequence of the DNA deposited under
 CC American Type Culture Collection (ATCC) accession number in a list given
 CC in the specification. Also included are vectors and host cells for
 CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
 CC extracellular domains and mature sequences, methods of detecting PRO
 CC proteins, methods for stimulating the release of TNF-alpha (tumour
 CC necrosis factor alpha) from human blood, (and the proliferation of
 CC differentiation of chondrocyte cells, the proliferation of, or gene
 CC expression in pericyte cells, the release or proteoglycans from
 CC cartilage, proliferation of inner ear utricular supporting cells, the
 CC proliferation of T-lymphocyte cells, the release of a cytokine from
 CC peripheral blood mononuclear cells (PBMC), or the proliferation of
 CC endothelial cells), a method for modulating the uptake of glucose or free
 CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
 CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
 CC cells, a method for detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, AIDS (acquired
 CC immunodeficiency syndrome), cancer, or diabetic complications. The
 CC nucleic acids are useful as hybridisation probes, in chromosome and gene
 CC mapping, and in generating antisense RNA or DNA. The polypeptides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
 CC are useful in tissue typing. The present sequence encodes a PRO protein
 CC of the invention
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCAGCAAGCTTGAGGCAACAC 60
 Db 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCAGCAAGCTTGAGGCAACAC 60
 QY 61 AATCTATCAGGAAGAAGAAAGAAAAAACCAGAACCTGCACAAAAAGAGAAAAAGAG 120
 Db 61 AATCTATCAGGAAGAAGAAAGAAAAAACCAGAACCTGCACAAAAAGAGAAAAAGAG 120
 QY 121 AAGAAAAAAATCATGAAAAATCCAGCCAAATGACAAATCTCTCTTGGGCAAT 180
 Db 121 AAGAAAAAAATCATGAAAAATCCAGCCAAATGACAAATCTCTCTTGGGCAAT 180
 QY 181 CTTACGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGC 240
 Db 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGC 240
 QY 241 CACCTTCCCAAGCTATGGAACAAGTCGGTCGGCAGGGGGAGAGCGCCACCTCAG 300
 Db 241 CACCTTCCCAAGCTATGGAACAAGTCGGTCGGCAGGGGGAGAGCGCCACCTCAG 300

PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-JUN-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Baton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341960/32.
DR P-PSDB; ABU79804.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 2; Fig 51; 255pp; English.
XX
CC The invention relates to an isolated, secreted/transmembrane polypeptide,
CC termed PRO polypeptide, having at least 80% sequence identity to a
CC sequence selected from any one of the 37 sequences appearing as ABU79779
CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
CC under any one of the ATCC numbers given in the specification. Also
CC included are an isolated nucleic acid molecule having at least 80%
CC sequence identity to a sequence selected from any one of the 37 cDNA
CC sequences defined in the specification (or encoding the mature PRO
CC protein or a PRO protein extracellular domain), a PRO expression vector,
CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
CC antibodies and a method for linking a bioactive molecule to a cell
CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,

CC radiolabel or an antibody and causes the death of the cell. PRO or the
CC antibody is useful for modulating at least one biological activity of
CC cell expressing the above polypeptides. PRO is useful for identifying
CC agonists or antagonists of PRO, for preparing a variant of PRO, as
CC molecular weight markers for protein electrophoresis purpose and PRO
CC nucleic acid is useful for recombinantly expressing those markers. PRO is
CC also useful as therapeutic agent. PRO is useful in assays to identify
CC other proteins or molecules involved in binding interaction. PRO nucleic
CC acid is useful as hybridisation probes, in chromosome and gene mapping,
CC in generation of antisense RNA and DNA, in the preparation of PRO
CC polypeptide, in gene therapy, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes the PRO and for the genetic
CC analysis of individuals with genetic disorders, for chromosome
CC identification, as a chromosome marker, and for generating probes for
CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
CC Western analysis. The antibody is useful in diagnostic assays for PRO,
CC e.g. detecting its expression in specific cells, tissues or serum, for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. PRO or Ab is useful for the preparation of medicament for
CC treating conditions which is responsive to the PRO polypeptide or anti-
CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
CC present sequence encodes a PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTTCGACAACTTGAGAGCAAC 60
DB 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTTCGACAACTTGAGAGCAAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180
DB 121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180
QY 181 CTTTCAGGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGC 240
DB 181 CTTTCAGGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGC 240
QY 241 CACCTTCCCAAGCTATGGACAAAGTACGCTCGGAGGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGGACAAAGTACGCTCGGAGGGGGAGAGCGCCACCTCAG 300
QY 301 GTGCACTATTGCAACCCGGGTCCACCCGGGTGGCTGCTTAAACCGCAGCACCCTCTTA 360
DB 301 GTGCACTATTGCAACCCGGGTCCACCCGGGTGGCTGCTTAAACCGCAGCACCCTCTTA 360
QY 361 TGCTGGGATGACAAAGTGGTGGTCTGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 TGCTGGGATGACAAAGTGGTGGTCTGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GCAGTACAGCATTCAGAGATCCAGAACGTGTGTATGATGATGATGATGATGATGATGATGAT 480
DB 421 GCAGTACAGCATTCAGAGATCCAGAACGTGTGTATGATGATGATGATGATGATGATGATGAT 480
QY 481 GGTGAGACAGACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
DB 481 GGTGAGACAGACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
QY 541 CAAATTTCTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCAC 600
DB 541 CAAATTTCTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCAC 600
QY 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTACTTCTTGGAGACACATCTCTCCCAAGC 660
DB 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTACTTCTTGGAGACACATCTCTCCCAAGC 660

Db	601	CTGCATAGCAACTGGTAGACACGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660	ID	ADA45894 standard; cDNA; 1679 BP.
Qy	661	GGTTGGCTTTGTGAGTGAAGACGAACTACTTGGAAATTCAGGGCATCAACCCGGGAGCAGTC	720	XX	
Db	661	GGTTGGCTTTGTGAGTGAAGACGAACTACTTGGAAATTCAGGGCATCAACCCGGGAGCAGTC	720	XX	ADA45894;
Qy	721	AGGGGACTACAGAGTGCAGTGCCTCAATGAGCTGCGCGCCGCTGGTACCGAGAGTAAA	780	DT	20-NOV-2003 (first entry)
Db	721	AGGGGACTACAGAGTGCAGTGCCTCAATGAGCTGCGCGCCGCTGGTACCGAGAGTAAA	780	XX	Novel human secreted and transmembrane protein PRO337 cDNA.
Qy	781	GGTCAACCGTGAATTCACCATATCATTTCAGAAAGCCAAAGGTTCAGGTGTCCTCCGCTGGG	840	XX	Human; secreted and transmembrane protein; PRO; gene; ss;
Db	781	GGTCAACCGTGAATTCACCATATCATTTCAGAAAGCCAAAGGTTCAGGTGTCCTCCGCTGGG	840	KW	Tumour necrosis factor alpha release; TNF-alpha release;
Qy	841	ACAAAGGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900	KW	glucose uptake modulator; FFA uptake modulator;
Db	841	ACAAAGGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900	KW	cell proliferation stimulator; cell differentiation stimulator;
Qy	901	CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACACAGACCTTT	960	KW	cell differentiation inhibitor; cytokine release stimulator;
Db	901	CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACACAGACCTTT	960	KW	lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
Qy	961	CCTCTCAAACTCATCTTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGCT	1020	KW	cervical tumour; liver tumour; chromosome mapping; gene mapping;
Db	961	CCTCTCAAACTCATCTTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGCT	1020	XX	gene therapy; chromosome identification; chromosome marker.
Qy	1021	GGCTTCCCAAGCTGGGCGCACCAATGCCAGCATCATGCTATTGCTCAGGGGCGGT	1080	OS	Homo sapiens.
Db	1021	GGCTTCCCAAGCTGGGCGCACCAATGCCAGCATCATGCTATTGCTCAGGGGCGGT	1080	XX	US2003022328-A1.
Qy	1081	CAGCGAGTGAGCAACGCGCAGCTCAGGAGGCGAGGCTCGCTCTGGCTGCTGCTCTTCT	1140	PD	30-JAN-2003.
Db	1081	CAGCGAGTGAGCAACGCGCAGCTCAGGAGGCGAGGCTCGCTCTGGCTGCTGCTCTTCT	1140	XX	16-APR-2002; 2002US-00123904.
Qy	1141	GGTCTTGCACTGCTTCTCAATTTTGAATGTGAGTGCCACTTCCCGGAAAGGCT	1200	XX	31-MAR-1997; 97WO-US005230.
Db	1141	GGTCTTGCACTGCTTCTCAATTTTGAATGTGAGTGCCACTTCCCGGAAAGGCT	1200	PR	12-JUN-1998; 98WO-US012456.
Qy	1201	GCCGCCACCCACCCACCAACACACACACGATGGCAACACGACGACGACCAATCAGATA	1260	PR	14-JUL-1998; 98WO-US014552.
Db	1201	GCCGCCACCCACCCACCAACACACACACGATGGCAACACGACGACGACCAATCAGATA	1260	PR	28-AUG-1998; 98WO-US017888.
Qy	1261	TATACAAATGAAATTTAGAAGAAACACACGCTCATGGGACAGAAATTTGAGGGGGAAC	1320	PR	10-SEP-1998; 98WO-US018824.
Db	1261	TATACAAATGAAATTTAGAAGAAACACACGCTCATGGGACAGAAATTTGAGGGGGAAC	1320	PR	14-SEP-1998; 98WO-US019093.
Qy	1321	AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCTTGCAGATA	1380	PR	14-SEP-1998; 98WO-US019094.
Db	1321	AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCTTGCAGATA	1380	PR	14-SEP-1998; 98WO-US019177.
Qy	1381	TTTAGGTACAATGGAGTTTCTTTTCCCAACGGGGAAGAACACACGACACACCCGCTTGGGA	1440	PR	16-SEP-1998; 98WO-US019330.
Db	1381	TTTAGGTACAATGGAGTTTCTTTTCCCAACGGGGAAGAACACACGACACACCCGCTTGGGA	1440	PR	17-SEP-1998; 98WO-US019437.
Qy	1441	CCCAGTCAAGTGCATCGTCAACCTTTTGGTSCCAGTGTGGGCAAGGCTCAGCCTC	1500	PR	07-OCT-1998; 98WO-US021141.
Db	1441	CCCAGTCAAGTGCATCGTCAACCTTTTGGTSCCAGTGTGGGCAAGGCTCAGCCTC	1500	PR	29-OCT-1998; 98WO-US022991.
Qy	1501	TCTGCCACAGTGTGCCCGCCAGTGGACATCTGGAGTGGCCATCCCAATTCATCA	1560	PR	29-OCT-1998; 98WO-US022992.
Db	1501	TCTGCCACAGTGTGCCCGCCAGTGGACATCTGGAGTGGCCATCCCAATTCATCA	1560	PR	01-DEC-1998; 98WO-US024855.
Qy	1561	GTCCATAGACGACAAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGCGGCACTTTG	1620	PR	01-DEC-1998; 98WO-US025108.
Db	1561	GTCCATAGACGACAAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGCGGCACTTTG	1620	PR	05-JAN-1999; 99WO-US000106.
Qy	1621	GTAGACTGTGCCACACCGCGTGTGTGTGAACCTGTGAATTAATAAGAGCAAAAAA	1679	PR	08-MAR-1999; 99WO-US005028.
Db	1621	GTAGACTGTGCCACACCGCGTGTGTGTGAACCTGTGAATTAATAAGAGCAAAAAA	1679	PR	10-MAR-1999; 99WO-US005190.

PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 22-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023528.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00815744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00865028.
 PR 25-MAY-2001; 2001US-00865034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-584997/55.
 DR P-PSDB; ADA45895.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 2; Fig 375; 659pp; English.
 XX
 CC The invention describes 305 nucleic acids encoding PRO (secreted and
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the
 CC release of TNF-alpha from human blood, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating the proliferation or differentiation of chondrocyte cells,
 CC for stimulating the proliferation of or gene expression in pericyte

CC cells, for stimulating the release of proteoglycans from cartilage, for
 CC stimulating the proliferation of inner ear utricular supporting cells,
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
 CC the release of a cytokine from PBMC cells, for inhibiting the binding of
 CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
 CC cells, for stimulating proliferation of endothelial cells, for detecting
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 CC are useful for isolating genomic and cDNA nucleotide sequences or
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 CC in assays to identify other proteins or molecules involved in binding
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 CC and gene mapping, in generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptide, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, in gene therapy, for
 CC chromosome identification, as chromosome marker, and for generating
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
 CC a novel human secreted and transmembrane PRO polypeptide.
 XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCACAACTTGAGAGCAACAC 60
 DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCAGCAAGCTTGAGAGCAACAC 60
 QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 QY 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATTCCTCTCTTGGCAAT 180
 DB 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATTCCTCTCTTGGCAAT 180
 QY 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGC 240
 DB 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGC 240
 QY 241 CACCTTCCCAAGCTATGGAACAGTGCCTGCGCAGCGGGGAGAGCCCACTTCAG 300
 DB 241 CACCTTCCCAAGCTATGGAACAGTGCCTGCGCAGCGGGGAGAGCCCACTTCAG 300
 QY 301 GTGCACATATTGACAAACCGGGTCACCCGGTGGCTTAAACCGCAGCACCCTCTCTA 360
 DB 301 GTGCACATATTGACAAACCGGGTCACCCGGTGGCTTAAACCGCAGCACCCTCTCTA 360
 QY 361 TGCTGGGAATGCAAGTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 TGCTGGGAATGCAAGTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACCTGCTC 480
 DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACCTGCTC 480
 QY 481 GGTGCAGACAGCAACACCCAGCAAGCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
 DB 481 GGTGCAGACAGCAACACCCAGCAAGCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
 QY 541 CAAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCAC 600
 DB 541 CAAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCAC 600
 QY 601 CTGCATAGCAACTGGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCCAAGC 660

QY 661 GTTGGCTTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGSCATCACCCGGGAGCAGTC 720
Db 661 GTTGGCTTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGSCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTACAGTGCAGTGCCTCAATGACGTGGCCCGGCCCGGTGACGGAGAGTAAA 780
Db 721 AGGGGACTACAGTGCAGTGCCTCAATGACGTGGCCCGGCCCGGTGACGGAGAGTAAA 780
QY 781 GGTCAACCGTGAATATCCACCATATCTTCAGAGCCCAAGGTGACAGTGTCCCGGTGG 840
Db 781 GGTCAACCGTGAATATCCACCATATCTTCAGAGCCCAAGGTGACAGTGTCCCGGTGG 840
QY 841 ACAAAGGGGACACTGCACTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGA 900
Db 841 ACAAAGGGGACACTGCACTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGA 900
QY 901 CAAGATGACAAAGAGACTGATGAGGAGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGATGACAAAGAGACTGATGAGGAGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
QY 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAATGCTCTGAACATGACTATGGAACTACACTTGGT 1020
Db 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGT 1020
QY 1021 GGCTTCCAAAGCTGGGCCACACCAATGCGAGCATATGCTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCTTCCAAAGCTGGGCCACACCAATGCGAGCATATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGGAGGTGAGCAACGCGCAGTGCAGGAGGCGAGGCTGCTGGCTGCTGCTCTTCT 1140
Db 1081 CAGGAGGTGAGCAACGCGCAGTGCAGGAGGCGAGGCTGCTGGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGCACCTGCTTCTCAATTTTGAATGTGAGTGCCACTTCCGCCACCCGGGAAAGGCT 1200
Db 1141 GGTCTTGCACCTGCTTCTCAATTTTGAATGTGAGTGCCACTTCCGCCACCCGGGAAAGGCT 1200
QY 1201 GCCGCCACCCACCAACCAACAGCAAGATGCGAACACCGACAGCAACCAATCAGATA 1260
Db 1201 GCCGCCACCCACCAACCAACAGCAAGATGCGAACACCGACAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAATTAGAAGAAACACAGCCTCTATGGGACAGAAATTTGAGGGGGGGAAC 1320
Db 1261 TATACAAATGAATTAGAAGAAACACAGCCTCTATGGGACAGAAATTTGAGGGGGGGAAC 1320
QY 1321 AAGAATACCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
Db 1321 AAGAATACCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
QY 1381 TTTAGGTACATGAGTGTCTTTTCCCAACCGGAGAGAACACAGCAGACACCCGGCTTGA 1440
Db 1381 TTTAGGTACATGAGTGTCTTTTCCCAACCGGAGAGAACACAGCAGACACCCGGCTTGA 1440
QY 1441 CCCACTGCAAGCTGCATGTCGCACTCTTTGGTGGCCAGTGTGGCAAGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGCTGCATGTCGCACTCTTTGGTGGCCAGTGTGGCAAGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTGCCTCCCAAGTGGCAATTTTGGAGCTGGCCATCCCAATTTCAATCA 1560
Db 1501 TCTGCCACAGAGTGCCTCCCAAGTGGCAATTTTGGAGCTGGCCATCCCAATTTCAATCA 1560
QY 1561 GTCCATAGACAGCAAGATGAGACCTTCGGCCCAAGCGTGGCGCTGGGGCACTTTG 1620
Db 1561 GTCCATAGACAGCAAGATGAGACCTTCGGCCCAAGCGTGGCGCTGGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCGCGGTGTGTGTGAACCTGAAATTAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCGCGGTGTGTGTGAACCTGAAATTAAGAGCAAAAAA 1679

RESULT 28
ADA76325
ID ADA76325 standard; cDNA; 1679 BP.
XX

AC ADA76325;
XX 20-NOV-2003 (first entry)
XX Human PRO polynucleotide #188.
XX Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.
XX Homo sapiens.
XX US2003073212-A1.
XX 17-APR-2003.
XX 16-APR-2002; 2002US-00123903.
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 29-OCT-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 23-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 22-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 2000WO-US000219.
XX 05-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004414.
XX 22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005074.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013709.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001US-00806520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00870792.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00896992.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001US-00892116.
PR 29-JUN-2001; 2001US-00902106.
PR 09-JUL-2001; 2001US-00902173.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PA (GETH) GENENTECH INC.
XX
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski P, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-687639/65.
DR P-PSDB; ADA76326.
XX
XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX
XX
PS Claim 2; Fig 375; 659pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for

CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC the proliferation of or gene expression in pericyte cells, for stimulating
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	100.0%;	Score 1679;	DB 8;	Length 1679;
	Matches 1679;	Conservative	0;	Mismatches	0;	Gaps
QY	1	GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCTTGTGCACAAAGCTTGAGAGCAAC	60			
DB	1	GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCTTGTGCACAAAGCTTGAGAGCAAC	60			
QY	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120			
DB	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120			
QY	121	AAGAAAAAAATCATGAAAAACCATCCAGCCAAATAATGCAAAATTTCTCTCTTGGGCAAT	180			
DB	121	AAGAAAAAAATCATGAAAAACCATCCAGCCAAATAATGCAAAATTTCTCTCTTGGGCAAT	180			
QY	181	CTTACGGGGCTGGCTGTCTGTGTCTTTCAGAGAGTGCCCGTGGCAGGAGATGC	240			
DB	181	CTTACGGGGCTGGCTGTCTGTGTCTTTCAGAGAGTGCCCGTGGCAGGAGATGC	240			
QY	241	CACCTTCCCAAAGCTATGGACAAAGTACGTCAGTCGGCAGGGGAGAGCGCCACCTCAG	300			
DB	241	CACCTTCCCAAAGCTATGGACAAAGTACGTCAGTCGGCAGGGGAGAGCGCCACCTCAG	300			
QY	301	GTGCATATTGACAAACCGGGTCACCCGGTGGCTGGCTGCTTAAACCGCAGCACCATCTCTA	360			
DB	301	GTGCATATTGACAAACCGGGTCACCCGGTGGCTGGCTGCTTAAACCGCAGCACCATCTCTA	360			
QY	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTTCGGTGGTCTCTCTGAGCAACACCAAC	420			
DB	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTTCGGTGGTCTCTCTGAGCAACACCAAC	420			
QY	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC	480			
DB	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC	480			
QY	481	GGTGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540			
DB	481	GGTGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540			
QY	541	CAAAATTGTAGAGATTTCTTCCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCAC	600			
DB	541	CAAAATTGTAGAGATTTCTTCCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCAC	600			

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QY 601 CTGCATAGCAACTGCTAGACACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGCATAGCAACTGCTAGACACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
QY 661 GGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCAGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCAGGAGCAGTC 720
QY 721 AGGGGACTACGAGTGCAGTGCTCAATGAGTGGCGCGCGCTGTGTACGGAGAGTAAA 780
Db 721 AGGGGACTACGAGTGCAGTGCTCAATGAGTGGCGCGCGCTGTGTGTACGGAGAGTAAA 780
QY 781 GGTCAACCGTGAATTCACCATATCAATTTCAAGAACCAAGGGTACAGGTGTCCCGTGGG 840
Db 781 GGTCAACCGTGAATTCACCATATCAATTTCAAGAACCAAGGGTACAGGTGTCCCGTGGG 840
QY 841 ACAAAAGGGGACCTGAGTGTGAAGCTCAGAGTCCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGA 900
Db 841 ACAAAAGGGGACCTGAGTGTGAAGCTCAGAGTCCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGA 900
QY 901 CAAGGATCACAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGGATCACAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
QY 961 CCTCTCAAAATCTCTTCTTCAATGCTCTGAACTGACTATGGGAACTACACTTGGCT 1020
Db 961 CCTCTCAAAATCTCTTCTTCAATGCTCTGAACTGACTATGGGAACTACACTTGGCT 1020
QY 1021 GGCTTCCAAAGCTGGGCAACACCAATGCGAGCATCATGCTATTGGTCAGGCGCGT 1080
Db 1021 GGCTTCCAAAGCTGGGCAACACCAATGCGAGCATCATGCTATTGGTCAGGCGCGT 1080
QY 1081 CAGCGAGTGTAGCAACGCGCAGTGTGAGGAGGCGAGGCTGCTGCGTGTGCTCTTCT 1140
Db 1081 CAGCGAGTGTAGCAACGCGCAGTGTGAGGAGGCGAGGCTGCTGCGTGTGCTCTTCT 1140
QY 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCGGGAAGGCT 1200
Db 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCGGGAAGGCT 1200
QY 1201 GCGCCACCAACCCACCAACACACAGCAATGCAACGACAGCAACCAATCAGATA 1260
Db 1201 GCGCCACCAACCCACCAACACACAGCAATGCAACGACAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAAATTTAGAGAAACACACAGCCTCATGGGACAGAAATTTGAGGGGGGAAAC 1320
Db 1261 TATACAAATGAAATTTAGAGAAACACACAGCCTCATGGGACAGAAATTTGAGGGGGGAAAC 1320
QY 1321 AAAGAATACTTTGGGGGAAAGAGTTTAAAGAAATTTGAAATTTGCTTTGCAGATA 1380
Db 1321 AAAGAATACTTTGGGGGAAAGAGTTTAAAGAAATTTGAAATTTGCTTTGCAGATA 1380
QY 1381 TTTAGGTACAAATGAGTTTCTTTTCCCAACGCGGAGAGACACAGCACCCCGCTTGA 1440
Db 1381 TTTAGGTACAAATGAGTTTCTTTTCCCAACGCGGAGAGACACAGCACCCCGCTTGA 1440
QY 1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTTGTGTCAGTGTGGGCAAGGCTCAGGCTC 1500
Db 1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTTGTGTCAGTGTGGGCAAGGCTCAGGCTC 1500
QY 1501 TCTGCCACAGAGTGCCTCCCAAGTGGAAATTTCTGAGCTGGCCATCCCAAAATCAATCA 1560
Db 1501 TCTGCCACAGAGTGCCTCCCAAGTGGAAATTTCTGAGCTGGCCATCCCAAAATCAATCA 1560
QY 1561 GTCCATAGACGCAACAGATGAGACCTTCCGCGCCCAAGCGTGGCGTGGGCACTTTG 1620
Db 1561 GTCCATAGACGCAACAGATGAGACCTTCCGCGCCCAAGCGTGGCGTGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCGCGTGTGTTGTGAACAGTGAATTAAGAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCGCGTGTGTTGTGAACAGTGAATTAAGAGAGCAAAAAA 1679
```

RESULT 29

ABT44288
ID ABT44288 standard; cDNA; 1679 BP.

XX AC ABT44288;

DT 06-NOV-2003 (first entry)

XX Human PRO337 cDNA.

DE XX PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; ss;
KW differentiation; dermal fibroblast; tumour; gene therapy; gene;
KW cytosstatic.

OS Homo sapiens.

XX US2003050448-A1.

XX 13-MAR-2003.

XX 28-AUG-2002; 2002US-00230414.

XX 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-521818/49.

DR P-PSDB; ABU72290.

XX New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.

PS Claim 2; Fig 125; 315pp; English.

XX The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, the stimulation of human dermal fibroblast cell
CC proliferation and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
CC cDNA of the invention

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 8; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTCTCTTCAGCAAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60

Db 1 GTTGTCTCTTCAGCAAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60

QY 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGCACAAAAGAAAGAAAG 120

Db 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGCACAAAAGAAAGAAAG 120

QY 121 AAGAAAAAAATCATGAAACCATCCAGCCAAATTCGCAATTTCTCTTTGGCAAT 180

Db 121 AAGAAAAAAATCATGAAACCATCCAGCCAAATTCGCAATTTCTCTTTGGCAAT 180

QY 181 CTTACGGGGCTGGCTGCTCTGTGTCTTCCAAGGAGTGCCCGTGGCGAGATGC 240


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PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US030095.
PR 16-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006894.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US0796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001WO-US0082706.
PR 14-MAR-2001; 2001WO-US008689.
PR 22-MAR-2001; 2001WO-US016744.
PR 05-APR-2001; 2001WO-US028366.
PR 10-MAY-2001; 2001WO-US0854208.
PR 18-MAY-2001; 2001WO-US0854280.
PR 18-MAY-2001; 2001WO-US0860216.
PR 25-MAY-2001; 2001WO-US086028.
PR 25-MAY-2001; 2001WO-US0866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US0872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001WO-US0874503.
PR 14-JUN-2001; 2001WO-US0882636.
PR 19-JUN-2001; 2001WO-US0886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001WO-US0887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PR PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-521854/49.
XX P-PSDB; ADA18976.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
XX e.g., tumors.
XX
XX Claim 2; Fig 375; 660pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
XX prostate, rectal, cervical and liver tumours). The polynucleotides are
XX useful in molecular biology, including uses as hybridisation probes, in
XX chromosome and gene mapping, in generating antisense RNA and DNA and in
XX gene therapy. The polynucleotides may also be used in preparing PRO
XX polypeptides by recombinant techniques and in generating either
XX transgenic animals or knock-out animals which are useful in the
XX development and screening of therapeutically useful reagents. The PRO
XX polypeptides or antibodies are used in preparing a medicament for
XX treating a condition responsive to the polypeptides or antibodies, such
XX as tumours, for modulating the uptake of glucose or FFA by adipocyte
XX cells, for stimulating the proliferation of or gene expression in
XX pericyte cells, for stimulating the release of proteoglycans from
XX cartilage, for stimulating the proliferation of inner ear utricular
XX supporting cells, for stimulating the release of cytokines from PBMC
XX cells, for inhibiting the binding of A-peptide to factor VIIA, for
XX inhibiting the differentiation of adipocyte cells and for stimulating the
XX proliferation of endothelial cells. This sequence represents a human PRO
XX polynucleotide of the invention. Note: The sequence data for this patent
XX is also available in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCACCAAGTTGAGAGCAAC 60
|
Db 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCAGCAAGTTGAGAGCAAC 60
|
Qy 61 AATCTATCAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
|
Db 61 AATCTATCAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
|
Qy 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCACAAATCTATCTCTTGGGCAAT 180
|
Db 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCACAAATCTATCTCTTGGGCAAT 180
|
Qy 181 CTTCAAGGGGTGGTCTCTGTGTCTCTTTCAGAGAGTGCCTGCGCAGGAGATGC 240
|
Db 181 CTTCAAGGGGTGGTCTCTGTGTCTCTTTCAGAGAGTGCCTGCGCAGGAGATGC 240
|
Qy 241 CACCTTCCCAAGACTATGACACGTCGACGTCGAGGTCGCGCAGGGGAGAGCCGCTCAG 300
|
Db 241 CACCTTCCCAAGACTATGACACGTCGACGTCGAGGTCGCGCAGGGGAGAGCCGCTCAG 300
|
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QY	301	GTGCACCTATTGACAAACCGGGTACCCGGGTGGCTGGCTAAACCGCAGACACCATCTCTTA	360
Db	301	GTGCACCTATTGACAAACCGGGTACCCGGGTGGCTGGCTAAACCGCAGACACCATCTCTTA	360
QY	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTCCGGTGGTCTCTTGAGCAACACCCAAAC	420
Db	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTCCGGTGGTCTCTTGAGCAACACCCAAAC	420
QY	421	GCAGTACAGCATCGAGATCGAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTC	480
Db	421	GCAGTACAGCATCGAGATCGAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTC	480
QY	481	GGTGCGACAGACAAACCCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540
Db	481	GGTGCGACAGACAAACCCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540
QY	541	CAAAATGTAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTAC	600
Db	541	CAAAATGTAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTAC	600
QY	601	CTGCATAGCAACTGGTAGACACGAGCCTACGGTTACTTTGAGACACATCTCTCCAAAGC	660
Db	601	CTGCATAGCAACTGGTAGACACGAGCCTACGGTTACTTTGAGACACATCTCTCCAAAGC	660
QY	661	GGTTGGCTTTGTGAGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC	720
Db	661	GGTTGGCTTTGTGAGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC	720
QY	721	AGGGGATAGAGTGCAGTGCCTCCAAATGACGTGGCGGCCCGTGGTACGGAGAGTAAA	780
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QY	781	GGTCACCGTGAACCTATCCACATACATTTCCAAAGCCCAAGGTACAGGTGTCCCGTGGG	840
Db	781	GGTCACCGTGAACCTATCCACATACATTTCCAAAGCCCAAGGTACAGGTGTCCCGTGGG	840
QY	841	ACAAAAGGGGACACTCGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
Db	841	ACAAAAGGGGACACTCGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
QY	901	CAAGGATGACAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAAAACAGACCTTT	960
Db	901	CAAGGATGACAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAAAACAGACCTTT	960
QY	961	CCTCTCAAAACTCATCTTCTCAATCTCTCGAATGACTATGGGAACTACACTTGGCT	1020
Db	961	CCTCTCAAAACTCATCTTCTCAATCTCTCGAATGACTATGGGAACTACACTTGGCT	1020
QY	1021	GGCTCCAAAGAGTGGGCAACCAATGCCAGCATCATGCTATTTGGTCCAGGGCCGT	1080
Db	1021	GGCTCCAAAGAGTGGGCAACCAATGCCAGCATCATGCTATTTGGTCCAGGGCCGT	1080
QY	1081	CAGCGAGGTGAGCAACGCGACGTGAGGAGGGCAGGCTGGCTGGCTGGCTCTTCT	1140
Db	1081	CAGCGAGGTGAGCAACGCGACGTGAGGAGGGCAGGCTGGCTGGCTGGCTCTTCT	1140
QY	1141	GGTCTTGACCTGCTTCTCAAAATTTTGTATGTGAGTGCACATTCGCCACCCGGGAAAGGCT	1200
Db	1141	GGTCTTGACCTGCTTCTCAAAATTTTGTATGTGAGTGCACATTCGCCACCCGGGAAAGGCT	1200
QY	1201	GGCGCCACCAACCAACCAACAGCAATGGCAACCCGACAGCAACCAATCAGATA	1260
Db	1201	GGCGCCACCAACCAACCAACAGCAATGGCAACCCGACAGCAACCAATCAGATA	1260
QY	1261	TATACAAATGAATTAGAAGAACACAGCCTCATGGGACAGAAATTTAGGGAGGGGAAAC	1320
Db	1261	TATACAAATGAATTAGAAGAACACAGCCTCATGGGACAGAAATTTAGGGAGGGGAAAC	1320
QY	1321	AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTCAGAAATTCGCTTGCAGATA	1380
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Search completed: May 28, 2004, 15:50:35
Job time : 751.61 secs

QY	1381	TTTAGCTACAATGGAGCTTTTCTTTTCCCAACCGGGAAGAACACAGACACACCCGGCTTGA	1440
Db	1381	TTTAGCTACAATGGAGCTTTTCTTTTCCCAACCGGGAAGAACACAGACACACCCGGCTTGA	1440
QY	1441	CCCACTGCAAGCTGCATCGTGAACCTCTTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC	1500
Db	1441	CCCACTGCAAGCTGCATCGTGAACCTCTTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC	1500
QY	1501	TCCTGCCACAGAGTGCCTCCCACTGTGGAACATTTCTGAGCTGGCCATCCCAAAATTCATCA	1560
Db	1501	TCCTGCCACAGAGTGCCTCCCACTGTGGAACATTTCTGAGCTGGCCATCCCAAAATTCATCA	1560
QY	1561	GTCCATAGAGACGAAACAGAAATGAGACCTTCCGSCCCCAAGCGTGGCGCTGGGCACTTTG	1620
Db	1561	GTCCATAGAGACGAAACAGAAATGAGACCTTCCGSCCCCAAGCGTGGCGCTGGGCACTTTG	1620
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Result No.	Query #			DB	ID	Description
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2	1679	100.0	1679	9	US-09-978-697-522	Sequence 522, App
3	1679	100.0	1679	9	US-09-978-192A-522	Sequence 522, App
4	1679	100.0	1679	9	US-09-999-832A-522	Sequence 522, App
5	1679	100.0	1679	10	US-09-978-189-522	Sequence 522, App
6	1679	100.0	1679	10	US-09-978-608A-522	Sequence 522, App
7	1679	100.0	1679	10	US-09-978-585A-522	Sequence 522, App
8	1679	100.0	1679	10	US-09-978-191A-522	Sequence 522, App
9	1679	100.0	1679	10	US-09-978-403A-522	Sequence 522, App
10	1679	100.0	1679	10	US-09-578-56A-522	Sequence 522, App
11	1679	100.0	1679	10	US-09-999-83A-522	Sequence 522, App
12	1679	100.0	1679	10	US-09-981-915A-522	Sequence 522, App
13	1679	100.0	1679	10	US-09-978-82A-522	Sequence 522, App
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; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/085697
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7, 8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 CACCTTCCCAAGCTATGGAACAAACGTGACGGTCCCGGAGGGGAGAGCGCCCTCAG 300
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Db 301 GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTA 360
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Db 361 TGTCTGGGAATGACAAAGTGTGCTCTCGCTCTCGCTGGTCTCTTCTGAGCAACACCCAAAC 420
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Db 421 GCAGTACAGCATCGAGATCCAGAAACGTGATGTATGACAGGGGCGCTTACACCTGTCTC 480
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us-10-017-084a-522.rnpb

Tue Jun 1 09:37:49 2004

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Db	1021	GGCTCCAAAGCTGGCCACACCAATGCGCAGCATCATGCTATTTGGTCCAGGCGCCGT	1080	APPLICANT: Stewart, Timothy A.
QY	1081	CAGCGAGGTAGCAAGCGCAGCTGCGAGGAGGCGAGGCTGGCTGCTGCTCTTCT	1140	APPLICANT: Tumas, Daniel
Db	1081	CAGCGAGGTAGCAAGCGCAGCTGCGAGGAGGCGAGGCTGGCTGCTGCTCTTCT	1140	APPLICANT: Williams, P. Mickey
QY	1141	GGTCTTGACCTGCTTCAAAATTTGATGAGTGCCTTCCCAACCCCGGGAAGGCT	1200	APPLICANT: Wood, William J.
Db	1141	GGTCTTGACCTGCTTCAAAATTTGATGAGTGCCTTCCCAACCCCGGGAAGGCT	1200	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
QY	1201	GGCGCCACCCACCCACCAACACACAGCAATGCGCAGCAGCAGCAACATCAGATA	1260	FILE REFERENCE: P2630PIC27
Db	1201	GGCGCCACCCACCCACCAACACACAGCAATGCGCAGCAGCAGCAACATCAGATA	1260	CURRENT APPLICATION NUMBER: US/09/978,697
QY	1261	TATCAAAATGAATAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC	1320	CURRENT FILING DATE: 2001-10-16
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Db	1501	TCTGCCACAGAGTCCGCCAGTGGAAACATTTCTGGAGTGGCCATCCCAATTCATCA	1560	PRIOR APPLICATION NUMBER: 60/077632
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QY	1621	GTAGACTGTGCCACACGCGCTGTGTGTGAAACGTGAAATTTAAAGAGCAAAAAA	1679	PRIOR FILING DATE: 1998-03-11
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RESULT 2

US-09-978-697-522

Sequence 522, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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QY 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTATGAAGGAAACAAATATTAGCTCAC 600
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; Sequence 522, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
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7	PRIOR APPLICATION NUMBER: 60/085579
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7	PRIOR APPLICATION NUMBER: 60/085573
7	PRIOR FILING DATE: 1998-05-15
7	PRIOR APPLICATION NUMBER: 60/085704
7	PRIOR FILING DATE: 1998-05-15
7	PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 9; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7.8e-22;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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	Db								
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	Qy								120
61	AATCTATC	GGAAGA	AGAAAA	AAAA	CCGAACT	TGC	CAAAAA	AGAAAA	AGAG
	Db								120
121	AAGAAAAA	AAATCAT	GTAAAA	CCAT	TCGAC	CAAAA	AAATGC	CAAA	TCTATCTCTTGGCAAT
	Qy								180
121	AAGAAAAA	AAATCAT	GTAAAA	CCAT	TCGAC	CAAAA	AAATGC	CAAA	TCTATCTCTTGGCAAT
	Db								180

QY 181 CTTCAAGGGGCTGCTCTCTGTCTCTTCCAGAGTGCCTGCGGAGCGGATGC 240
Db 181 CTTCAAGGGGCTGCTCTCTGTCTCTTCCAGAGTGCCTGCGGAGCGGATGC 240
QY 241 CACCTTCCCAAGCTATGACAACTGACGCTGCGGAGGGGAGAGCGCCACCTTCAG 300
Db 241 CACCTTCCCAAGCTATGACAACTGACGCTGCGGAGGGGAGAGCGCCACCTTCAG 300
QY 301 GTGCACATATTGACAAACCGGGTACCCCGGGTGGCTTGGCTTAAACCGCAGCACTTCTCTA 360
Db 301 GTGCACATATTGACAAACCGGGTACCCCGGGTGGCTTAAACCGCAGCACTTCTCTA 360
QY 361 TGCTGGGAATGACAAAGTGGTCTTGGATCTCTCGGTGGTCTTCTGAGCAACCCCAAC 420
Db 361 TGCTGGGAATGACAAAGTGGTCTTGGATCTCTCGGTGGTCTTCTGAGCAACCCCAAC 420
QY 421 GCAGTACAGCATCAGATCCAGAACTGAGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCAGATCCAGAACTGAGTGTATGACGAGGGCCCTTACACCTGCTC 480
QY 481 GGTGCAGACAGAACCAACCAAGACCTTAGGGTCCACTCATTTGTGCAAGTATCTCC 540
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QY 541 CAAAAATTGTAGAGATTTCTTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCAC 600
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QY 601 CTGATAGCAACTGGTGTAGACAGAGCCTACGGTACTTTGGAGACACATCTTCCCAAGC 660
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QY 661 GGTGGCTTTGTGAGTGAACCACTTGTGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAACCACTTGTGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTAGAGTGCAGTGCCTTCCATGATGCTGGCGCGCGCTGGTACGGAGAGTAA 780
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QY 781 GGTCAAGTGAATCTCCACATACATTTTCAAGGCAAGGGTACAGGTGTCCCGGTGG 840
Db 781 GGTCAAGTGAATCTCCACATACATTTTCAAGGCAAGGGTACAGGTGTCCCGGTGG 840
QY 841 ACAAAGGGGACACTGAGTGTGAGCCTCAGCAGTCCCTCAGCAGATTCAGTGGTA 900
Db 841 ACAAAGGGGACACTGAGTGTGAGCCTCAGCAGTCCCTCAGCAGATTCAGTGGTA 900
QY 901 CAAGGATGACAAAGACTGATTGAAAGGAAAGGGGTGAAAGTGGAAACAGACCTTT 960
Db 901 CAAGGATGACAAAGACTGATTGAAAGGAAAGGGGTGAAAGTGGAAACAGACCTTT 960
QY 961 CTTCTCAAACTCATCTTCTTCAATGTCTGAACTGACTATGGGAACTACACTGGGT 1020
Db 961 CTTCTCAAACTCATCTTCTTCAATGTCTGAACTGACTATGGGAACTACACTGGGT 1020
QY 1021 GGCCTCCAAAGCTGGGCGACACCAATGCCAGCATCTGCTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCCTCCAAAGCTGGGCGACACCAATGCCAGCATCTGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGCAGGTGAGCAACCGGACGCTCGAGGAGGGCAGGCTGGTCTGGCTGCTCTTCT 1140
Db 1081 CAGCAGGTGAGCAACCGGACGCTCGAGGAGGGCAGGCTGGTCTGGCTGCTCTTCT 1140
QY 1141 GGTCTTGCACCTGCTTCTCAAAATTTGATGTAGTGCACATTTCCCAACCGGAAAGGCT 1200
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QY 1201 GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
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QY 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAC 1320
Db 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAC 1320
QY 1321 AAAGAATACTTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAAAATTTGCTTTGCAGATA 1380
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QY 1381 TTTAGGTACAATGAGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCCGCTTGA 1440
Db 1381 TTTAGGTACAATGAGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCCGCTTGA 1440
QY 1441 CCACCTGCAAGCTGATCGTGAACCTCTTGTGTCAGTGTGGCAAGGGCTCAGCCTC 1500
Db 1441 CCACCTGCAAGCTGATCGTGAACCTCTTGTGTCAGTGTGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCCCAACAGAGTGCCTCCCAACGTCGGAACATTTCTGAGCTGGCCATCCCAAAATTTCAATCA 1560
Db 1501 TCTGCCCAACAGAGTGCCTCCCAACGTCGGAACATTTCTGAGCTGGCCATCCCAAAATTTCAATCA 1560
QY 1561 GTCCATAGAGACGAAACAGAAATGAGACCTTCCGGGCCCAAGCGTGGCGCACTTTG 1620
Db 1561 GTCCATAGAGACGAAACAGAAATGAGACCTTCCGGGCCCAAGCGTGGCGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAAACGTTGAAATTAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAAACGTTGAAATTAAGAGCAAAAAA 1679

RESULT 4

US-09-999-832A-522
; Sequence 522, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311

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3	PRIOR FILING DATE: 1997-11-21	4	PRIOR APPLICATION NUMBER: 60/081952
4	PRIOR APPLICATION NUMBER: 60/077450	5	PRIOR FILING DATE: 1998-04-15
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10	PRIOR APPLICATION NUMBER: 60/077649	11	PRIOR FILING DATE: 1998-04-21
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21	PRIOR FILING DATE: 1998-03-20	22	PRIOR APPLICATION NUMBER: 60/083336
22	PRIOR APPLICATION NUMBER: 60/078939	23	PRIOR FILING DATE: 1998-04-27
23	PRIOR FILING DATE: 1998-03-20	24	PRIOR APPLICATION NUMBER: 60/083322
24	PRIOR APPLICATION NUMBER: 60/079294	25	PRIOR FILING DATE: 1998-04-28
25	PRIOR FILING DATE: 1998-03-25	26	PRIOR APPLICATION NUMBER: 60/083392
26	PRIOR APPLICATION NUMBER: 60/079656	27	PRIOR FILING DATE: 1998-04-29
27	PRIOR FILING DATE: 1998-03-26	28	PRIOR APPLICATION NUMBER: 60/083495
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29	PRIOR FILING DATE: 1998-03-27	30	PRIOR APPLICATION NUMBER: 60/083496
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42	PRIOR APPLICATION NUMBER: 60/080105	43	PRIOR FILING DATE: 1998-04-29
43	PRIOR FILING DATE: 1998-03-31	44	PRIOR APPLICATION NUMBER: 60/083742
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47	PRIOR FILING DATE: 1998-03-31	48	PRIOR APPLICATION NUMBER: 60/084414
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49	PRIOR FILING DATE: 1998-03-31	50	PRIOR APPLICATION NUMBER: 60/084441
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51	PRIOR FILING DATE: 1998-04-01	52	PRIOR APPLICATION NUMBER: 60/084637
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58	PRIOR APPLICATION NUMBER: 60/081070	59	PRIOR FILING DATE: 1998-05-07
59	PRIOR FILING DATE: 1998-04-08	60	PRIOR APPLICATION NUMBER: 60/084600
60	PRIOR APPLICATION NUMBER: 60/081049	61	PRIOR FILING DATE: 1998-05-07
61	PRIOR FILING DATE: 1998-04-08	62	PRIOR APPLICATION NUMBER: 60/084627
62	PRIOR APPLICATION NUMBER: 60/081071	63	PRIOR FILING DATE: 1998-05-07
63	PRIOR FILING DATE: 1998-04-08	64	PRIOR APPLICATION NUMBER: 60/084643
64	PRIOR APPLICATION NUMBER: 60/081195	65	PRIOR FILING DATE: 1998-05-07
65	PRIOR FILING DATE: 1998-04-08	66	PRIOR APPLICATION NUMBER: 60/085339
66	PRIOR APPLICATION NUMBER: 60/081203	67	PRIOR FILING DATE: 1998-05-13
67	PRIOR FILING DATE: 1998-04-09	68	PRIOR APPLICATION NUMBER: 60/085338
68	PRIOR APPLICATION NUMBER: 60/081229	69	PRIOR FILING DATE: 1998-05-13
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1 PRIOR APPLICATION NUMBER: 60/085573
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7, 8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTCTCTTCAGCAAAACAGTGGATTTAAATCTCTTTGCAAAAGCTTTGAGAGCAACAC 60
DB 1 GTTGTCTCTTCAGCAAAACAGTGGATTTAAATCTCTTTGCAAAAGCTTTGAGAGCAACAC 60

QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AAGAAAAAATCATGAAACCAATCCAGCCAAAAATGCAAAATTCATCTCTTTGGCAAT 180
DB 121 AAGAAAAAATCATGAAACCAATCCAGCCAAAAATGCAAAATTCATCTCTTTGGCAAT 180

QY 181 CTTACGGGGTGGCTGTCTGTCTCTTTCAAGAGTGCCTCGGCGGAGGAGATGC 240
DB 181 CTTACGGGGTGGCTGTCTGTCTCTTTCAAGAGTGCCTCGGCGGAGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGACAACTGAGGTCGGCGGGGGAGGCGGCAACCTCTAG 300
DB 241 CACCTTCCCAAGCTATGACAACTGAGGTCGGCGGGGGAGGCGGCAACCTCTAG 300

QY 301 GTGCACATTTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCAACCTCTCTA 360
DB 301 GTGCACATTTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCAACCTCTCTA 360

QY 361 TGTGGGAATGACAGTGGTCTGATCTCTCGGCTGGCTCTTCTGAGCAACACCCAAAC 420
DB 361 TGTGGGAATGACAGTGGTCTGATCTCTCGGCTGGCTCTTCTGAGCAACACCCAAAC 420

QY 421 GCAGTACAGCATCGAGATCCAGAACTGGATGTATGACGAGGCGCTTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACTGGATGTATGACGAGGCGCTTTACACCTGCTC 480

QY 481 GGTGAGAGAGCAACCAACCAAGACCTTAGGGTCCACCTCATTTGTCAAGTATCTCC 540
DB 481 GGTGAGAGAGCAACCAACCAAGACCTTAGGGTCCACCTCATTTGTCAAGTATCTCC 540

QY 541 CAAAAATTGTAGATTTCTTCAGATATCTCATTATGAGGAAACAAATTTAGGCTCAC 600
DB 541 CAAAAATTGTAGATTTCTTCAGATATCTCATTATGAGGAAACAAATTTAGGCTCAC 600

QY 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACATCTCTCCCAAGC 660
DB 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTGAGTGAAGACAAATCTTTGAAATTCAGGGCATCAACCGGAGCAGTC 720
DB 661 GGTGGCTTTGTGAGTGAAGACAAATCTTTGAAATTCAGGGCATCAACCGGAGCAGTC 720

QY 721 AGGGGACTAGAGTGCAGTGCCTTCCATGAGCTGGCGGCGGCTGGTACGGAGTAA 780
DB 721 AGGGGACTAGAGTGCAGTGCCTTCCATGAGCTGGCGGCGGCTGGTACGGAGTAA 780

QY 781 GGTACCGGTGAATCTATCCACCATACATTTTCAGAAAGCAAGGTTACAGGTGTCCTCCGTGG 840
DB 781 GGTACCGGTGAATCTATCCACCATACATTTTCAGAAAGCAAGGTTACAGGTGTCCTCCGTGG 840

QY 841 ACAGAGGGGACACATGAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATCCAGTGGTA 900
DB 841 ACAGAGGGGACACATGAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATCCAGTGGTA 900

QY 901 CAAGGATGACAAAGACTGATTGAAGAGAAAGAGGGGTGAAGTGGAAAAAGACCTTT 960
DB 901 CAAGGATGACAAAGACTGATTGAAGAGAAAGAGGGGTGAAGTGGAAAAAGACCTTT 960

QY 961 CCTCTCAAAATCTCATCTTCTCAATGTCTGAAATGATGAGTATGGAATCTACCTGGT 1020
DB 961 CCTCTCAAAATCTCATCTTCTCAATGTCTGAAATGATGAGTATGGAATCTACCTGGT 1020

QY 1021 GGCCTCCAAAGCTGGGCAACCAATGCGCAGCATCATGCTATTTGGTCCAGGGCGCT 1080
DB 1021 GGCCTCCAAAGCTGGGCAACCAATGCGCAGCATCATGCTATTTGGTCCAGGGCGCT 1080

QY 1081 CAGCAGGTGAGCAACCGGCACTGCGAGGAGGCGCTGCGTCTGGCTGCTCTTCT 1140
DB 1081 CAGCAGGTGAGCAACCGGCACTGCGAGGAGGCGCTGCGTCTGGCTGCTCTTCT 1140

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DB 1261 TATACAAATGAAATTTAGAAAGAAACAGCTCATGCGGAGAGAAATTTGAGGAGGGGAAC 1320

QY 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTCGAAATTCGCTTTGAGATA 1380
DB 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTCGAAATTCGCTTTGAGATA 1380

QY 1381 TTTAGTACAAATGAGTCTTTTCCCAACCGGGAAGAAACAGCAGACACCCGGCTTGA 1440
DB 1381 TTTAGTACAAATGAGTCTTTTCCCAACCGGGAAGAAACAGCAGACACCCGGCTTGA 1440

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RESULT 5

US-09-978-189-522
; Sequence 522, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697
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Best Local Similarity 100.0%; Pred. No. 7.8e-22;
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QY 241 CACCTTCCCAAGCTATGCAAAACGTCGCGTCCGCGAGGGGAGCGCCACCTCTCAG 300
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QY 301 GTGCATATTGACAAACCGGTACCCGGGTGGCTGGCTGCTGCTGCTGCTGCTGCTGCT 360
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RESULT 8

US-09-978-191A-522
; Sequence 522, Application US/09978191A
; Publication No. US20030050239A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

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; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

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; APPLICANT: Kuo, Sophia S.

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; APPLICANT: Pan, James

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; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/084637
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTCTTCCAGCAAAACAGTGGATTAAATCTCTTGCACAACTTGGAGCAACAC 60
DB 1 GTTGTGCTCTTCCAGCAAAACAGTGGATTAAATCTCTTGCACAACTTGGAGCAACAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAATTCCTATCTCTTGGCAAT 180
DB 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAATTCCTATCTCTTGGCAAT 180
QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGGAGTGCCCGTCCGCGAGGAGATGC 240
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QY 241 CACCTTCCCAAGCTATGGAACAACTGACGGTCCGGGAGGAGGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGGAACAACTGACGGTCCGGGAGGAGGAGCGCCACCTCAG 300
QY 301 GTGCACATTATGCAACACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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QY 361 TGCTGGGAATGCAAGTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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QY 421 GCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGAGAGGGGCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGAGAGGGGCTTACACCTGCTC 480
QY 481 GGTGCAGACAGCAACACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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QY 541 CAAAATTGTAGAGATTCTTTAGATATCTCCATTAATGAGGGAACAATATTAGCCTCAC 600
DB 541 CAAAATTGTAGAGATTCTTTAGATATCTCCATTAATGAGGGAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCAACTGGTAGACAGAGCGGTACCTTGGAGACACATCTCTCCCAAGC 660
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Db 601 CTGATAGCAACTGGTAGACAGAGCCCTACGTTACTTGGAGACACATCTCTCCCAAGC 660
QY 661 GGTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATACCCGGGAGCAGTC 720
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QY 721 AGGGGACTACAGTGCAGTGCCTCCATGAGTGGCGCGCGCGCTGTACGGAGAGTAA 780
Db 721 AGGGGACTACAGTGCAGTGCCTCCATGAGTGGCGCGCGCGCTGTACGGAGAGTAA 780
QY 781 GGTCAACCGTGAACATCACCATATCATTTAGAGCCCAAGGGTACAGGTGTCCCGTGGG 840
Db 781 GGTCAACCGTGAACATCACCATATCATTTAGAGCCCAAGGGTACAGGTGTCCCGTGGG 840
QY 841 ACAAAGGGGACATGCGAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATTCAGAGTGTA 900
Db 841 ACAAAGGGGACATGCGAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATTCAGAGTGTA 900
QY 901 CAAGGATCACAAAGACTGATTGAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGGATCACAAAGACTGATTGAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
QY 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGT 1020
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Db 1081 CAGGAGGTGAGCAACGACGCTCGAGGAGGAGCGCTGCGTCTGCGTCTCTTCT 1140
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QY 1321 AAAGAAATCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
Db 1321 AAAGAAATCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGCCCTTGCAGATA 1380
QY 1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAACGGGAAGACACAGCACACCCGGCTTGA 1440
Db 1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAACGGGAAGACACAGCACACCCGGCTTGA 1440
QY 1441 CCCACTGCAAGCTGCATCGTCAACCTCTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC 1500
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QY 1561 GTCCATAGACGACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGGGCCTTTG 1620
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QY 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAACGTGAATATAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAACGTGAATATAAGAGCAAAAAA 1679

US-09-978-403A-522
; Sequence 522, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7,8e-22;

Mismatches 0; Indels 0; Gaps 0;
Matches 1679; Conservative 0;

QY 1 GTTGTCTCTTCAGCAAAAACAGTGGATTAAATCTCTTTCGCAAGCTTGAGAGCAAC 60

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QY 61 AATCTATCAGGAAGAAAGAAAACCGAACCTGCAAAAAGAGAAAGAAAGAG 120

Db 61 AATCTATCAGGAAGAAAGAAAACCGAACCTGCAAAAAGAGAAAGAAAGAG 120

QY 121 AAGAAAAAATCATGAAACCATCCAGCAAAAATGCAAAATTCATCTCTTGGCAAT 180

Db 121 AAGAAAAAATCATGAAACCATCCAGCAAAAATGCAAAATTCATCTCTTGGCAAT 180

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Qy 241 CACCTTCCCAAAGCTATGGAACAACGTCACGGTCCGGCAGGGGAGAGCGCCACCTCAG 300
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Qy 361 TGCTGGGAATGACAAAGTGGTGGCTGGATCCCTGGCTGGTCTTCTGAGCAACACCCCAAC 420
Db 361 TGCTGGGAATGACAAAGTGGTGGCTGGATCCCTGGCTGGTCTTCTGAGCAACACCCCAAC 420
Qy 421 GCAGTACAGATCGAGATCCAGAAACGTGATGTGATGACGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGATCGAGATCCAGAAACGTGATGTGATGACGAGGGCCCTTACACCTGCTC 480
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Db 1321 AAAGAATACTTTGGGGGAAAGAGTTTTTAAAAAGAAATTTGAAAAATTTGCTTGCAGATA 1380
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Qy 1621 GTAGACTGTGCCACCAACCGGCTGTGTGTGAAACGTGAAATATAAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACCGGCTGTGTGTGAAACGTGAAATATAAAAGAGCAAAAAAAA 1679

RESULT 10

US-09-978-564A-522
; Sequence 522, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364

[illegible]

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Garney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCAAGCTTTGAGAGCAAC 60

QY      61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB      61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY      121 AAGAAAGAAATCATGAAACCATCCAGCAAAATGCAATTTCTTTGGGCAAT 180
DB      121 AAGAAAGAAATCATGAAACCATCCAGCAAAATGCAATTTCTTTGGGCAAT 180

QY      181 CTTTCAGGGGCTGGCTGCTGTCTGTCTCTTCCAGAGGTGCCCGTCCGAGGGAGATGC 240
DB      181 CTTTCAGGGGCTGGCTGCTGTCTGTCTCTTCCAGAGGTGCCCGTCCGAGGGAGATGC 240

QY      241 CACCTTCCCAAGTATGGCAACAGTGAACGTGACGTCCGGCAGGGGAGCGCCACCTCAG 300
DB      241 CACCTTCCCAAGTATGGCAACAGTGAACGTGACGTCCGGCAGGGGAGCGCCACCTCAG 300

QY      301 GTGCACTATTGCAACCGGCTACCGGGTGGCTGGCTTAACCGGAGCACCCTCTTA 360
DB      301 GTGCACTATTGCAACCGGCTACCGGGTGGCTGGCTTAACCGGAGCACCCTCTTA 360

QY      361 TCGTGGGAATGCAAGTGTGCTGTGATCCTCGCGTGTCTTCTTGAGCAACACCAAC 420
DB      361 TCGTGGGAATGCAAGTGTGCTGTGATCCTCGCGTGTCTTCTTGAGCAACACCAAC 420

QY      421 GCAGTACAGATCGAGATCCAGAAAGTGTGATGACGAGGGCCCTTACACCTGCTC 480
DB      421 GCAGTACAGATCGAGATCCAGAAAGTGTGATGACGAGGGCCCTTACACCTGCTC 480

QY      481 GGTGAGACAGAAACCAACCAAGAGCTCTAGGGTCACTCTATTTGGAAGTATCTCC 540
DB      481 GGTGAGACAGAAACCAACCAAGAGCTCTAGGGTCACTCTATTTGGAAGTATCTCC 540

QY      541 CAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACATATTTAGCCTCAC 600
DB      541 CAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACATATTTAGCCTCAC 600

QY      601 CTGCATAGCAACTGGTAGACAGAGCTTACGTTTACTTTGGAGACACATCTCTCCCAAGC 660
DB      601 CTGCATAGCAACTGGTAGACAGAGCTTACGTTTACTTTGGAGACACATCTCTCCCAAGC 660

QY      661 GGTGGCTTTGTGAGTGAAGACGAATACTTTGGAATTTAGGGCATCACCGGGAGCAGTC 720
DB      661 GGTGGCTTTGTGAGTGAAGACGAATACTTTGGAATTTAGGGCATCACCGGGAGCAGTC 720

QY      721 AGGGGACTACGAGTGCAGTGCCTCAATGAGTGGCCGCCGCCGCTGAGGAGTAAA 780
DB      721 AGGGGACTACGAGTGCAGTGCCTCAATGAGTGGCCGCCGCCGCTGAGGAGTAAA 780

QY      781 GGTCAACCGTGAACATATCCACCATATATTTCAAGAGCCAAAGGTACAGGTGTCGCCGTGG 840
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QY      841 AAAAAAGGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTTCCAGTGTGA 900
DB      841 AAAAAAGGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTTCCAGTGTGA 900

QY      901 CAAGGATGACAAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAACAGACCTTT 960
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QY      961 CCTCTCAAAACTCATCTTTCTTCAATGTCTCTGAACATGACTATATGGAACTACACTTGGCT 1020
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QY      1021 GGCCTCCAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGTCAGGGGCCGT 1080
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QY      1081 CAGCAGGTGAGCAACAGGACGCTCGAGGAGGAGGCTGCTGCTGGCTGCTCTTCT 1140
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QY      1141 GGTCTTGCACTGCTTCTCAAAATTTTGAATGTGAGTGCACCTTCCCAACCGGGGAAAGGT 1200
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QY      1321 AAAGAAATCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGAAATTTGAAATTTG 1380
DB      1321 AAAGAAATCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGAAATTTGAAATTTG 1380

QY      1381 TTTAGGTACAAATGGAGTTTTTCTTTTCCCAAGGGGAAAGACACACAGCACACCGGCTTGA 1440
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QY      1501 TCTGCCCAACAGAGTGCCTCCACGCTGGAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
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1021 GGCCTTCCAAAGCTGGGCCACCAATTCAGCATCATGCTATTTGGTCCAGGCGCGGT 1080
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Db 1321 AAAGAATACTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
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US-09-978-824-522

; Sequence 522, Application US/09978824

; Publication No. US20030055216A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Fred. No. 7.8e-22; Indels 0; Gaps 0;
Matches 1679; Conservative 0; Mismatches 0;

Qy 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60
Db |||||
Qy 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60
Db |||||
Qy 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACTTGACAAAAGAGAAAGAAAG 120
Db |||||
Qy 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACTTGACAAAAGAGAAAGAAAG 120
Db |||||
Qy 121 AAGAAAAAATCATGAAAAACCATCCAGCAAAATGCAAAATCTATCTTTGGGCAAT 180
Db |||||
Qy 121 AAGAAAAAATCATGAAAAACCATCCAGCAAAATGCAAAATCTATCTTTGGGCAAT 180
Db |||||
Qy 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGGCCGTGCGCAGCGAGATGC 240
Db |||||
Qy 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGGCCGTGCGCAGCGAGATGC 240
Db |||||
Qy 241 CACCTTCCCAAGCTATGGACAACTGACCGTCCGACAGGGGGAGAGCGCCACCTCAG 300
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Qy 601 CTGCATAGCACTGGTAGACAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
Db |||||
Qy 601 CTGCATAGCACTGGTAGACAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
Db |||||
Qy 661 GGTGGCTTTGTAGTGAAGACGAATACCTTGAAATTCAGGGGCAATCACCCTGGGAGAGTC 720
Db |||||
Qy 661 GGTGGCTTTGTAGTGAAGACGAATACCTTGAAATTCAGGGGCAATCACCCTGGGAGAGTC 720
Db |||||

QY	721	AGGGGACTACGAGTGCAGTGCCTTCCAATGACGTGGCCGCGCCGTGGTACGGAGAGTAAA	780
Db	721	AGGGGACTACGAGTGCAGTGCCTTCCAATGACGTGGCCGCGCCGTGGTACGGAGAGTAAA	780
QY	781	GGTCACGGTGAATAATCCACCATACATATTCAGNAAGCCAAAGGTACAGGTGTCCCGTGGG	840
Db	781	GGTCACGGTGAATAATCCACCATACATATTCAGNAAGCCAAAGGTACAGGTGTCCCGTGGG	840
QY	841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
Db	841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
QY	901	CAAGGATGACAAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960
Db	901	CAAGGATGACAAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960
QY	961	CCTCTCAAAACTCATCTTTCTTAATGTCTCTGAACATGACTATGGGAACTACACTTGCCT	1020
Db	961	CCTCTCAAAACTCATCTTTCTTAATGTCTCTGAACATGACTATGGGAACTACACTTGCCT	1020
QY	1021	GGCCTCCAAACAAGTGGCCGACACCAATGCCAGATCATGTATTTGGTCCAGGCGCCT	1080
Db	1021	GGCCTCCAAACAAGTGGCCGACACCAATGCCAGATCATGTATTTGGTCCAGGCGCCT	1080
QY	1081	CAGCGAGGTGAGCAACCGCAGCTCGAGGAGGGCAGCGTGGCTGTGGCTGTGCTCTTCT	1140
Db	1081	CAGCGAGGTGAGCAACCGCAGCTCGAGGAGGGCAGCGTGGCTGTGGCTGTGCTCTTCT	1140
QY	1141	GGTCTTGCACTGCTTCTCAAATTTTGATGTAGTGCACCTTCCCAACCGGGAAGGCT	1200
Db	1141	GGTCTTGCACTGCTTCTCAAATTTTGATGTAGTGCACCTTCCCAACCGGGAAGGCT	1200
QY	1201	GCCGCGACACCCACCAACACAAACAGCAATGGCAACACCGACAGCAACCAATCAGATA	1260
Db	1201	GCCGCGACACCCACCAACACAAACAGCAATGGCAACACCGACAGCAACCAATCAGATA	1260
QY	1261	TATACAAATGAAATTTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC	1320
Db	1261	TATACAAATGAAATTTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC	1320
QY	1321	AAAGAATACTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCATGAGATA	1380
Db	1321	AAAGAATACTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCATGAGATA	1380
QY	1381	TTTAGGTACAAATGAGATTTTCTTTCCCAACCGGAAGAACACAGCACACCCGCTTGA	1440
Db	1381	TTTAGGTACAAATGAGATTTTCTTTCCCAACCGGAAGAACACAGCACACCCGCTTGA	1440
QY	1441	CCCCTGCAAGCTGCATCGTGCAACCTCTTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC	1500
Db	1441	CCCCTGCAAGCTGCATCGTGCAACCTCTTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC	1500
QY	1501	TCTGCCACAGAGTGCCTCCACAGTGGAACTTCTGGAGCTGGCCATCCCAATTCATCA	1560
Db	1501	TCTGCCACAGAGTGCCTCCACAGTGGAACTTCTGGAGCTGGCCATCCCAATTCATCA	1560
QY	1561	GTCCATAGAGACGAACGAATGAGACCTTCCGCGCCCAAGCGTGGCGCTGGGGCACTTTG	1620
Db	1561	GTCCATAGAGACGAACGAATGAGACCTTCCGCGCCCAAGCGTGGCGCTGGGGCACTTTG	1620
QY	1621	GTAGACTGTGCCACCAACCGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA	1679
Db	1621	GTAGACTGTGCCACCAACCGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA	1679

RESULT 14

RESULT 14
US-09-918-585A-522

US-09-518-383A-322
: Sequence 522, Application US/09918585A

Sequence 322, Application US/03/03/0030060406A1
Publication No. US20030060406A1

GENERAL INFORMATION:

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APPLICANT: ASIKEMAZI, AVI
APPLICANT: Baker Kevin P.

APPLICANT:	Botstein, David
APPLICANT:	Deenoyers, Luc
APPLICANT:	Eaton, Dan
APPLICANT:	Ferrara, Napoleon
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J.
APPLICANT:	Kljasin, Ivar J.
APPLICANT:	Kuo, Sophia S.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pan, James;
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Shelton, David L.
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tumas, Daniel
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION:	Acids Encoding the Same
FILE REFERENCE:	P2630PlCl
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CURRENT FILING DATE:	2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7.8e-22; Mismatches 0; Indels 0; Gaps 0;
Matches 1679; Conservative 0;

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Db	1	GTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCAAAAGCTTTGAGCAACAC	60
QY	61	AATCTATCAGGAAAGAAAGAAAGAAACCGAACCTTGACAAAAGAGAAAGAG	120
Db	61	AATCTATCAGGAAAGAAAGAAAGAAACCGAACCTTGACAAAAGAGAAAGAG	120
QY	121	AAGAAAAAATCATGAAAAACCATCCAGCAAAATGACAAATTTCTTTGGGCAAT	180
Db	121	AAGAAAAAATCATGAAAAACCATCCAGCAAAATGACAAATTTCTTTGGGCAAT	180
QY	181	CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTCGCGCAGCGGAGATGC	240
Db	181	CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTCGCGCAGCGGAGATGC	240
QY	241	CACCTTCCCAAGCTATGGAACAAGTACGCTCGCGGAGGGGGAGAGCGCCACCTTCAG	300
Db	241	CACCTTCCCAAGCTATGGAACAAGTACGCTCGCGGAGGGGGAGAGCGCCACCTTCAG	300

QY 301 GTGCACCTATTGACAAACGGGCTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTCTA 360
Db 301 GTGCACCTATTGACAAACGGGCTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTCTA 360
QY 361 TGCTGGGAATGACAAAGTGGTGGCTGAGTCCCTCGCGTGGTCTCTCTGAGCAACACCCAAAC 420
Db 361 TGCTGGGAATGACAAAGTGGTGGCTGAGTCCCTCGCGTGGTCTCTCTGAGCAACACCCAAAC 420
QY 421 GCAGTACAGCATCAGATCCAGATCCAGACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCAGATCCAGATCCAGACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
QY 481 GGTGACAGACACCAACCCAAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCC 540
Db 481 GGTGACAGACACCAACCCAAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCC 540
QY 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Db 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCACTGCTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
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QY 661 GGTGGGCTTTGTGAGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTGGGCTTTGTGAGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTACAGTGGAGTGCTCTCAATGAGTGGCGCGCCGCTGGTACGAGAGTAAA 780
Db 721 AGGGGACTACAGTGGAGTGCTCTCAATGAGTGGCGCGCCGCTGGTACGAGAGTAAA 780
QY 781 GGTCAACGTAACATCCACCATACATTTCAAGAGCCAAAGGTTACAGTGTCCCGGTGGG 840
Db 781 GGTCAACGTAACATCCACCATACATTTCAAGAGCCAAAGGTTACAGTGTCCCGGTGGG 840
QY 841 AAAAAAGGGGACATGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db 841 AAAAAAGGGGACATGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
QY 901 CAAGGATGACAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACACAGCTTT 960
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Db 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACTTGGT 1020
QY 1021 GGCTTCCAAAGCTGGGCCACACCAATGGCAGCATCATGTATTTGGTCCAGGGCGGT 1080
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QY 1081 CAGCGAGTGAACGACGCTGAGGAGGCGAGCTGCTGCTGGCTGGCTGCTCTTCT 1140
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QY 1141 GGTCTTGACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
QY 1201 GCCGACACACACCAACCAACAGCATTTGGCAACACCGACAGCAACCAATCAGATA 1260
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QY 1261 TATCAAAATGAATTAGAAGAAACACAGCTCATCTGGGACAGAAATTTGAGGGAGGGAAAC 1320
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QY 1321 AAAGAAATCTTTGGGGGAAAGAGTGTAAAAAAGAAATTTGAAATTTGCTTGCAGATA 1380
Db 1321 AAAGAAATCTTTGGGGGAAAGAGTGTAAAAAAGAAATTTGAAATTTGCTTGCAGATA 1380

QY 1381 TTTAGTGTACAAATGAGAGTCTTTTCTTTTCCCAAAACGGGAAGAACACAGACACACCCGGCTTGA 1440
Db 1381 TTTAGTGTACAAATGAGAGTCTTTTCTTTTCCCAAAACGGGAAGAACACAGACACACCCGGCTTGA 1440
QY 1441 CCACCTGCAAGCTGCAATCGTGGCAACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC 1500
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QY 1501 TCTGCCACACAGAGTGGCCCAACGTCGAAACATTTCTGGAGCTGGCCATCCCAAAATTTCAATCA 1560
Db 1501 TCTGCCACACAGAGTGGCCCAACGTCGAAACATTTCTGGAGCTGGCCATCCCAAAATTTCAATCA 1560
QY 1561 GTCCATAGAGACCAACAGAAATAGACCTTCCCGCCCAAGCGTGGCGTGGCGGACCTTTG 1620
Db 1561 GTCCATAGAGACCAACAGAAATAGACCTTCCCGCCCAAGCGTGGCGTGGCGGACCTTTG 1620
QY 1621 GTAGACTGTGCCACCAACGCGGTGTGTGTGAAACGTTGAAATAAAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACGCGGTGTGTGTGAAACGTTGAAATAAAAAGAGCAAAAAA 1679

RESULT 15

US-09-978-423A-522

; Sequence 522, Application US/09978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C21

; CURRENT APPLICATION NUMBER: US/09/978,423A

; CURRENT FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

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; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7.8e-22;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTTGTGCTTCAGCAAAACAGTGGATTTAAATCTCTTGCCACAGCTTGAGAGCAAC 60
Db 1 GTTGTGCTTCAGCAAAACAGTGGATTTAAATCTCTTGCCACAGCTTGAGAGCAAC 60
Qy 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Db 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Qy 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATATGCAATTCCTTTGGGCAAT 180
Db 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATATGCAATTCCTTTGGGCAAT 180
Qy 181 CTTACGGGGTGGCTGCTCTGTGTCTCTTCCAGAGAGTCCCGTGGCGAGGAGATGC 240
Db 181 CTTACGGGGTGGCTGCTCTGTGTCTCTTCCAGAGAGTCCCGTGGCGAGGAGATGC 240
Qy 241 CACCTTCCCAAGCTATGCAACACGTGACGGTCCGGCAGGGGAGAGCGCCCTCAG 300
Db 241 CACCTTCCCAAGCTATGCAACACGTGACGGTCCGGCAGGGGAGAGCGCCCTCAG 300
Qy 301 GTGCACATATTGACAAACCGGGTACCGGGTGGCTTGAACCGGAGACCATTCCTTA 360
Db 301 GTGCACATATTGACAAACCGGGTACCGGGTGGCTTGAACCGGAGACCATTCCTTA 360
Qy 361 TGCTGGGAATGACAAAGTGGTGGCTGATCTCTCGGGTGGCTCTCTGAGCAACCCAAAC 420
Db 361 TGCTGGGAATGACAAAGTGGTGGCTGATCTCTCGGGTGGCTCTCTGAGCAACCCAAAC 420
Qy 421 GCAGTACAGCATCAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Qy 481 GGTGAGACAGACAAACCCCAAGACCTTAGGGTCCACCTCATTTGTGAGATCTCTCC 540
Db 481 GGTGAGACAGACAAACCCCAAGACCTTAGGGTCCACCTCATTTGTGAGATCTCTCC 540
Qy 541 CAAATTTGAGATTTCTTCAGATATCTCCATTAATGAAGGAACATATAGCCTCAC 600
Db 541 CAAATTTGAGATTTCTTCAGATATCTCCATTAATGAAGGAACATATAGCCTCAC 600
Qy 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
Db 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
Qy 661 GGTGGCTTTGTGAGTGAAGCAATATCTGGAATTCAGGGCATCCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGCAATATCTGGAATTCAGGGCATCCCGGGAGCAGTC 720
Qy 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCCCGCGCGGTGACGAGAGTAAA 780
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Qy 781 GGTCACTGGTGAATTCACCAATATTCAGAACCCAGGGTACAGGTGTCCTCCGGTGG 840
Db 781 GGTCACTGGTGAATTCACCAATATTCAGAACCCAGGGTACAGGTGTCCTCCGGTGG 840
Qy 841 ACAAAGGGGACACTGAGTGTGAGCCCTCAGACGTCCCTCAGCAGAAATTCAGTGTGA 900
Db 841 ACAAAGGGGACACTGAGTGTGAGCCCTCAGACGTCCCTCAGCAGAAATTCAGTGTGA 900
Qy 901 CAAGGATGACAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
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RESULT 16

US-09-978-193A-522

; Sequence 522, Application US/09978193A

; Publication No. US20030073624A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Flivaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

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; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Kenneth L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C6
CURRENT APPLICATION NUMBER: US/09/978,193A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/084639

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Qy		361	TGCTGGGGAATGACAAGTGGTGGCTGGATCTCTCGCGTGGTCTCTTCTGAGCAACACCCAAC	420
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Qy		421	GCAGTACAGCATCGAGATCCAGAAAGTGGATGTGTATGACAGGGGCCCTTACACCTGCTC	480
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RESULT 17

US-09-999-830A-522

Sequence 522, Application US/09999830A

Publication No. US20030077700A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

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APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PIC70

CURRENT APPLICATION NUMBER: US/09/999,830A

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

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Best Local Similarity 100.0%; Pred. No. 7.8e-22;
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Db 61 AATCTATCAGGAAAGAAAGAAAGAAACCCGAACTGCAAAAAAGAAAGAAAGAG 120

Qy 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAAATGCAAAATCTCTTTGGGCAAT 180
Db 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAAATGCAAAATCTCTTTGGGCAAT 180

Qy 181 CTTACGGGGCTGGCTCTCTGTCTCTTCCAAGAGTGCCTGCGCAGCGAGATGC 240
Db 181 CTTACGGGGCTGGCTCTCTGTCTCTTCCAAGAGTGCCTGCGCAGCGAGATGC 240

Qy 241 CACCTTCCCAAGCTATGACAAACGTGACCGGTCCGGGAGAGGGGAGAGCCCTCAG 300
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Qy 601 CTGCATAGCAACTGGTATGACAGAGCCCTAGTTACTTTGAGAGACATCTCTCCAAAGC 660
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Db 781 GGTCAACCGTGAACATATCCACCATATATTTCCAGAGCCAGAGGTACAGGTGTCCCGTGGG 840
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Db 841 ACAAAGGGGACACTGCACTGTGAGACCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTA 900
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RESULT 19

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; Sequence 522, Application US/09978187B
; Publication No. US20030096744A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C5
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;; PRIOR APPLICATION NUMBER: 60/085697
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Db 121 AAGAAAAAAATCATGAAAAACATCCAGCCAAAAATGACAAATTCATTCTTTGGGCAAT 180
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Db 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATTTGGAGAGAAATTTAGGGAGGGAAC 1320
Qy 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTGCAGATA 1380
Db 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTGCAGATA 1380
Qy 1381 TTTAGGTACATGAGTTTCTTTTCCCAACGGGAGAACACAGCAGCAGCCGCTTGA 1440
Db 1381 TTTAGGTACATGAGTTTCTTTTCCCAACGGGAGAACACAGCAGCAGCCGCTTGA 1440
Qy 1441 CCCACTGCAAGTGCATCGTCAACCTCTTTTGGTGCAGAGTGGGCAAGGCTCAGCCTC 1500

Db 1441 CCCACTGCAAGTGCATCGTCAACCTTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC 1500
Qy 1501 TCTGCCACAGAGTGCCTCCACAGTGGAAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGCCTCCACAGTGGAAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
Qy 1561 GTCCATAGAGACGAACGAATGAGACCTTCCGGGCCAAGCGTGGCGTGGCGGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACGAATGAGACCTTCCGGGCCAAGCGTGGCGTGGCGGCACTTTG 1620
Qy 1621 GTAGACTGTGCCACCAACCGCGTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACCGCGTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA 1679

RESULT 20

US-09-978-643A-522
; Sequence 522, Application US/09978643A
; Publication No. US20030104998A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P16
; CURRENT APPLICATION NUMBER: US/09/978,643A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-643A-522

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGTCCTTTCAGCAAAACAGTGGATTTTAAATCTCTTTCGCAAAAGCTTGAGAGCAAC 60
Db 1 GTTGTGTCCTTTCAGCAAAACAGTGGATTTTAAATCTCTTTCGCAAAAGCTTGAGAGCAAC 60
Qy 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Db 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Qy 121 AAGAAAAAATCATGTGAAACCATCCAGCCAAATATCAATTTCTTCTTGGGCAAT 180

Db 121 AGAAAAAATCATGAAACCATGAGCAAAATGCAATCTCTTTGGCAAT 180
QY 181 CTTTCAAGGGCTGGCTCTGTGTCTCTTCAAGGAGTGCCTGCGCAGCGAGATGC 240
Db 181 CTTTCAAGGGCTGGCTCTGTGTCTCTTCAAGGAGTGCCTGCGCAGCGAGATGC 240
QY 241 CACTTCCCAAGCTATGAGCAACAGTGAAGTGCCTGCGCAGGGGAGAGCCACCTTCAG 300
Db 241 CACTTCCCAAGCTATGAGCAACAGTGAAGTGCCTGCGCAGGGGAGAGCCACCTTCAG 300
QY 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGTCTTAAACCGCAGACCAATCTCTTA 360
Db 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGTCTTAAACCGCAGACCAATCTCTTA 360
QY 361 TGCTGGGAATGACAAGTGGTGCCTGGATCTCTCGGTGGTCTTCTTGAGCAACACCCAAAC 420
Db 361 TGCTGGGAATGACAAGTGGTGCCTGGATCTCTCGGTGGTCTTCTTGAGCAACACCCAAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACCTGTGATGATGAGGAGGCGCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCGAGATCCAGAACCTGTGATGATGAGGAGGCGCTTACACCTGCTC 480
QY 481 GGTGACAGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
Db 481 GGTGACAGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
QY 541 CAAAATTGTAGAGATTTCTTCAGATATCTTCAGATATCTTCAGATATCTTCAGATATCTTC 600
Db 541 CAAAATTGTAGAGATTTCTTCAGATATCTTCAGATATCTTCAGATATCTTCAGATATCTTC 600
QY 601 CTGCATAGCACTGGTACAGCAGACGCTACCGTTACTTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGCATAGCACTGGTACAGCAGACGCTACCGTTACTTTGGAGACACATCTCTCCCAAGC 660
QY 661 GTTGGCTTTCTGAGTGAAGACGATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GTTGGCTTTCTGAGTGAAGACGATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGACTACAGTGCAGTGCCTCAATGAGTGGCGCGCCGCTGAGTGCAGGAGTAA 780
Db 721 AGGGACTACAGTGCAGTGCCTCAATGAGTGGCGCGCCGCTGAGTGCAGGAGTAA 780
QY 781 GGTACCGTGAACATCCACCATATCTTCAAGTGCAGGAGTGCAGGAGTGCAGGAGTGCAG 840
Db 781 GGTACCGTGAACATCCACCATATCTTCAAGTGCAGGAGTGCAGGAGTGCAGGAGTGCAG 840
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTTCAGAGTCCCTCAGCAGAAATCCAGTGGTA 900
Db 841 ACAAAGGGGACACTGCAGTGTGAAGCCTTCAGAGTCCCTCAGCAGAAATCCAGTGGTA 900
QY 901 CAAGATGACAAAGACTGATTGAAGGAAAGAAAGGAGTGAAGTGAAGGAGGAGGAGTGA 960
Db 901 CAAGATGACAAAGACTGATTGAAGGAAAGAAAGGAGTGAAGTGAAGGAGGAGGAGTGA 960
QY 961 CCTCTCAAAACCTCATCTTCAATGTCTCTGAAATGAGTGAAGTGAAGTGAAGTGAAGT 1020
Db 961 CCTCTCAAAACCTCATCTTCAATGTCTCTGAAATGAGTGAAGTGAAGTGAAGTGAAGT 1020
QY 1021 GGCCTCCCAAGCTGGGCGCACCAATGCGGAGTCAATGATGATGATGATGATGATGATGAT 1080
Db 1021 GGCCTCCCAAGCTGGGCGCACCAATGCGGAGTCAATGATGATGATGATGATGATGATGAT 1080
QY 1081 CAGCGAGGTGAGCAACCGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 CAGCGAGGTGAGCAACCGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GGTCTTGACCTGCTTCTCAATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 1141 GGTCTTGACCTGCTTCTCAATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 GCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260

Db 1201 GCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
QY 1261 TATACAAATGAATTTAGAGAAACACAGCCTCATGGACAGAAATTTTGGAGGAGGGAAC 1320
Db 1261 TATACAAATGAATTTAGAGAAACACAGCCTCATGGACAGAAATTTTGGAGGAGGGAAC 1320
QY 1321 AAAGATACTTTGGGGGAAAGAGTTTTTAAAAAGAAATTTGAAAATTCCTTTGACAGATA 1380
Db 1321 AAAGATACTTTGGGGGAAAGAGTTTTTAAAAAGAAATTTGAAAATTCCTTTGACAGATA 1380
QY 1381 TTTAGGTA CAATGGAGTTTTTCTTTTCCAAAACGGGAAGAACACAGACACCCCGCTTGA 1440
Db 1381 TTTAGGTA CAATGGAGTTTTTCTTTTCCAAAACGGGAAGAACACAGACACCCCGCTTGA 1440
QY 1441 CCACCTGCAAGCTGCATCGTGAACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC 1500
Db 1441 CCACCTGCAAGCTGCATCGTGAACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCCCAACAGAGTGGCCCCACCGTGAACATTTCTGAGCTGGCCATCCCAAAATCAATCA 1560
Db 1501 TCTGCCCAACAGAGTGGCCCCACCGTGAACATTTCTGAGCTGGCCATCCCAAAATCAATCA 1560
QY 1561 GTCCATAGAGACAAACAGATGAGACCTTCCGGCCCAAGCGTGGCGTGGGCAAGGGCTTGG 1620
Db 1561 GTCCATAGAGACAAACAGATGAGACCTTCCGGCCCAAGCGTGGCGTGGGCAAGGGCTTGG 1620
QY 1621 GTAGACTGTGCCACCAAGCGGTGTGTGTGAAACGTGAAATATAAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAAGCGGTGTGTGTGAAACGTGAAATATAAAAGAGCAAAAAAAA 1679

RESULT 21
US-09-978-375A-522
; Sequence 522, Application US/09978375A
; Publication No. US20030130181A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gersitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P26301C24
; CURRENT APPLICATION NUMBER: US/09/978,375A
; PRIORITY FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C2
CURRENT APPLICATION NUMBER: US/09/978,298A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640

[illegible]

us-10-017-084a-522.rnpb

RESULT 23

US-09-978-188A-522
Sequence 522, Application US/09978188A

Publication No. US20030139328A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C8
CURRENT APPLICATION NUMBER: US/09/978,188A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/079664
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495

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181	CTTACGGGGCTGGCTGCTCTGTGTCTCTTCCAAAGAGATGCCCGTGGCAGCGAGATGC	240
241	CACCTTCCCAAAAGCTATGACAAACGTCGCGTCCGGAGGGGGAGAGCGCCACCTCTCAG	300
241	CACCTTCCCAAAAGCTATGACAAACGTCGCGTCCGGAGGGGGAGAGCGCCACCTCTCAG	300
301	GTGCACATATTGACAAACCGGGTCCACCCGGGTGGCTTGGCTAAACCGCAGCACCATCTCTA	360
301	GTGCACATATTGACAAACCGGGTCCACCCGGGTGGCTTGGCTAAACCGCAGCACCATCTCTA	360
361	TGCTGGGAATGACAAAGTGGTGGCTTGGATCTCGGGTGGTCTTCTGAGCAACACCCAAAC	420
361	TGCTGGGAATGACAAAGTGGTGGCTTGGATCTCGGGTGGTCTTCTGAGCAACACCCAAAC	420
421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC	480
421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC	480
481	GGTGCAGACAGCAACCAACAGACCTCTAGGGTCCACTTATGTGCAAGTATCTCC	540
481	GGTGCAGACAGCAACCAACAGACCTCTAGGGTCCACTTATGTGCAAGTATCTCC	540
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661	GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATACCCGGGAGCAGTC	720
721	AGGGGACTACGAGTGCAGTGCTCCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAA	780
721	AGGGGACTACGAGTGCAGTGCTCCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAA	780
781	GGTACCGTGAACACTATCCACATFACATTTAGAGCCAGGGTACAGGTGTCCTCCGTTGG	840
781	GGTACCGTGAACACTATCCACATFACATTTAGAGCCAGGGTACAGGTGTCCTCCGTTGG	840
841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC18
; CURRENT APPLICATION NUMBER: US/09/978,681A
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Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1621 GTAGACTGTGCCACCAACGCGGTGTGTGAAACGTTGAAATTAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACGCGGTGTGTGAAACGTTGAAATTAAGAGCAAAAAAAA 1679
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RESULT 26

US-09-999-829A-522

; Sequence 522, Application US/09999829A

; Publication No. US20030195344A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuc, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C61

; CURRENT APPLICATION NUMBER: US/09/999,829A

; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 522

; LENGTH: 1679

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-999-829A-522

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTGTGCAAGCTTGAGAGCAAC 60
QY 61 AATCTATCAGAAAGAAAGAAAGAAACCGACCTGACAAAAAGAAAGAAAG 120
Db 61 AATCTATCAGAAAGAAAGAAAGAAACCGACCTGACAAAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCCCAAAATGCACAATCTCTCTTGGGCAAT 180
Db 121 AAGAAAAAATCATGAAACCATCCAGCCCAAAATGCACAATCTCTCTTGGGCAAT 180
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us-10-017-084a-522.rnpb

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC13
CURRENT APPLICATION NUMBER: US/09/978,544A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

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2	PRIOR APPLICATION NUMBER: 60/084414
3	PRIOR FILING DATE: 1998-05-06
4	PRIOR APPLICATION NUMBER: 60/084441
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19	PRIOR FILING DATE: 1998-05-07
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28	PRIOR APPLICATION NUMBER: 60/085700
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30	PRIOR APPLICATION NUMBER: 60/085689
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35	PRIOR FILING DATE: 1998-05-15
36	PRIOR APPLICATION NUMBER: 60/085573
37	PRIOR FILING DATE: 1998-05-15
38	PRIOR APPLICATION NUMBER: 60/085704
39	PRIOR FILING DATE: 1998-05-15
40	PRIOR APPLICATION NUMBER: 60/085697

QY	421	GCAGTACAGCTCGAGATCCAGAA	CGTGCATCTGTATGACGAGGCGCCCTTACACCTGCTC	480	
DB	421	GCAGTACAGATCGAGATCCAGAA	CGGTGATGTGTATGACGAGGCGCCCTTACACCTGCTC	480	
QY	481	GGTGCAGACAGACAAC	CCACCCAAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCC	540	
DB	481	GGTGCAGACAGACAAC	CCACCCAAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCC	540	
QY	541	CAAAAATTGTAGAGATTTCTT	CAGATATCTCCATTATGAAGGAA	CAAATATTAGCCTCAC	600
DB	541	CAAAAATTGTAGAGATTTCTT	CAGATATCTCCATTATGAAGGAA	CAAATATTAGCCTCAC	600
QY	601	CTGCATAGCAACTGTGTAGAC	CCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAAGC	660	
DB	601	CTGCATAGCAACTGTGTAGAC	CCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAAGC	660	
QY	661	GGTTGGCTTTGTGAGTGAAG	ACGAATACTTTGGAAATTCAGGGGATCACCCGGAGCAGTCT	720	
DB	661	GGTTGGCTTTGTGAGTGAAG	ACGAATACTTTGGAAATTCAGGGGATCACCCGGAGCAGTCT	720	
QY	721	AGGGGACTACGAGTCAGTGCCT	CCAATGACGTGGCGCGCGTGGTACGGAGAGTAAA	780	
DB	721	AGGGGACTACGAGTCAGTGCCT	CCAATGACGTGGCGCGCGTGGTACGGAGAGTAAA	780	
QY	781	GGTCACCGTGAACCTATCC	ACATATTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGG	840	
DB	781	GGTCACCGTGAACCTATCC	ACATATTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGG	840	
QY	841	ACAAAGGGGACACTGCAAGT	GTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTTA	900	
DB	841	ACAAAGGGGACACTGCAAGT	GTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTTA	900	
QY	901	CAAGGATGACAAAGAATCTA	TTGAAGAAAGAGGGGTGAAAGTGGAAACAGACCTTT	960	
DB	901	CAAGGATGACAAAGAATCTA	TTGAAGAAAGAGGGGTGAAAGTGGAAACAGACCTTT	960	
QY	961	CCTCTCAAAACTCATCTTT	CTAATGCTCTGAACATGACTATGGGAACTACACTTTCGT	1020	
DB	961	CCTCTCAAAACTCATCTTT	CTAATGCTCTGAACATGACTATGGGAACTACACTTTCGT	1020	
QY	1021	GGCTCCAAACAAGCTGGCG	CCACCAATGCGAGCATCATCTATTTGGTCCAGGCGCGGT	1080	
DB	1021	GGCTCCAAACAAGCTGGCG	CCACCAATGCGAGCATCATCTATTTGGTCCAGGCGCGGT	1080	
QY	1081	CAGCGAGGTGAGCAAC	CGGCA	CGTGCAGAGAGGCGAGGTGCTGTGGCTGTGCTCTTCT	1140
DB	1081	CAGCGAGGTGAGCAAC	CGGCA	CGTGCAGAGAGGCGAGGTGCTGTGGCTGTGCTCTTCT	1140
QY	1141	GGTCTTGCACTGCTCTCAAA	TTTTGATGTGAGTGCCACTTCCCAACCCGGGAAAGGCT	1200	
DB	1141	GGTCTTGCACTGCTCTCAAA	TTTTGATGTGAGTGCCACTTCCCAACCCGGGAAAGGCT	1200	
QY	1201	GCCGCCACCAACCA	CCACCAACAGCAATGGCAACCCGACAGCAACCAATCAGATA	1260	
DB	1201	GCCGCCACCAACCA	CCACCAACAGCAATGGCAACCCGACAGCAACCAATCAGATA	1260	
QY	1261	TATACAAATGAATTAGA	AGAAACACAGCCTCATGGGACAGAAATTTGAGGGGGGGAAC	1320	
DB	1261	TATACAAATGAATTAGA	AGAAACACAGCCTCATGGGACAGAAATTTGAGGGGGGGAAC	1320	
QY	1321	AAAGAAATCTTTGGGGG	AAAAAGATTTTAAAAAAGAAATTTGAAAAATTCGCTTGCAGATA	1380	
DB	1321	AAAGAAATCTTTGGGGG	AAAAAGATTTTAAAAAAGAAATTTGAAAAATTCGCTTGCAGATA	1380	
QY	1381	TTTAGGTACAAATGAGTTT	CTTTTCCAAAACGGGAAGAAACACAGCACACCCGGCTTGGTA	1440	
DB	1381	TTTAGGTACAAATGAGTTT	CTTTTCCAAAACGGGAAGAAACACAGCACACCCGGCTTGGTA	1440	
QY	1441	CCCACTGCAAGCTGCAT	CGTGCACCTTTTGGTGGCAGTGTGGGCAAGGGCTCAGGCTC	1500	
DB	1441	CCCACTGCAAGCTGCAT	CGTGCACCTTTTGGTGGCAGTGTGGGCAAGGGCTCAGGCTC	1500	
QY	1501	TCTGCCCAACAGAGT	GCCCAACGTCGAGTGGCCATCTCGAGCTGGCCATCCCAAAATTCATATCA	1560	

Db 1501 TCTGCCACAGAGTGGCCCACTGGAGCACTTCTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCAAGCGGTGTGTGTAACGTTGAATATAAAGACCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAAGCGGTGTGTGTAACGTTGAATATAAAGACCAAAAAA 1679

RESULT 29

US-09-978-665A-522
/ Sequence 522, Application US/09978665A
/ Publication No. US20030199437A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C19
/ CURRENT APPLICATION NUMBER: US/09/978,665A
/ CURRENT FILING DATE: 2001-10-16
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
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1	PRIOR FILING DATE: 1998-04-27	QY	121	AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAATTTCTATCTCTTGGGCAAT	180
1	PRIOR APPLICATION NUMBER: 60/083392	Db	121	AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAATTTCTATCTCTTGGGCAAT	180
1	PRIOR FILING DATE: 1998-04-29	QY	181	CTTTCAGGGGCTGGCTCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGC	240
1	PRIOR APPLICATION NUMBER: 60/083495	Db	181	CTTTCAGGGGCTGGCTCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGC	240
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1	PRIOR APPLICATION NUMBER: 60/083554	Db	241	CACCTTCCCAAGCTATGGAACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTTCAG	300
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1	PRIOR FILING DATE: 1998-04-29	QY	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACAGGGGCGCTTACACCTGCTC	480
1	PRIOR APPLICATION NUMBER: 60/083500	Db	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACAGGGGCGCTTACACCTGCTC	480
1	PRIOR FILING DATE: 1998-04-29	QY	481	GGTGCAGACAGAAACCAACCGGCTCTAGAGTCTCTAGAGTCTCTAGAGTCTCTAGAGTCTCT	540
1	PRIOR APPLICATION NUMBER: 60/084366	Db	481	GGTGCAGACAGAAACCAACCGGCTCTAGAGTCTCTAGAGTCTCTAGAGTCTCTAGAGTCTCT	540
1	PRIOR FILING DATE: 1998-05-05	QY	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCTCAC	600
1	PRIOR APPLICATION NUMBER: 60/084411	Db	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCTCAC	600
1	PRIOR FILING DATE: 1998-05-06	QY	601	CTGCATAGCAACTGGTAGACAGAGCCTACGGTTTACTTTGGAGACACATCTCTCCCAAGC	660
1	PRIOR APPLICATION NUMBER: 60/084600	Db	601	CTGCATAGCAACTGGTAGACAGAGCCTACGGTTTACTTTGGAGACACATCTCTCCCAAGC	660
1	PRIOR FILING DATE: 1998-05-07	QY	661	GTTTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGGCATCACCGGGGAGCTC	720
1	PRIOR APPLICATION NUMBER: 60/084627	Db	661	GTTTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGGCATCACCGGGGAGCTC	720
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1	PRIOR FILING DATE: 1998-05-07	QY	781	GTTCAACCGTGAATATCCACCATACATTTCAAGAACCAAGGGGTACAGGTGTCCCGTGGG	840
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1	PRIOR FILING DATE: 1998-05-13	QY	841	ACAAAGGGGACATGCGAGTGTGAGCTCAGAGTCCCTCAGCAGAAATTCAGAGTGA	900
1	PRIOR APPLICATION NUMBER: 60/084646	Db	841	ACAAAGGGGACATGCGAGTGTGAGCTCAGAGTCCCTCAGCAGAAATTCAGAGTGA	900
1	PRIOR FILING DATE: 1998-05-13	QY	901	CAAGGATCAAAAGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960
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1	PRIOR FILING DATE: 1998-05-15	QY	961	CCTCTCAAAACCTCATCTTCTCAATGTCTGTAACATGACTATGGAACCTACCTGCGT	1020
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1	PRIOR FILING DATE: 1998-05-15	QY	1021	GGCTTCCAAAGCTGGGGCCACCAATGCCAGCATCATGCTATTGTTCCAGGGCGCGT	1080
1	PRIOR APPLICATION NUMBER: 60/084653	Db	1021	GGCTTCCAAAGCTGGGGCCACCAATGCCAGCATCATGCTATTGTTCCAGGGCGCGT	1080
1	PRIOR FILING DATE: 1998-05-15	QY	1081	CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCGGCTGCGTCTGGCTGCTCTTCT	1140

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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6436.482 Million cell updates/sec

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1032	61.5	1032	4	US-09-700-397-1
3	939	55.9	939	4	US-09-700-397-5
4	704.6	42.0	6075	4	US-09-023-655-1366
5	703	41.9	70000	4	US-09-851-896-3
6	701.1	41.8	5532	2	US-08-475-035-3
7	701.1	41.8	5532	4	US-09-676-6108-17
8	700.9	41.7	14770	4	US-09-220-132-30
9	699.2	41.6	5092	4	US-09-620-312D-153
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23	695	41.4	4079	4	US-09-016-434-1174
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26	694.5	41.4	6856	4	US-09-566-921-42
27	694.2	41.3	5364	4	US-09-620-312D-345

28	694.2	41.3	7672	4	US-09-220-132-24
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83	691.8	41.2	14086	3	US-08-652-877-83
84	691.7	41.2	4003	3	US-08-991-840A-3
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ALIGNMENTS

RESULT 1

US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
; LOCATION: (130)..(1161)
; NAME/KEY: sig_peptide
; LOCATION: (130)..(213)
; NAME/KEY: mat_peptide
; LOCATION: (214)..()
US-09-700-397-2

Query Match 99.5%; Score 1671.3; DB 4; Length 1693;

Best Local Similarity 99.9%; Pred. No. 5.7e-26;

Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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767 GTACGAGAGTAAAGGTACCGTGAATCTATCCACATATTTTCAAGAGCAAGGGTACA 826
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541 GTACGAGAGTAAAGGTACCGTGAATCTATCCACATATTTTCAAGAGCAAGGGTACA 600
QY
827 GGTCTCCCGTGGGACAAAGGGGACACTGAGTGTGAAGCCTCAGCAGTCCCTCAGCA 886
Db
601 GGTCTCCCGTGGGACAAAGGGGACACTGAGTGTGAAGCCTCAGCAGTCCCTCAGCA 660
QY
887 GAATTCAGTGGTACAAAGGATGACAAAGAGCTGATTGAAGGAAAGAGGGGTGAAAGTG 946
Db
661 GAATTCAGTGGTACAAAGGATGACAAAGAGCTGATTGAAGGAAAGAGGGGTGAAAGTG 720
QY
947 GAAACAGACCTTCTCTCCTCAAACTCATCTCTTCTCAATGTCTTGAACATGACTATGG 1006
Db
721 GAAACAGACCTTCTCTCCTCAAACTCATCTCTTCTCAATGTCTTGAACATGACTATGG 780
QY
1007 AACTACACTTCTGCTGGCTCCCAAGCTGGGACACACCAATGCCAGCATCATCTATT 1066
Db
781 AACTACACTTCTGCTGGCTCCCAAGCTGGGACACACCAATGCCAGCATCATCTATT 840
QY
1067 GGTCCAGGCGCTGACGAGGTGAGCAACGGCAGCTGAGGAGGGGAGGCTGGCTGG 1126
Db
841 GGTCCAGGCGCTGACGAGGTGAGCAACGGCAGCTGAGGAGGGGAGGCTGGCTGG 900
QY
1127 CTGCTGCTCTTCTGCTGCTGCACTGCTTCAATTT 1165
Db
901 CTGCTGCTCTTCTGCTGCTGCACTGCTTCAATTT 939

RESULT 4

US-09-023-655-1366
; Sequence 1366, Application US/09023655
; Patent No. 6607879

GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENE BANK
; CLONE: g35787
; US-09-023-655-1366

Query Match 42.0%; Score 704.6; DB 4; Length 6075;
Best Local Similarity 36.8%; Pred. No. 0.00023;
Matches 1443; Conservative 0; Mismatches 159; Indels 2320; Gaps 411;

QY 1 GT-----TGCTCTCTTCAG-----CAAAAC 20
Db 2110 GTGAGAGATGT-TCTTCAGCTCCCTCACCAGCGCGCTCTACACGCTGACCATTAAC 2168
QY 21 -----AGTGG-----ATTTAAT--CTCTTTGCA--CAAG-----CT----- 48
Db 2169 TACAAGGAGTGGCAAGTATGAAATCACTCTT-CAGCCAAAGCGGACAGTGCCTGACA 2227
QY 49 ---T-----GAG-----AGCAACACA-----A-T-CTAT----- 67
Db 2228 AAGTCCAGGAGTCACTGTTAGCACTCAGCCAGGAGTACTATTTAAGGGTATCTCGG 2287
QY 68 -----CA--GGAAA--GA-----AAG-----AAGAAAAAACCAGAACCT 98
Db 2288 TGCACTGCCACTGGAGACTTTGATCACTATGAAGTCACTTAAACAAAAAC--AACTT 2345
QY 99 GA--CAA--AAAAG-----A--AGAAAAAGAA----- 119
Db 2346 CATTCAAACTAAAGCATTCCTCAAGTCAAGAAAAAGAAATGTATTTTTCAGCTAGTCCC 2405
QY 120 --GA-----AG-----AAAAA--A-AATCATGA-----AAC 141
Db 2406 TGGACGGTTGTACAGTGTCTCTTACTACAAAGTGGACAAT-ATGAAGCCAAATGAAC 2464
QY 142 -----CA--TCC--AGCC--AA-----AA-AT--GC-ACA-----A 162
Db 2465 AAGGGAATGGAGACAAATTTCCAGAGCCTCTTAAGGATCTAACTTGGCAACAGGACA 2524
QY 163 TT-----CT--ATCT--CTTGGGCA--ATCTTACGGGGCTG----- 193
Db 2525 CTGAGGACTTGCATGTGACTTGGTCAGAGC-TAATGGGAGATGTCGACCAATATGAGATC 2583
QY 194 --GCTGCTCT--GTGT--CTC--TTC-----CAA-G 215
Db 2584 CAGCTCTCTCAATGACATGAAGATTTCTCTCTTTTTCACCTTGTAAATACCGGAAC 2643
QY 216 GAGT-----GCC-----CGTG-GGC-- 229
Db 2644 GAGTATCATTTACTTCCCTTAACACAGGCGGCCAATACAAATTTCTTGTCTTGGAGATT 2703
QY 230 AGCGGAGAT-----GC--CA-CCTTC-----CC-----CAAA 253

Db 2704 AGCGGGATGTACAGCAGTCTTCAATGAGGGCTTACAGTCTCTAGTGTCTCAAA 2763
QY 254 -----GCT-----ATGCA-CAAC-----G-TGACGGT-----CCGGCA-----279
Db 2764 AATAATTCACATTTCTCCAAATGAGCAACAGATAGCCTGACGGTGAATGG-ACTCCTGG 2822
QY 280 -GGGGAGAGCG-----CC-ACCC-----TCAGG-----TG-----303
Db 2823 TGGGGGAGA-CGTTGATTCTCTACACGGTGTCCGCAATTCAGGCACAGTCAAAAGTTGACT 2881
QY 304 --C--ACTATT-----G-----ACA-----A--CCGG-----320
Db 2882 CTCAGACTATTCCAAAGCAGCTCTTTGAGCACACGTTCCACAGACTGGAGCGCGGAGC 2941
QY 321 -----TCA-----CC-----CGGGTGGCTG-----GCTAAA-----342
Db 2942 AGTACCAGATCATGATGCTCAGTCAGTCAGCGGT-CCCTGAAGATCAGATAAATGGTGT 3000
QY 343 -CCG-CAG--CACATC-CTC-----TA--TGCTGGGAATG-----ACA--AGT-----377
Db 3001 GGGCGACAGTTCACGATCTGTCCAAGGAGTAATTCAGACAATGCATACAGCAGTTAT 3060
QY 378 -----G--GT-----GC--CTGG-----ATCCCTGC-394
Db 3061 TCTTAATATGATGTCGCAAAAGCTGCTGTGGCGAAGATATGATATCTCT-GCT 3119
QY 395 -----G-----TGG--TCCTTCTGAGCAACAC-----CCA-----AAC-420
Db 3120 TCTAAGTAAATGGAATCTTCTGCGCAACATCAGAGCCAGCCACACTAAGCAACA 3179
QY 421 -----GCAG--TA--CA--GC-----AT--CGAGATCCAGA-----AC-----GTGG-449
Db 3180 CAAATTTGAAGATCTAAACACCGGCAAGAAATACAGATACAGATCTTAACCTGTCTAGTGG 3239
QY 450 A-----TGCTATGACGAGG--GCCCTTACACT-----GCTCG-----GT-----GCAG-----487
Db 3240 AGGCTCTTTA-G-CAAGAGAGCC--AGA-CTGAAGCC--AGA-CTGAAGCC-CAAGACAGTCCAGCAGTGT 3293
QY 488 -----ACAGACAA--CCACCACAAAG--ACCT-----CTAGGGTCC 518
Db 3294 CACCGACCTGAGGATCAGAGAGACTCCACC--AGGCACCTGTCTCTCCGT--GGACC 3348
QY 519 ACCTCA-----TTGTGCAAGTATCT-----CCCA-A-----AAT-T 547
Db 3349 GCCTCAGAGGGGAGCTCAGCTGGTACAA-CATCTTTTGTACAAACCCAGATGGGAATCT 3407
QY 548 -----GTAGAGA-T-----TT-----CT--T-CAGA--TATC--TCCATTAA--TG-----578
Db 3408 CCAGGAGAGAGCTCAGTTGACCCACTAGTCAGAGCTTCTCTTTCCA-GAACTTGCTAC 3466
QY 579 AAGG-GA-----ACAAATAT-----TAGCCTCAC-----CTG-C--AT-AG-----608
Db 3467 AAGGCAGAAATGACAAAGATGGTATGTA-ACTCAGTGGGAGCTGCTAATGAGTCT 3525
QY 609 --CA-A-CTGGTAGACCAG--AGCCTAGGTTACTTGGAGACATCTC-----TCC 654
Db 3526 TTCATATTTGGTAGAACAGTCCAGCCT-CTGT-----GAG--TCATCTCAGGGGGTCC 3576
QY 655 CAAAGCGG-----TTGGCTT-----TGTGAGTGAAGAC-----GAAT-686
Db 3577 --AATCGGACACGACAGACAGCCTTTGG-TTCAACTG-GAGTCCAGCCTCTGGGGACTT 3632
QY 687 --ACTT-----G--GA-----AATTC--AGGCATC-----ACCCGGGAGC 716
Db 3633 TCACITTTTATGAGTGAATCTCTATATCCCAATGGCA-CAAGAAGGAATCTGAA--3689
QY 717 AGTCAGGGGACT-AC-GAGT-GCAGT-----GCC-----TCC--AATG-----AGTGGC 756
Db 3690 AGACAAGGACCTGACGGAGTGGCGTTTCAAGCCCTTGTCTCTGGAAGGAAGTACGT-GC 3748
QY 757 CGCGCCCGTGGT-----AC--GGAG-----AG--TAAAGTTCAC--CG-----TGAA 792
Db 3749 TGTG--GGTGGTAACTCACAGTGGAGATCTAGCAATAAA-GTCACAGCGGAGACAGAA 3805

QY 793 CTA--TCCA-----CCA-----TA-----CATTT-----CA--G--AA-----GCC 817
Db 3806 C-AGCTCCAAAGTCTCCCAAGTCTTATGTCAITTTGCTGACATTCACAAACACATCTTTGGCC 3864
QY 818 A--A--GGGTACAGGTGTCCCC-G--TGG--GAC--AAAAGGGGAC--A-CTGCAAGTGT 862
Db 3865 ATCAGTGGAAAGG-GCCCCAGACTGGACAGACTACAA--CGACTTTAGCTGCAAGT-3920
QY 863 GAAGCCTCA-----GCA-----GT-----CCCC--CAGCAG-AATTC-----892
Db 3921 GTTGGC-CAGAGATGACATTTACTGTCTTCAACCCCTTACAAACAGAAATCAGAGGAC 3979
QY 893 -CA--GTG-----GTACAAAGATGA-----CAA-----AAGAC-----917
Db 3980 GCATTTGTATAGTCTTGTCTCCAGGA-GATCTATCAATCAAGTCAAGATGTCTAGT 4038
QY 918 --TGATT-----GAAGGAA--AG-AAA-----GGG-----GTG-----AAG--TG 946
Db 4039 GGTGATTCCTGAA--AACTTACAGCAACCAATTTTGGATCTGTGAGGACAAAGCCTG 4096
QY 947 ---GA--AAACAGACT--TT-CC--TCTCAAAACT-----CAT--C--TTCTT 981
Db 4097 ACAAGATACAAA--ACCTGCATTCGCGCCTCAGAACTCCACGGCAATGCTGTCTT 4153
QY 982 CAATGTCT-CTGA-----AC-----ATG-----ACTAT-----GGGAAT--ACAC--1014
Db 4154 GGATCCCTCTCTGATCTGACTTTGATGGTTATGATTTGAATGCCGGAATAATGGACCC 4213
QY 1015 -----TTGCTGGGCTCCAAACAAGCTGG-GCCACACAA--TGC-CAGCATC--AT 1059
Db 4214 AAGAAAGTTGAGT--TTTCCAGAAAGCTGGAGAAAGAAATCTCTGCTCAACATCATGAT 4271
QY 1060 GCTATT-----TG--GTCC-----AG-GC-----GCCG--T--CAG 1083
Db 4272 GCTAGTGGCCCAATAAGAGGTACCTGGTGTCCATCAAGTGCAGTGGCGGCGATGACCAG 4331
QY 1084 CGAGGTG-----AGCAACGGCACGT-----CGAGGAGGGCAG--GC-----1117
Db 4332 CGAGTGGTTGAG--ACAGCAC-TATCAATGA--TAGACCGCCGCCCTCTCCACG 4385
QY 1118 -----TGCGTCTG-----GCTGCT-----GC-----CT-----CTT--1138
Db 4386 CCCACACATTCGTGTGAATGAAAGGATG-TGCTAATTAGCAAGTCTTCCATCAACTTTA 4444
QY 1139 CTGGTC--TTGCACCTGCTTC-----TCAAT--TT-----1165
Db 4445 CT-GTCAACTGCAGCTGGTTTCCAGCACCAATGGAGCTGTGAATACTTTCACAGTGGTG 4503
QY 1166 -----TGATG-----TGAG-T--GCCA-----CT--TCC--CC 1186
Db 4504 GTGAGAGAGGCTGATGGCAGTGTGAGTGTGAAGCCAGACAGCAGCACCCTCTCCCTCC 4563
QY 1187 -ACCCGG-G-AAAGC-----TGCGGCCA-----CCACC 1212
Db 4564 TACCTGGAGTACAGGCAAAATGCCCTCCATTCGGGTGATCAGACTAAATTTTGGCCAGC 4623
QY 1213 A-----CC-----A-CC-AACA-CAAC-----AGCA-----1230
Db 4624 AAATGTCGGAATACTTAACAGCAACTCCAAGAGTTTAAATTAAGCTTTGGAGCAGAG 4683
QY 1231 ATGG-----C-----AACAC-CGA-----CAGCAA-----1249
Db 4684 ATGGAGACTTAGGTGGAAGAGCGATCCCACTCAGCAAAATTTCTGTGTGAGGACCACTG 4743
QY 1250 -----CC-----AATCAG-AT--A--TATACA-A-----ATGA-----1271
Db 4744 AAGCCACACACTGCTACAGAAATCAGCATTCGAGCTTTTACACAGCTCTTGTATGAGGAC 4803
QY 1272 -----AATT-----AG-----A-----AGAAACA-----1285
Db 4804 CTGAAGGAATTCACAAAGCCACTCTATTTCAGACACATTTTTTTTCTTTTACCATCTACT 4863

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QY 1286 ---CAG---CCT-----C 1292
Db 4864 GAATCAGAGCCCTTGTGGAGCTATTGAAGTGTGAGTGTGCTCTGTTTAAATTGGC 4923
QY 1293 ATG-----G-GACAGAAATT-----TG----- 1308
Db 4924 ATGCTAGTGGCTGTGTTGGCTTATTGTAATCTGACAGACAGAAAGTGAAGCCATGTCGAGAA 4983
QY 1309 AG-----G-CAG-----GGGAACAAAGA-----AT-----ACTT----- 1331
Db 4984 AGACCCCTGCGCGCTGCTGAGCATTCGTAGGATC-----GACCATTAATCTGTCACCTTAAAC 5040
QY 1332 -TGG-----GGAA-----AAGAGTT-TT-----A-AAAAAGAAA-----TTGAA--- 1364
Db 5041 CTGGCCAGAAAGGTAAACCGAAACTTCTTGTCCATAAATAAATACAGTCTTGAAGGG 5100
QY 1365 -AATT-----GC-----CT-----TGCAGATA--TT--T--AGG--TAC----- 1389
Db 5101 CATTTATGAAGCTACAGGCTGACTCCAACTACCTTCTATCCNAGGAATACGAGGAGTTA 5160
QY 1390 AA-----TGG-----AGT-----TT-----TCTT----- 1403
Db 5161 AAGAGCTGGGCCGGAACCACTGATGTGACATTGCACCTCTTCCCGGAGATAGAGGAAA 5220
QY 1404 -----TT-CCCA-----ACGGGA-----AGA- 1419
Db 5221 AATCGATACAAATATATTGCTTATGATGCCACGGAGTGAAGCTCTCCAATGTAGAT 5280
QY 1420 -----ACA-----CAGC-ACA-CCC-GGC----- 1435
Db 5281 GATGATCTTGTCTGACTACATCAATGCCAGCTACATCCCTGGCAACAACCTCAGAGA 5340
QY 1436 -----TT-----GGACC-----CACTG-----CAAG-----CTG-----CATCGT 1460
Db 5341 GAATACATTGTCACTCAGGAGCCGCTTC-CTGGACCACCAAGATGACTTCTGGAAAATGGT 5399
QY 1461 G-----CAACTCTT--TGGTG--CCAGTGT-----GGGC----- 1486
Db 5400 GTGGGAACAAACGTTCAACAATCGTCTGATGGTGACCCAGTGTGTTGAGAAGGCCGAGT 5459
QY 1487 -AAG-----GGCTCAG-----CCTCT----- 1502
Db 5460 AAGTGTGACCATTAATCTGAGC-CAGCGACACAGGATTCCTCTACTATGGGACCTCATCC 5518
QY 1503 TGC-----C-CACAGAT--GCC--CC--ACGTGGAAACATTTCTGG----- 1536
Db 5519 TGCAGATGCTCTCAGAGTCCGCTCTGCTGA-GTGGACCATCCGGAGTTTAAGATATGC 5577
QY 1537 -----AGC-TG-GC-----CATC--CCAAATTC--AT-----CA 1560
Db 5578 GGTGAGGAACAGCTTGTATGACACAGACTCATCGGCCACTTTCATATACGGTGTGGCCA 5637
QY 1561 GTCCATAGAGAC--GAA-----CA-----GA--A-----TGAGACCT----- 1588
Db 5638 GACCATGAGTCCAGAAACCCAGCTCTCTGATCCAGTTTGTGAGAACTGTCAAGGAC 5697
QY 1589 -TC-----C-GGCCCAAGC-GTG--GCCGTGC-----GG 1612
Db 5698 TACATCAACAGAACCCGGGTGTGGGCCCA--CTGTGTGTGCACTGCAGTGTGTGG 5755
QY 1613 GCA-----CT-----TTGG-----TAGACT----- 1627
Db 5756 GTAGGACTGGAACCTTATTGCAATTTGAGACCGCAATCTCCAGAGTTAGACTCCAAAGACT 5815
QY 1628 -----GTGC-----CAC-----CAC--GG----- 1639
Db 5816 CTGTGGACATTTATGAGCAGTGCACGACCTTAAGACTTTCACAGGGTTCAATGGTCCAGA 5875
QY 1640 C---GTGT--GT-TGTGAA---AC-----GTGAATATAAA-----AGAGCAA-AA 1674
Db 5876 CTGAGTGTCAATGATGTCTCACTACATCAGTGTG--TAAGAGATGTCTCTCAGAGCAAGA 5932
QY 1675 A-----AAAA 1679
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Db 5933 AGCTACGAGTGAACAAGAAA 5954

RESULT 5

US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RIS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match 41.9%; Score 703; DB 4; Length 70000;

Best Local Similarity 40.5%; Pred. No. 0.031;

Matches 1394; Conservative 0; Mismatches 196; Indels 1854; Gaps 388;

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QY 1 GTTG-----TG-----TCCT-----TCAG-----CAA 17
Db 49493 GTTGGCCAGGCTGGTCTCGAAGCTCTGGCTCAGGTGATCTGACCATCTTGGCCTCCAA 49434
QY 18 A-----A-----CAG-TGG-----ATTT-----AAAT 33
Db 49433 AGTGTGTGTATACAGAGCCACTGCAGCTGGCCAGTTATTTTAAAGTTTTTAAAAAAT 49374
QY 34 CTCCTT-----GCACA-----A-GC-----TTG----- 50
Db 49373 TT--TTAATTTAATTTTGTGGGTACATAGTACCATATATATTATTATTATTATTT 49316
QY 51 ---A-GA-----GCA-----ACAC-----AA--TCTATCA-GG-AA--AG-- 75
Db 49315 TAAATGAATTAATATTTTGAAATTTTCACACTTTTAAATTTCTAAATGTTAAATATAGAT 49256
QY 76 AAGAAA-----GA-AAAAACC-----GAACCTCAGAAAA--AGAAGAA 114
Db 49255 AAGAAAAATCCAGATGATTAAAAAATCTTTGTGATCTCT--CAATAATTTTTCAGAGTATA 49198
QY 115 AAGAAGAAGAAA-----AAAAATCATGAAAC-----CA-TCCA-----GCC- 150
Db 49197 AAG-GGATCAATAGAGCCAAAGAACTTGAGAACTGTGAGTTAGATCATTCNAGGGCCC 49139
QY 151 -----AAAAATG--CACAAT-----CTAT-----CTCTT 173
Db 49138 ACCAGTGTCTAAAAATGTCCACAGTTTCAAAATGAACATAITTTATAGTTTCAGCCTTTT 49079
QY 174 GGGCAA-----TCTTC-ACG--G-----GG-----CTGGCTG-CTC--TGT 203
Db 49078 GGGCAACAACTCTCTTCCAGTTTGTGACCTTTGGTATATAAAACAGGATGTCTCTGAATGT 49019
QY 204 GTCTCT--TCCAAG-----GAGTGCCCGTG-----CGCA-----G--CGGAGATGC 240
Db 49018 GTC-CTGATC--AGCTTTTAGAT--CCCGGGGTCTCTCATGTTCTGTCACTGACA--C 48965
QY 241 -C-----AC--CTTC--CCCAAA-----GCTATGGACAACTG--ACGGT--C- 274
Db 48964 TCAGTAAACAGACTTCTGTACATACGGTATTCTATAGAAAACGTGCACACGGTGGGGG 48905
QY 275 CGS-----CAG-----GGGG-----AGAGCG-----CCACCTTC 298
Db 48904 CGGTGGCTCACGCCCTGTATCCAGACTTTTGGGGTGCACAG-GCGGGTGGATCA---TG 48849
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QY	299	AGGTGCACTA---TTGA-----CAAC-CGGG---TC-----ACCCGGGTGGCC---	334
DB	4848	AGGT-CAGGAGTTTGAGACCAGCTGGCCAAACACAGGAGTTTGAGACCAGCTGGCCAAC	48790
QY	335	TGG-----CTAA---AC-----C-GCA-----GCAC-----	351
DB	48789	GTGGTGAACCCCGTCTCTACTAAATAAATAAATAAGCTGGGCATGGTGCCACGTGCC	48730
QY	352	--CA-TC-----CT-CT-----ATGCTG-GGAATGACAA-----	375
DB	48729	TGCAGTCCCAGCTACTTTGGGAGGCTCAGGACAGAGATCGCTTGAACTGGGAGCGGAG	48670
QY	376	---GTGCT--GCCTGGATC-----CTC--GGGTGG-----TCCT	402
DB	48669	GTGTGTGTGAGCGGAGATCGCGCACTGCACCTCCAGCTGGCGCAGAGTGGGAGACTCCA	48610
QY	403	TCT-G-----AG--CA--ACACCCA-----AACGCAGTA-----	426
DB	48609	TCTCGAAAAAAGATATATGCACACATATGTCTGTAACACAGTAACGTCTCTCTCT	48550
QY	427	-C-AG-----CA--TCGAGAT-----CCAGAAAGCT-----	447
DB	48549	GCTAGGTTTAATATGTTCTACTCTAGATGTGTAACACACAGTAAGGGCTTTGAGGCA	48490
QY	448	GGA--TGCTGT---AT-----GACGA--G---GGC-CCTTACAC--CTGCTCGG--	482
DB	48489	GGAAGTGTGTTCTATAATAAACCAACGAATATGCTGGCACCCTGCCACAGGCTGCTGGC	48430
QY	483	TGCA-----GACAG--ACAAACCAACCA-----AAGA-----	506
DB	48429	TGCACACTCAGGCTTTGGCTTGCAGGATCTTACGCTCCAGGGAAGATGAGAGCAACA	48370
QY	507	-----C-----CT--CTAGGGTC-----CACCT--	522
DB	48369	CGGGACCACTGAAGGAGCAGGATGCTCACTCGGGCCAGTACTGCGTGTCTACTTAA	48310
QY	523	--CATT-----GTG--CAAGTATCTCCA-AAATGTAGAGATTCTT-CAGATA--	566
DB	48309	GACATCTGTAGAGGTGACCAAGTGTCCACCATAAATTTTCCACAACCTTCCAGATAA	48250
QY	567	---T---CTCCATT---A-ATGA-----AGG-GA-----ACA-----	587
DB	48249	GTATTGACACCACATTTTCCAGATGAGGAATTCAGGCTGACAGTGCATGCTTGTCT	48190
QY	588	-----A--TAT-----TAG-----CCTCACCTG-CAT---AG---CA---	610
DB	48189	CAGGGCCAGTCTATGCCAGAGCTGTCATTTTCCCTCTCTGTCATGCAAGTGCCTAAT	48130
QY	611	-----ACTGCT---AG--ACCGAGGCTAC-----G-GTTACTT---G--GAGA	643
DB	48129	GGGGGACACAGGTGGAAAGGTATCCACAGCACACAGAGGTGGTGTATTTTGGGCTCAGA	48070
QY	644	---CACAT-----CTCTCCCAA-----AG-C--GGT-----TG-GCTTT--GTG--	673
DB	48069	GGGGGACTTGGAGGCT-TCTTGAGGGAGAGTCAAGGTCTGAAGTCAAGTCTTGGGTGG	48011
QY	674	-AG-TGA-----A--GACGA-----ATAC--TTGGAA-----ATTGAG	700
DB	48010	AAGATGATTGGAGCAGCTGCATAGGAGGAGACAGTGGGAGGAGGCTCCAGTCCG	47951
QY	701	G-----GCAT--CACCGGG-----A-GCA-GTCA--GG-----GGACT-A	729
DB	47950	GACAGCCCTCTGCAATCCACCGGGGCCCAAGGACAGCACGCGCTCTGGGCTCA	47891
QY	730	---CGA-----GTCCA-----GTGC-CTCCAAATGACGTG---CCGCG--	760
DB	47890	CCGACATGGCCAGGTGCAGGGGGTGTTCGCGTGTCTCC--G-CG-GGCATCCGGTT	47836
QY	761	---CCGCTGG-----TACCG-AGAGT-AAAG-----G--TCAC-----CGTG	790
DB	47835	GGCCCGGTGGTCAGCAGCACTATGGCACAGTCGAAAGCGGTTCGCATCACCGCACGTG	47776
QY	791	AA-----CTATCCACCATACA-----TTTCAGAA-----	814

47775	DB	CAGGGCCGGTGTTC	CGGAGCTGGTGT	GTGTACAGTTCAGCCCGGTTTCAGCAGCAT	47771
815	QY	-----GCCA-----	AGG-----GT-----ACAGG-----	-----TG-----	830
47715	DB	GGGGCCATCTCGGGAGAGCGT	CAGGCTGAGTTAGCA	CAGGCACTCGGGGAGCTGCCG	47656
831	QY	TTCCCGTGGGACAAAGGGGAC	ACTG-CA-----G-----TGTGAGCCT-CAGCAGT-C--	877	
47655	DB	ACCCC--GGGACA--CGTGGCACTGCCACTT	CTGCTCTGAGAGGCTACAG-GTACTG	47602	
878	QY	-----CCCTCAGC-AGA-ATTCCAGTGGTA-----CA-----AG-----	904		
47601	DB	GGATGTTGAAAGCGCT-AGCAAGAGGATTCAGGGGCGAGCCCCAGTTCTTAGGGGGGCC	47543		
905	QY	-----GA--TG-----A-CA--A-----AAGACTGATTGAAGG-----AAAG--AAAG--	935		
47542	DB	TAGACTGCGCTCCCATCCATCAGCATCCCAAGACT-----AGGACAAAGCCCAAGA	47489		
936	QY	-G-GGTGA-----AAGTGGAAAC--AGACCTTTCTCT-----CTCAA--AACTCA-	974		
47488	DB	TGTGCTGACTGTTTAAAGAGG---CTTCTGGTCTCTTCTAGTGC-CAACAGAACCCAC	47434		
975	QY	TCCTTCTT-CAA-----TCTCTCTGAA-CA-----TG-A-----	999		
47433	DB	TCTCTTGCAAGGCTCCTCTGGGCGCTGTC-CTGAAGCACCCCGTCCCTGCATCCCTC	47375		
1000	QY	CTATGGGAAC-----TA-----CACTTG--CGTGG-----CCT--	1025		
47374	DB	CCT--GGAAACCTGCAAGGTATCACCTCTCACTGGGCGCTTGGCAATGCACATCCCTGG	47318		
1026	QY	-----CC-----AACA-----AGC-----TGG-GCCACA-----CDAATG-	1049		
47317	DB	CAGAGCTTGGAAACAGGAGGGAGCGCTGGCTTTGGAGTCA	CAGACCTGAGGCCAAAGC	47258	
1050	QY	CCAG--CA-TCAT-----GCT-----ATT--TG-----GT--CCAGGCGC-CGTC	1081		
47257	DB	CCAGCTTCACTCATCCAGCTGCCTCGGCTTGGATGGGTCACTGTAGCCATGTGCATTC	47198		
1082	QY	AG-----C-----GA--GG--TG--AG--CA--ACGGCACGT-----C-----	1104		
47197	DB	AGGGCTTCTGTGAAGATGGGAATGCAAGTCCCACTC	CACAGCATGTGATGCAATGAGT	47138	
1105	QY	GA-----GG-AGGGC--A-----GGC-----TGC-----GT-----C	1123		
47137	DB	GACCAAACTACAGGAAGGCGCTGACTCGGTGCTCGGTCTCTGGAATGCAGAGTACCC	47078		
1124	QY	T--GGCT-GC--TG--CCT--CTTCTGG-----TC-----TTG-----C-----AC-CTG	1153		
47077	DB	TGAGGCTGGCAGTGCCCTCCCTCGTGGCCATCACATTCAGAAAGTAGGCCATGAACTCTG	47018		
1154	QY	-----C-ATC-----TCAATTTTGAT-----GTAGTG--CCA-----CTTCC--CC	1186		
47017	DB	GGGATCCCAATTCTCTGTCAAGCTGTGCTCTCTGTGTA-TGAGACAGAGGCGCTCCATCC	46959		
1187	QY	ATCC-----GGGAA-----AG-GCTGGC--GCCA-----	1207		
46958	DB	TCCAGGAGGACAGAGCTTAGTTAGGGGAGAACTCAGAGAGATGCCACCGAGGCTC	46899		
1208	QY	-----CCACCACCAACACAAACAGCAATGGCAACACCGACAGCA	1248		
46898	DB	CCTGTGTGTCAGCTAGGCCCGACCAACCACCAAC-CA-CCAT--CATCATC--CATCA	46846		
1249	QY	--ACCA--ATCA-----GAT-----AT-AT-A-----CAA-ATGA--AATTAGAG-----	1280		
46845	DB	TCATCATCATCTTGATGGTTAATAATGATGTCACTTGATTGGATT-GAAGGATGT	46787		
1281	QY	AAA-----CACAGCC-----TCAT-----GGG-----AC-AG--AA-ATTGCA	1309		
46786	DB	AAAGTATTGAC--CCTGGGTGTGC-TGAGAGGGTGTCTAACGGAGATTACATTGCA	46730		
1310	QY	G-----GGAGGGGAA--CAAAGA-ATA--CTT-----TGGG-GGG-----AA--A-----	1341		

Db 46729 GTCAGTAGGGAAGGC--AGACCTACCCTTAATCTGGGTGGCCACCACCTAATCAGCTGC 46572
Qy 1342 -AG-----AG-TTTTAAA-----AAGAAAT-TGAAAA-----TT-GC 1370
Db 46671 CAGACGCCAGATATAAAGCAGCAGAAATAATGTGAARAGCTAGACTGGCTTAGC 46612
Qy 1371 CTTCAG-----ATATTT---AGGTACAAATGGAGTTTCTTT---TTCC---CAAAAGGGA-- 1416
Db 46611 CTCCAGCTACATCTTCTCCGGTGC--TGGA--TGCTTCTGCCCTCAAC--ATC 46560
Qy 1417 AGA--ACA-----CAGCACACCGG--CTTGAC-----CCAC-----TGC 1448
Db 46559 AGACTCCAACTCCTTCAGC--CTCGGACTTGGACTGGCTTCTCTTCTCAGCTTGC 46503
Qy 1449 AA--GC-----TG--C-----ATCGT-----C-----AA--CCTCTT 1470
Db 46502 GATGGCTATTGTGGGACCTTGTGATCTGTGAGTTAATGTCTCTTAATAATCCCTT 46443
Qy 1471 TGGTGCCAGTGGGCAAG--GGCTCA--GCCTCTCTGCCCA--CA-----GAGTGCC--- 1517
Db 46442 TAG--GCCA-----GGCAGGTGGCTCAGCCTATAATCCAGCACTTTGGGAG--GCCAAG 46390
Qy 1518 -CAGTGCAGTGGGCAAG--GGCTCA--GCCTCTCTGCCCA--CA-----GAGTGCC--- 1517
Db 46389 CAGGAGATCAGGAG-----TCAGGAGATCGAGACCATCTCTGCTAACACGCTGAAC 46335
Qy 1558 -TCAGTC-----C-ATAGACAGCAACAGAAATCAG-----ACCT-----T 1589
Db 46334 CTC-GTCTCTACTAAATATC-AAAAAATTAGCCGGGTGTGGCGGGCGCTGTAGT 46277
Qy 1590 CC-----GGC-----CCA--AGCOTGGC--G---CTGGC--GGCA--CTTTG- 1620
Db 46276 CCGAGTACTCAGGAGGCTGAGGAGGAGATGGCATGAACCTGGGAGGAGAGC-ITGC 46218
Qy 1621 -GT-----AGACTGTGCCAC--CA--CGCGGTGTGTGA--AACTGTA----- 1658
Db 46217 AGTGAGCAAGATTGTGCACTGCACTCCAGCCTG-G--GGACAGAGCGAGACTCCGTC 46161
Qy 1659 --AATAAAAGAGCAAA-AAAAA 1679
Db 46160 TCAAAAAAATA--AATAAAAAA 46139

RESULT 6

US-08-475-035-3
; Sequence 3, Application US/08475035
; Patent No. 5985553
; GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Peirymann, David G.
; REGISTRATION NUMBER: 33,438

; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3816
; US-08-475-035-3

Query Match 41.8%; Score 701.1; DB 2; Length 5532;
Best Local Similarity 39.3%; Pred. No. 0.00023;
Matches 1387; Conservative 0; Mismatches 196; Indels 1943; Gaps 374;

Qy 1 GTTGTGTGCC--TTTCAG-----C-AAAACAG--TGGA-----TTT----- 29
Db 1395 GTT-TTGTGTGATTCAGGCTTGGCCTGAAAACAGGACGACCTCCATGCTTTTGAGAAC 1453
Qy 30 ---AAATC-T-----CCTTGC-ACA-----AG-----CTTG-AG-----AGC- 55
Db 1454 TAGAATCATACGCGGCGAGCAAGCAACATGCTCAGTTTCTCTTGCACTGCTCAGCC 1513
Qy 56 ---AACACA--ATC-----TA-----TC-AGAAAGAA-----AGA-- 82
Db 1514 TGAACATAAATCCTTTGGGATTACGCTCCCTCAAGGAGATAAGTGTGAGATGTGATAA 1573
Qy 83 -----GAAAAAACCAGAACCTG---A--CAAA-A-AAGAA---GAAAAAGAA----- 119
Db 1574 TTTCAGGAAACAAA---AATTGTGTATGCAATACATATACTGGAATA---AATGTT 1628
Qy 120 ---GA-----AGAAAA-AAAAT-----CA-----TCAAAACCATCCAGC--C 150
Db 1629 TGGGACCTCCGGTCAGAAACCAAAATTTATAAGCAACAGAGGTGAAAA---CAGCTGC 1683
Qy 151 AA-----AAATGCACATTTCT---ATCTTTGGGCAATCTTCAGC--GGCTGGCTG- 197
Db 1684 AAGGCCACAGGC-CAGGTCTGCCATGCTTTGTGC--TC-CCCCGAGGGCT-GCTGGGGCC 1738
Qy 198 -----C-----TCTGTGTCTCTT-CCAAGGAGTG-C--CCGTGCGCAGCGGA----- 235
Db 1739 CGGAGCCCGAGGACTGCTCTCTTGCC--GGAATGTGAGCCGAG--GCAG--GGATGGCTG 1794
Qy 236 GA-----TGCCACCTTC-----CCCAA---AGCTA-TGACAAAC-----GTG---A 269
Db 1795 GACAAGTGCAAGCTTCTGGAGGGTGAGCCCAAGGAGTTTGTGAGAACTCTGAGTGCA 1854
Qy 270 CGGT-----CC--GG-----CAGG--GGGAGAGC 289
Db 1855 CAGTGCCACCCAGAGTGCCTGCTCAGGCCATGAACATCACTGACAGAGCGG-GACC 1913
Qy 290 -GCCACCTC-----CAG-GTG--CACT--ATTGA-----CAACCGGGTCA-----CC 325
Db 1914 AGACA-ACTGTATCCAGTGTGCCCACTACATTCAGCGCCCTCCCTGGTCAAGACCTGCC 1972
Qy 326 CGG-----GT-----GG-----CCTGG-CT--AA--ACCGGAG----- 348
Db 1973 CGGAGGAGTCAATGGGAGAAAAACAACACCTGTCTGGAAGTA-CGACAGACGCGGCCAT 2031
Qy 349 -----CA-----CCATC--CT-----ATG-CTGG-----GAA--- 369
Db 2032 GTGTGCCACCTGTGCCATCAAACTGCACTACGATGCACTGGGCCAGGCTTTGAAGGC 2091
Qy 370 TG-----ACAAAGTGGTGCCT--GGATCC-----TCGC-----GTGG-----TCCT 402
Db 2092 TGTCCAAAGATGG-GCCTAAGATCCCGTCCATCGCACTGGGATGTGGGGGCCCCCTCT 2150
Qy 403 -----T-----CTGAGCAAC-ACC-----CA-----AA--CGCAGTACAGCATC 433

Db	2151	CTTGTGCTGTGTGTGGCCCTGGGATCGGCTCTTTCATGCGAAGCGC	---	CA-CATC	2205
Qy	434	GAGATCCAGA	---ACG-T---GGA---TG-TGTATGACGAGG---	GCC-CT	469
Db	2206	G---TTGGAAGCGGACCGCTGGGAGGCTGCTGCAAGGAGGAGCTTTGTGAGACCTCT	---	2261	
Qy	470	TAACAC	---CT---	GCTC	---
Db	2262	TACACCCAGTGGAGAAGCTCCCAACCAAGCTCTCTTGAGGATCTTGAGGAACTGTAATT	---	2321	
Qy	493	CAACCAACCCAAAGCC	---T-CTAGG---	TC-CAC	---
Db	2322	CAA-----AAAGATCAAAGTGCT-GGGCTCCGTGGGTTCGGCAGCGTGTATAAGGAC	---	2374	
Qy	522	TC---AT-----TGTCAAAGT---ATCTCCC-----	---	582	
Db	2375	TCTGGATCCAGAAGTGGAGAAAGTTAAAT-TCCGCTCGCTATCAAGGAATT-AAAGA	---	2432	
Qy	554	-----ATTTCCTC-----A-GATAT-CTCCATTA-----TGAAG-	---	582	
Db	2433	AGCAACATCTCCGAAGCAACAAGGAATCCTCGATGAAGCCTACGTGATGCCAGCGT	---	2492	
Qy	583	GAACAA-----T-----ATTAGCCTCACTGCA---TAGCAACTGG	---	615	
Db	2493	GGACAACCCCACTGTGCGCCCTGTGGGCATCTGCTCACTTCCACCGT-GCAACTCA	---	2551	
Qy	616	TAGAC-CAG---A-G-CCTACGGTT-----ACT---T---GGAGACAC-----A	---	647	
Db	2552	T-CAGCAGCTCATGCGCTTCGGCTGCTCTGGACTATGTCCGGGA-ACACAAGACAA	---	2609	
Qy	648	TCT---CTCCCAAGCGGT---TGGCT---TTGTGAGTG-----AAG---ACGAA	---	685	
Db	2610	TATTGGCTCCCA-----GTACCT-GCTCAACTGTTGTGCAGATGCCAAGGGCATGAA	---	2663	
Qy	686	-TACTTGGA-A-----ATTCAAG-GCATCACCCGGGA---GCAGTCAGG---GGACT	---	728	
Db	2664	CTACTTGGAGCAGCGTGCCTT---GGTGCA---CCGGACCTGGCAGCAGGAAGTACT	---	2717	
Qy	729	-----ACAGTGCAG-TGCCTCA-ATGAC-G-----TGCGCGC--GCC--C-G-T-	---	765	
Db	2718	GGTGAAAC-ACCGCAGCATG--TCAAGATCAAGATTTTGG-GCTGGCCAACTGCTG	---	2772	
Qy	766	GGTACGG-AGAGTAAGGTCACCGTG-----AA---CTATCCA-----CC	---	801	
Db	2773	GGTGGGAAG-AGAATAACCATGCAGNAGGAGCAAGTGCCTATCACTGGATGCG	---	2831	
Qy	802	AT---A-CA-TTT---CAGAA-----GCCA-AG-----GG---TACAGGTG	---	830	
Db	2832	ATTGGATCAATTTTACAGAACTATATACCAACAGAGTGATGCTGGAGCTAC-GGGG	---	2890	
Qy	831	TCGCCG--TGGGA-----CAA---A-AGG-GGA--CACTG-CAGTG	---	861	
Db	2891	TGACCGTTTGGGAGTTGATGACCTTTGGATCCAAAGCCATATACGCGAATCCCTGCCAGC	---	2950	
Qy	862	TGAAG---CCTC-----AGCAG-----TCGCCCTCAG-----CAGA-----	---	888	
Db	2951	---AGATCTCTCCATCTCGAGAAAGGAGACGCT-CCCTAGCCACCATATGTACC	---	3006	
Qy	889	---AT-TC--CA-G---TGATCAA-----GGATGA-----CA-----AAA	---	914	
Db	3007	ATCGATGCTACATGATCATGTT-CAAGTCTGGATGATAGACGCAGATAGTCGCCCAA	---	3065	
Qy	915	G--AC-TGA-TTGA--A-AGAA-----AGA-----	---	932	
Db	3066	GTTCCTGTGATGATCATGAAATCTTCCAAATGGCCCGAGACCCCGCTACTTGT	---	3125	
Qy	933	A---AGGG--TGAAG-TGGA-----AA---ACAGAC-----CTT--T--	---	960	
Db	3126	CATTGAGGGGATGAAAGAATGCAATTGGCAAGTCTCTACAGACTCCAATCTACCGTGC	---	3185	
Qy	961	CCT-----CTCAA-AA-----CTCAT-----	---	975	

[illegible]

QY 1445 ---CTG---CAAGCTGCATC---GTGC---AAC-CT-----CCT---TGGT 1474
Db 4305 GGTCTCTGCTCAAG-GCTTCCTCACTGCAAAACACTAAGATCAAGAGGCTTCATGGC 4362
QY 1475 GCCAG-----TGT-----G-----GGCA-----AG---GGCTCAGCTCTC 1502
Db 4363 CCCAGAGCCGGATCGGTACTGATCAAGTCAATGCGAGGTACAGTAGGATAAGCCATC 4422
QY 1503 TG-CCC-----ACAGAG-----1513
Db 4423 TGTCTCTCTCTGGGCAAGAGAAACGAGGGGATGAATCTCTCTTAGACTTACTTTTG 4482
QY 1514 -----TGCCTCCACG-----TGGAAACA-----TTC-----TG---1535
Db 4483 TAAAAATGTCCCAAGGTACTTACTCCCACTGATGGACCAAGTGTCTTCCAGTCAATGAGC 4542
QY 1536 G-AG-CTG-----G-----CCATCCC-----AAATCA--AT-----CAGT 1562
Db 4543 GTTAGACTGACTGTTGTCTCTTCCATCCATTTGTTTGAACCTCAGTATGCGGCCCTGT 4602
QY 1563 C-----CAT-----AGAGAGCA---ACA---GAATGAGACC-----TTCCGGC 1594
Db 4603 CTGTGCTCATGAATCATGAGAGAGAGAGTGCACATCAATATATTAATCTCGGATTCAGC 4662
QY 1595 CCAAGCTGGCGCTGC---GGGACTTTGG---TAG---AC-----TGTG-----1630
Db 4663 CCA---CATTTG---GATTCATCAGCA---TTTGGACCAATAGCCACAGCTGAGATGTGAATA 4718
QY 1631 CC-----ACCAGCGGTGTGTGT-G---AAACG-----T 1656
Db 4719 CCTAAGGATACACCGCTTTGTTCTCGCAAAACGTATCTCTCTTAATTTGAGGCTCAGAT 4778
QY 1657 GAAAT--A--A-----AAAGAGCAAAA-----AAAA 1679
Db 4779 GAAATGCATCAGTCTCTTTGGGGCATAGATCAGAGACTACAAAA 4824

RESULT 7

US-09-676-610B-17
; Sequence 17, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 17
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (187)....(3819)
US-09-676-610B-17

Query Match 41.8%; Score 701.1; DB 4; Length 5532;
Best Local Similarity 39.3%; Pred. No. 0.00023;
Matches 1387; Conservative 0; Mismatches 196; Indels 1943; Gaps 374;

QY 1 GTTGTCTCC---TTTCAG-----C---AAAACAG---TGGG-----TTT-----29
Db 1395 GTP-TTTGTGATTGAGGCTTGGCTTGAAACAGAGGAGGACCTCCATGCTTTGAGAACC 1453
QY 30 ---AATC-T-----CCTTC-ACA-----AG-----CTTG-AG-----AGC- 55
Db 1454 TAGAATCATACGCGCAGACCAAGCAACATGCTCAGTTCTCTTTCGATCGTCAGCC 1513
QY 56 --AACACA--ATC-----TA-----TC-AGGAAGAA-----AGA-----AA 82

Db 1514 TGAACATAACATCTCTGGGATTACGCTCCCTCAAGAGATAAGTGATGGAGATGTGATA 1573
QY 83 -----GAAAAAACCCGAACCTG---A---CAAA-A-AAGAA-----GAAAGAA- 119
Db 1574 TTTCCAGGAACAAA---AATTTGTCTATGCAATATCAATTAATGGAATAA---AATCTTT 1628
QY 120 ---GA-----AGAAAA---AAAAAT-----CA-----TGAACACCATCCAGC--C 150
Db 1629 TGGGACCTCCGGTTCAGAAAAACAAAATATATAAGCAACAGAGGTGAAAA-----CAGCTGC 1683
QY 151 AA-----AAATGCACAAATCT---ATCTCTTTGGGCAATCTTTCAG-GGCTGGCTG- 197
Db 1684 AAGCCACAGGC-CAGGTCTGCCATGCTCTGTGC--TC-CCCCAGAGGCT-GCTGGGGCC 1738
QY 198 -----C-----TCTGTGTCTCTT-CCAAGAGTG-C---CGTCCGCGAGCGG- 235
Db 1739 CGGAGCCCGAGGACTGCTCTCTTTGCC--GGAATGTACGCGAG-GCAG-GGAATGCGTG 1794-
QY 236 GA---TGCCACCTTC-----CCCAA---AGCTA-TGGACAA-----GTG--A 269
Db 1795 GACAAGTGCAAGCTTCTGGAGGCTGAGCCAGGAGTTTGTGAGAACTCTGAGTGCTATA 1854
QY 270 CGGT-----CC---GG-----CAGG---GGGAGAGC 289
Db 1855 CAGTGCCACCAGAGTGCTCTCAGGCCATGAACATCACTGACACAGGACGGG-GACC 1913
QY 290 -GCCACCT---OAG-GTG---CACT---ATTGA-----CAACCGGTCA-----CC 325
Db 1914 AGACA-ACTGTATCCAGTGTGCCACTTACATTCAGCGGCCCTCTCTCATCGACACCTGCC 1972
QY 326 CGG-----GT-----GG-----CCTGG-CT--AA--ACCGGAG- 348
Db 1973 CGGAGAGTCACTGGGAGAAAAACAACCTCTGTCTGGAAGTA-CGACAGACCGCGCCAT 2031
QY 349 -----CA-----CCATC---CT---CT---ATG-CTCG- 369
Db 2032 GTGTGCCACTGTGCCATCAAACTGCACCTACGATGCATGGGCGAGCTTTGAAGGC 2091
QY 370 TG-----ACAGTGTGCTCT-GGATCC-----TGGC-----GTGG-----TCCT 402
Db 2092 TGTCCAAACGAATGG-GCCTAAGATCCGTCCTCCATCGCCACTGGGATGTTGGGGCCCTCT 2150
QY 403 -----T-----CTGAGCAAC-ACC-----CA---AA---CGCAGTACAGATC 433
Db 2151 CTTGCTGTGTGTGGCTTGGCCCTGGGATCGGCTCTCTCATCGAAGCGC---CA-CATC 2205
QY 434 GAGATCCAGA---ACG-T--GGA---TG-TGTATGACGAG- 469
Db 2206 G---TTGGAAGCGCAGCTGCGGAGGCTGCTGCAGGA-GAGGAGCTTGTGGAGCCTCT 2261
QY 470 TACAC-----CT-----GCTC-----GG-----TGCAG--ACAGA---492
Db 2262 TACACCCAGTGGAGAGCTCCCAACCAAGCTCTCTTGAAGATCTTGAAGAACTGAATT 2321
QY 493 CAACCAACCAAGACC---T-CTAGG-----TC---CAC-----C 521
Db 2322 CAA-----AAGATCAAGTCT-GGGCTCGGTGGCTTGGCAGCGGTGTATAGGGAC 2374
QY 522 TC---AT-----TGTGCAAGT---ATCTCCC-----AA---AATTTAGAG- 553
Db 2375 TCTGGATCCAGAGGTGAGAAAGTTAAAT-TCCCGTGTCTATCAAGAAAT-AGAGA 2432
QY 554 ---ATTCTTC-----A-GATAT-CTCATTTAA-----TGAAG-----582
Db 2433 AGCAACATCTCCGAAAGCCAAACAGGAAATCTCGATGAAGCCTACGTGATGGCCAGGT 2492
QY 583 GAACAA-----T-----ATTAGCTCACCTGCA---TAGCAACTGG 615
Db 2493 GGACAAACCCACGCTGTGCGCGCTGTGGGATCTGCTCCTCACCTCCACCGT-GCAACTCA 2551
QY 616 TAGAC-CAG---A-G-CCTACGGTT- 647

Db 2552 T-CAGCAGCTCATGCCCTTCGGCTGCTCTCGAGTATGTCGGGA-ACACAAAGACAA 2609
Qy 648 TCT---CTCCAAAGCGGT---TGCT---TTGTGAGTG-----AAG---ACGAA 685
Db 2610 TATTGGCTCCCA---GTACCT-GCTCACTGTGTGTGTGAGATCGCAAAAGGGCATGAA 2663
Qy 686 -TACTTGA-A-----ATTGAGG-GCATCACCCGGGA---GCAGTCAGG---GGACT 728
Db 2664 CTACTGTGAGGACCGTCGCTT---GGTGCA---CGCGACCTGGCAGCAGCAAGCTACT 2717
Qy 729 -----ACGAGTGAG-TGCTCCA-ATGAC-G-----TGCGCGC---GCC---C-G-T- 765
Db 2718 GGTGAAAC-ACCGCAGATG---TCAAGTACAGATTTGG---GCTGGCCAAATCGTG 2772
Qy 766 GGTACGG-AGAGTAAAGTCAACCGTG-----AA---CTATCCA-----CC 801
Db 2773 GGTGCGAAGAG-AAAGAATACCATGACAGAGGAGGCAAGTGCTTATCAAGTGGATGGC 2831
Qy 802 AT---A-CA-TTT---CAGAA-----GCCA-AG-----GG---TACAGGTG 830
Db 2832 ATTGGAATCAATTTTACACAGATCTATPACCCACAGAGTGTATGCTGGAGCTAC-GGGG 2890
Qy 831 TCCCGG-TGGGA-----CAA---A-AGG-GGA---CACTG-CAATG 861
Db 2891 TGACCGTTTGGAGTTGATGACCTTTGGATCCAAAGCCATATGACGGAATCCCTCCACG 2950
Qy 862 TGAAG---CCTC-----AGCAG-----TCCCTCAG-----CAGA----- 888
Db 2951 ---AGATCTCTCCATCCTGGAGAAAGGAGAACGCT-CCCTCAGCCACCATATGTACC 3006
Qy 889 ---AT-TC-CA-G---TGATACAA---GGATGA---CA-----AAA 914
Db 3007 ATCGATGTCATGATGATCATGTT---CAAGTGTGGATGATGACGACAGATGTCGCCCAA 3065
Qy 915 G--AC-TGA-TTGA-A-GGAA-----AGA----- 932
Db 3066 GTTCCGTGAGTTGATCATGCAATCTCCAAATGCGCCGAGACCCCGAGCGCTACCTTGT 3125
Qy 933 A---AGGG---TGAAG---TGA-----AA-----ACAGAC-----CTT---T--- 960
Db 3126 CATTCAGGGGATGAAGAATGCAATTTGCCAAGTCTTACAGACTCCAACTTCTACCGTGC 3185
Qy 961 CCT---CTCA-AA-----CTTGC-----CTCAT----- 975
Db 3186 CCTGATGATGAAGACATGACGACGAGTGGTGGATGCGACGAGTACCTCATCCACA 3245
Qy 976 -----CTTCTTCA-----ATGCTCTGA-----ACATGA---CTATG---GG 1006
Db 3246 GCAGGGCTTCTTCAGCAGCCCTCCAGTCAAGGACTCCCTCTCTGAGTCTCTGAGTGC 3305
Qy 1007 AACTA-CA-----CTTGC-----G---TGGCTCCAAACAGCTGGCC 1040
Db 3306 AACCGACAAATTCACCGTGGCTTGCATTGATGAGAAATGGGCTGCA--AAGCTGTCCC 3363
Qy 1041 A-CACCA--ATGCCAGCATATGC-----TATTTGTC-----CAGCGCGCTGACG 1084
Db 3364 ATCA--AGGAGACAGCTTCTTGAGGATA-CAGCTCAGACCCACAGCGCTTGA 3420
Qy 1085 GAGTGAGCA--ACGGCAC-----GT-----CGAG---G----- 1108
Db 3421 GAGGACAGCATAGACGACACCTTCTCCAGTGCCTGATACATAAACCTGCTCCGTTCC 3480
Qy 1109 --AGGCGAGCTCGTGTG---G---CTG-CT-----GCCTCT----- 1137
Db 3481 AAAAGGCCGCTGGCTCTGTGAGAAATCTGTCTATCACAATCAGCTCTGAACCCCGCG 3540
Qy 1138 -----T-CTGCTTGCAC-----CTGC-T-----T 1156
Db 3541 CCCAGCAGACCCACACTACACGAGACCCCCACAGCAGCTGCGAGTGGGCAACCCGAGTAT 3600
Qy 1157 CTCAA-ATTTT---G---A---TGTTG---AGTGCAC-TTC-----CCAC--- 1188
Db 3601 CTCAACACTGTCCAGCCACCTGTGTCAACAG---CACATTGACAGCCCTGCGCCACTGG 3657

Qy 1189 -CCGGAAAGGCTGCC-----GCC---ACCACC---ACCACCAACA----- 1222
Db 3658 GCCCAGAAAGGCGAGCCCAAAATTAGCTGTGACCAACCTGACTACAGCAGGACTTCTTT 3717
Qy 1223 --CAA-----C-AGC--AATGGC---AA---CACCGCAGC--AACCAAT-CAG-A 1258
Db 3718 CCCAAGGAGCCCAAGCCAAATGGCATCTTTAAGGGCTCC-ACAGCTGAA--AATGCAGAA 3774
Qy 1259 TA--TA--T-----ACAAA---TGAA---ATTAGA----- 1278
Db 3775 TACCTAAGGCTCGCGCCACAAAGCAGTGAAATTTATTGGAGCATGACCCGAGGATAGTA 3834
Qy 1279 -----AGA-----AA---CACAG-----CCT--- 1291
Db 3835 TGAGCCCTAAATPCCAGACTCTTTTCGATACCCAGGACCAAGCCACAGCAGGCTCTCCAT 3894
Qy 1292 -----CATG-----G---ACAGA-----AA---TTT--- 1307
Db 3895 CCCAACAGCCATGCCCGCATTTAGCTCTTAGACCCACAGACTGGTTTGGCAACGTTTACAC 3954
Qy 1308 -----G--AGGGAG-----GGGAA----- 1319
Db 3955 CGACTAGCAGAGTACTTCCACCTCGGCGACATTTTGGGAGTTGCAATTCCTTTGCT 4014
Qy 1320 -CAAA-----GAATA-----CTTTGGGGGA- 1339
Db 4015 TCAAACTGTGAAGCATTTACAGAAACGATCCAGCAAGAAATATTTGTCCTTTGAGCAGAA 4074
Qy 1340 -----AAAGAG-----TTTTAAAAAGAAATTTGAAA---AT-TGCCTTGCAGA 1378
Db 4075 ATTTAATCTTCAAGAGGTATATTTGNAAAAAA---AAAAAGTATATG---TGAGGA 4128
Qy 1379 TATTTA-----GGTA-CAATGGAGTTT-----CTT----- 1403
Db 4129 TTTTATATGATGGGATC-TTGGAGTTTTCATTTGCTGCTATTGATTTTACTTCAATG 4187
Qy 1404 ---TTCC--CAACGGGAGAA-----CAC----- 1423
Db 4188 GGTCTTCCAA---GGAAGAGCTGTGCTGTAGCACTTGCTACCTGAGTTCAATCCA 4244
Qy 1424 -----AGCACA--CC-C--GGCTT---GGA--C-----CCA-- 1444
Db 4245 GGCCCAACTGTGAGCAAGGAGCAGACAGCCAGTCTTCCAGAGGATGCTTGTATTCCAGT 4304
Qy 1445 ---CTG---CAAGCTGCATC--GTGC--AAC-CT-----CTT---TGCT 1474
Db 4305 GGTCTGTCTTCAAG--GCTTCCACTGCAAAACACTAAAGATCCAGAAAGGCTTCAATGGC 4362
Qy 1475 GCCAG-----TGT---G---GGCA---AG--GGCTCAGCCTCTC 1502
Db 4363 CCCAGCAGCCGATCGGTACTGTATCAAGTCAATGCGAGGTACAGTAGGATAAGCCATC 4422
Qy 1503 TG-CCC-----ACAGAG----- 1513
Db 4423 TGTCTCTTCTGGGCAAGAAAGAAACGAGGGGATGAAATTTCTTCTTAGACTTCTTTG 4482
Qy 1514 -----TGCCCCCAG-----TGGAACA-----TTC-----TG--- 1535
Db 4483 TAAAAATGTCCCGACGGTACTTACTCCCACTGATGGACAGTGGTTTCCAGTCATGAGC 4542
Qy 1536 G--AG-CTG-----G---CCATCCC-----AAATTC-A--AT-----CAGT 1562
Db 4543 GTTAGACTACTTGTGTGTCTTCCATTCATTTGTTTGAATCTAGTATGCGCCCTGT 4602
Qy 1563 C-----CAT-----AGAGACGA---ACA--GAATGAGACC-----TTCCGCGC 1594
Db 4603 CTTGTGTTCATGAATCAGCAGAGAGGATGACATCAATAATTAATCTCGATTCAGC 4662
Qy 1595 CCAAGCGTGGCTGC---GGGCACTTTGG---TAG---AC-----TGTTG--- 1630
Db 4663 CCA--CATTG-GATTTCATGCA-TTTGGACCAATAGCCCCACAGCTGAGAAATGTGAATA 4718

QY 1631 CC-----ACCAGCGGTGTGTGT-G-----AAACG-----T 1656
Db 4719 CCTAAGGATAACACCGCTTTTGTCTCGCAAAACGTTATCTCTTAATTTGAGGCTCGAT 4778
QY 1657 GAAT-A-A-----AAAGACAAAA-----AAAA 1679
Db 4779 GAATGATCAGGTCCTTTGGGCGATAGATCAGAAGACTACAAAA 4824

RESULT 8
US-09-220-132-30
; Sequence 30, Application US/09220132
; Patent No. 6508607
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07134-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 14770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-30

Query Match 41.7%; Score 700.9; DB 4; Length 14770;
Best Local Similarity 35.1%; Pred. No. 0.0016;
Matches 1459; Conservative 0; Mismatches 165; Indels 2531; Gaps 406;

QY 2 TTGTG-----TC-----CTTC-AG-CAAAAC-----AGTGGATT-----28
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QY 29 TAA-----ATCTCTTGCAAA-----GCTTGAG 52
Db 113 TAAGCCTATTAGAGTGCCTGAGGATATCACTTTTACAAAGGACCGGTGTGTGCTTGAG 172

QY 53 AG--C-----AA--CACAAT--CT-AT-CAG-----GAAAGAAAGAA-----81
Db 173 AGGATCTTTTAAATGCAATATATGGCTCATGAGCTTCAACATTAAGAA--AACAGGAT 231

QY 82 --AGAAA--AA-----AACGAA--CCTGCAAAAA-----107
Db 232 TTAGAAATCAATGCTGAA--GAAAGCCTGGAAGAAAAAGAAACACCGCAACGTCCTC 289

QY 108 -----GAAGAAAAAG-----AAG-----AAGA-----124
Db 290 GGGATCGGAAGAAAGTCTGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 349

QY 125 -----AAAAA-----ATC-----AT--GA 137
Db 350 ACCTTGAAGGCCCTCGACTACATAAAATGAGTTGACATCAACATTTGCAATCAGA 409

QY 138 A-----AA-----CCA-----TCCA-----GCCA-----151
Db 410 ATGGGTGACCTCTCCACCTTCTTCCAAAGAGGCCATGTAGAGGTGTTTCTGAGC 469

QY 152 -----AA--AATG-----CACA--ATT--CT 166
Db 470 TGCTGAGAGAGAGCAATGATGAGTACAAAGAAAGAAACACAGCTTTGCACT 528

QY 167 ATC--TCT--TGGGCA-----TCTT-----183
Db 529 ATCGCATCTTTGGCTGGGCAAGCAGAGGTGTTAAAGTCTTGGTTACAAATGAGGCCAAT 588

QY 184 -----CAC-----G--GG-----GC-----TGGCTGC-----T---199

Db 589 GTCAATGCAATCTCAGAATGTTTTCAGCCCATTTATATGTCAGCCAGGAAATATCAC 648
QY 200 CTG-----TGTTC-----TCTTC-----CAAGGAGTGC-----CC-GTGC-----G-----CAGCGGA 235
Db 649 CTGGAAGTTGTCAAGTTTCTTCTTGACATG--GTGCAAGCCAGAGCTAGCCACAGAGA 707
QY 236 --GATGC-CACC-----TTTC-----CCAA-----A 253
Db 708 TGGCTTTCACACCATTTGGCAGTGGCTTTTGCAACAAGTTCACGACCAAGTCGTTTGGCTCT 767
QY 254 GCTATGGACAAAGTGC-----GG-----TCCGGCAG-----GGG--284
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QY 285 -----AG-----AG-CGCCACCT-CAGGTGCACACTATTGACAA-----316
Db 822 CGCAAGAGACGACACAAAGCGCGCTCTGCTGCA--GAATGACAAATGCAATG 880
QY 317 -----C-----G-GG--TCAC--CG-----GG-----TG 331
Db 881 TGAATCAAGAGTGGCTTCACTCGCTCCACATAGTGTCTCACTATGGAATATCAATG 940
QY 332 --GCC-----TG--GCTAAACCG-----CA--GC-----AC--CA 353
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QY 365 G-GGA-----ATGACA-----AG-----TGG-----TGC-CT-----384
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QY 385 GGA-T--CCTC--GC--GTGGT-----CC-TTCT-----405
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Db 1181 AAACAAGATGGAATTTCTCATTGACATGCGGCACAAAGGGATCATTTAACTGCG 1240
QY 432 TCGAG-----ATCCAG--AA-----CGTGGATG--TGT-----ATGAC-----GAGGG 465
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QY 466 CCTTACAC-----CTGCTC-----GG-----TGC-----AG 487
Db 1301 CCC-TACAGTGGCTGCCCATCTGTGGCATTAACAAGTTGCCAAGTTCTCTTGGATAG 1359
QY 488 ACAGACACCAAC-----CCAAAGACTCTAGGG--TCCACCTATTGTGCAAGTATCTCC 540
Db 1360 AAAGCTAACCCCAATGCAAGCCCTGAATGGCTTTTACCCCTC-TT--CA--TATGCC 1413
QY 541 --CAA-----AAAT--GTA--GAGATTTCTTCAGA-----T-ATC--TCCA 572
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QY 573 -----TTA-----ATG-----AAGGG-----583
Db 1473 AGCTTAACGAGTGGGCTTACCCCAATTCATGTTGCTGCTTCATGGGCATGTAAA 1532
QY 584 -----AAC-AAT--AT--T--AGCTTAC-----600
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QY 601 -----CTGCA-----T-----AGC--AA-----CTGGT---616
Db 1593 AACAGCACTGCACATGGAGCTCGCTCGGCGCAAGCTGAAGTGTGCGGTATCTGGTACA 1652
QY 617 AGAC-----CAG-----AGC-----CTACGG-----TT---634

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Db 1713 CCGACTGGGAAAGACAGACATAGTACACAGCTGTTGCGACGAGGGGCAATCCAAATGC 1772
QY 658 AGC---GGT---T--- 664
Db 1773 AGCCCAACTCTGGGTGACACCCCACTTCCGCTTCCGCGGAGAGGGGCATGAGGATGT 1832
QY 665 GGC---TTTG---T---GAGTG---ARGACGAA---T 686
Db 1833 GCGCGGTTCTTGGATCATGGAGCGTCTTATCTATATAACAACAAGA---AAGGATTT 1890
QY 687 ACT---TGAAA---TT---CAG 700
Db 1891 ACTCTCTTTCATGTGGCAGCAAAATATGAAAGCTTGAAGTCGCCAATCTCTGCTACAG 1950
QY 701 ---G-GCATCACC---C-GGAGCAGTCAGGGGACT---ACGAGTGCA-GTGGC 742
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Db 2007 TGCACATTAGGATAATCAGAAAGTGGCCCTTCTGCTTTTGGACCAAGGAGCCTCACCTCA 2066
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Db 2067 CGCAGCCGCAAG-AATGGTTATATAGCCAC---TGAC-ATCGTCCCAAAAAGAACCCAGA 2122
QY 803 T-ACAT---TTCCAGAGCCAA-G---GGTAC---AG 827
Db 2123 TGGACATAGCAACAACTCTGCTGGAAATGTGTGATGTCACAGCAGTTACCCGGCAAG 2182
QY 828 G---TG---TCC---CGGT---GGGACA---A---AAGG---GGACA---CTGC 857
Db 2183 GAAATGCTTCGTTCCATCTCG---CAGCTCAGGAGGCGCAGTGGACATGTGTGCTGTC 2239
QY 858 ---AG---TGTGAAGCTCAGCAGT---CCC--- 879
Db 2240 TCCTCGGTAGAAATGCGGAATGTGAA-CCTGAGCAATAAGAGCGGCTGACCCCACTCCAT 2298
QY 880 ---CTCA---GCAGATTCAGTGGTA---CAAGG--- 905
Db 2299 TTGCTGCTCAGAGATCGAGTGAATGTGGCAGAGTCC---TCGTAAACCAAGGGGCTC 2356
QY 906 AT---GACAAA-A---G---ACTG-AT---TG---AAGGAA 929
Db 2357 ATGTGGACGCGCCAGACAAAGATGGATACACCACTGCAATGTGGCTGCCACTATGGAA 2416
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QY 956 ---CCTTTCTCTCAA---A-ACCTCA---TC 976
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QY 1018 ---CGTGGCTC---CAACA---AG---CTG--- 1036
Db 2595 CATTGCCCGGGCTCGGCTACATCTCAGTAGTGGACACCCCTGAAGATAGTACCCGAAGA 2654
QY 1037 ---GGCCACACC---AATG---CCGCA--- 1055
Db 2655 AACCATGACCAACTACTCTCAGAGAGACCAAAATGAATGTTCCAGAAACGATGAA 2714
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Db 2715 TGAAGTTCTTGATATGTCTGATGATGAATTCGTAAAGCCCAATGCCCTGAATGCTCAG 2774

QY 1083 ---GCG---AGGTGA---GCAA---CGG---CAC-G- 1102
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QY 1103 ---TC---G---AGGA---GGG---CAGGCTGC--- 1120
Db 2835 CAAATATCTTGGGCGACAGGACCTTAAGGAATGGGTGATGATTCCTGCTGCAGAGGG 2894
QY 1121 ---GTCT-GG---CTG-CTGCTC---TTC---T-G 1141
Db 2895 TTACATGGGCTTACTCTCGGAGCGGTTCTGCGAGCCCTCGCTCTCTCAGTTCGATAG 2954
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Db 2955 GTCTTACACCTTGAACAGAGCTCTATGCAAGGACGACATGATGAT-TGAAGAATCC 3013
QY 1174 ---GTGCCACTTCC---C---CACCGGGA--- 1195
Db 3014 TTGTGCCA---TCCAAGAGCAGCATCTAACATTCACAAAGGGAATTTGATCAGATTCTCT 3071
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QY 1250 CC---AATCA---GAT---AT-AT---A---CAAATG---A---AAT 1274
Db 3192 CCGTCATCAGGATGAGATCATCTCTCCAGCAAGTGTACGGCCCCCTCCTCGAAT 3251
QY 1275 ---TAGAAGA---AA---CACAGCTCATGG-GACAGAA 1303
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QY 1304 ---ATT---TG---A-GGG---AGGGGAACA- 1322
Db 3311 GAGGATAGCAGTAGGCTGTAGAAATGGTCTGTCAGGGGCACTATTTAGGCCCTG 3370
QY 1323 ---AG---AAT---ACTTTGGG---G-GGAAAAGA---GTT- 1347
Db 3371 TCATAGTGAATATCCCTCACTTTGGGTCCATGAGAGGAAAGAGAGAACTCATTTGTT 3430
QY 1348 TT-AA---AAAA---GAAA-TTGA---ATTGC---C---TTG-CAG---AT---A 1380
Db 3431 TTGAAAGTGAATATGGTGAACCTTGAAGGA---GCATCAGTTTGACAGCAAAATGAAGA 3488
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QY 664 TGGCT-----T---TG--TG--AGTGAAGCGAA--T-ACCTGGAATTCAGGG 702
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Db 2539 CTACCAATGTGGCTATGGGCTGTGAAGCTTTTGCRAAACAGCTGTGTGTTTCA-GGATC 2597
QY 775 AGTA-----AAGG-----TCACCGTGAACCT---ATCCAC----- 800
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QY 849 --GNACAC--TGCAGT-G-TG--AA-----GCC-----T-CAG 872
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QY 873 C---AGT---CC-----CCTCA-----CGAAGTT----- 891
Db 2835 CCAAGTTTGGCCAAAAGGGGAGATGGGCATCACTTAGAACCGCTCAGAGTTGGCTG 2894
QY 892 CCAGTGSTA-CA-AGGATGA-----CA-A-----AAGA-CTG 919
Db 2895 CCA-TCGTAGGAGGATGAGTTGCTGCTTCCCTGGCTCTCAGATGTGCCCAAGAGCTG 2953
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Db 2954 CTTCTGGCCAACTGGGTGGGAGCCAGGAAGCCCTGCAGCTGCATGAAGTCTACAG 3013
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Db 3014 GGTGAGATGTTGTTTGTGCTTCTGTGAGCTACTGTCCAGGCACTTGGAGGAAAAGCAG 3073
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Db 3074 --CTTTCAGAGGC-----AAAAGCTCTCTCTTACCA-----CACTTGGAAACCGGCAC 3123
QY 997 -----TGACT--A-TG-GGAA-----CTACA--CTTG----- 1017
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QY 1102 -----GTC--GAG--GA-----GG-----GCAGG-----CT--GC 1120
Db 3355 GCGGTGGTCCGAGGCTATGACTCAGGAGGCTTCACCATCATGCAAGAAAGTGTACTCAGC 3414
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QY 1148 ---CACCTGCTTCTCAAA--TTTTGA-----TG--TGA----- 1173
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Db 3591 GAACACTCTCTGTGAGCCAAAGCCAGCAGTTAGACACTGCCAGCACTGAAGAAAGCGAC 3650
QY 1242 --GA-----CAGC--AACCAA-----TCAGA--TATA-----T-ACA----- 1266
Db 3651 CTGAAACTTCTCAGCCAGAGCCAAACAGGCCCTTCAGAACTAGACTTGAGACTCAGAAAG 3710
QY 1267 AA--TGA--AA-----TTA--GA-----AGAA--CA--CAGCTC- 1292
Db 3711 AAGGTGAGCAATGCTGAGTACTTTTAAAGAGCTCTTTTCAAGAAAGCATCCAGTCTCC 3770
QY 1293 --A-TGGGACAGA-AA--TT--TGAGGGAGGGGAAACAAGAATACTTTTGGGG- 1337
Db 3771 AAAACT--CACAGAAACTGTGCTGA--AG-----TCCAG-AGACCTTGGCAGAAATG 3820
QY 1338 ---GA-----AAAGAT-----TTTAAA--AAAG-AAAT-----T 1361
Db 3821 ATCCGCAACACCAAAAGAGTCAACTCTGTAAATPCCACAGCAATGCTCTGTATAAGAT 3880
QY 1362 GAA-----AATTT-----G--CCT-TGCAGATATT-T-----AG-GT----- 1387
Db 3881 GAACCGGAGTAGAAGCAGAGCAGCCCTCTGAG--TTCTCAGAGCCAGTGTAAAGAA 3937
QY 1388 ---ACATGGAG---TTT-TCT-----TTTCCAAACGG-----GA----- 1416
Db 3938 GAAAAAAT-GAGCCACTTTCTCTGCTGAGTTAAACCAAAAGGCTTACCAGGCAATCA 3996
QY 1417 -AGAA--CA-----C-----AGCA--CA--CCCGG--CTTGGACCCA-----CTGCA 1449
Db 3997 GAGATGGCAAAATTTCTGAGAGCATTAAGGCTTGGCCCTT--CCAGATGTGTGGA 4053
QY 1450 -AGCTGCATCG---TG-----CA--A--CCTCTT--TGG-----TG--CCAGTG-- 1481
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QY 1482 TG-----GG--CAAGGGC--TCAG-----C-----CT-----C 1500
Db 4113 TGCAGCAGCAGGGCCCAAGAGCTCTTTCAGAAATACGCAACACGAAAACCTTACAGAGAC 4172
QY 1501 TCTGCCACAGA-----GTG-----CCCCAC-----G-----TG--GA 1527
Db 4173 ACTGC--CAGACCTTCTGTATGTGAATTTTTCACACCTTGAAGAAATTCGCAATTTGA 4229
QY 1528 -----ACAT-----TCTGAGCT-GGCCATC-CCA-A-ATTCAATC-AGTCCA 1565
Db 4230 AATGTTTGACATCTTTCACCTCTGAGTATGCCC-TCACCAGACATTCCTCTGCTGCC 4288
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Db 4289 TAGATGTTTTTGAGTAATCCAAAAGAAATACAAAAGGATTAAAGTTTGAATCAACCTG 4348
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Qy 1677 --AAA 1679
Db 4520 CCAAA 4524

RESULT 10

US-09-566-921-133
; Sequence 133, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 133
; LENGTH: 8734
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 256009.4
; NAME/KEY: unsure
; LOCATION: 500
; OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-133

Query Match 41.6%; Score 698.9; DB 4; Length 8734;
Best Local Similarity 41.6%; Pred. No. 0.00063;
Matches 1396; Conservative 0; Mismatches 176; Indels 1785; Gaps 413;
Qy 3 TGTGTC---CTTC-AG--CA-----AAAAGTGGAT-----TT----- 29
Db 141 TGTGTCGTGGCCTCAAGGTCACCTGGAA--AGTGGATCTGGAAGTAACATCCCTAAA 198
Qy 30 -----AAATCT-CCTT---GC---A-----CA-AG----- 46
Db 199 ATGAAGATCCCCAAATTTACCTTCTCTGGCCGTGAGCTGGTTGGCAGAGAAATGGGGTG 258
Qy 47 -----CTTT-----G-AGAG--CAACA--CAATCT-AT-CAGGA----- 72
Db 259 GATGTCATCTCCCTAAAGCAGAGCCAGCATCCAGCTGGTGGAGACGGCGAGTGGG 318
Qy 73 AGGA-----AAG-AAA--GAAGAAACC--G-----AA-----CCTGA-----CA- 102
Db 319 AAGAGTCTGAAGTCAAACTGMAAAGTCCAAAGTTTAAATGCTTCTCTGAGTATTTAT 378
Qy 103 -----AAA-----A-----A---GAAGAAAA---GAAGAG-----AAA-AAAAAT 132
Db 379 CTCCCAAGTTTCTATGCTCGAGCGTGAATTTGA--AAGGTCCCAATTCAGAT 436
Qy 133 -----CATGA-----AAA-----CCA-----TCCA-GCC-----AAA-----A 154
Db 437 GCTGACATGAATATCAAGCTCCCAAGATCTCCATGCTGATTTGACTTAAACTTGA 496
Qy 155 ATG-CACAA-----AT-----TTCT-----AT-----CTCTT 173
Db 497 AGNCCAAAGTGAAGGGGATGTGGATGTTTCTCTGCCCAAAATGGAAGGTGACCTCAA 556

Qy 174 GGCC---AAATCT---TCACGGGGC---TGG-C-----TGCTC-----TG-TGT 205
Db 557 GGGCCCAAGAGCTGACATCAAGGGCCCAAGTGGACATTAATGCTCCAGATGTTGATGT 616
Qy 206 -----CT-----T---CCAAGG---AGTGGCC---GTGC-GCA----- 230
Db 617 TCAGGCCCAAGCTGGCACCTGAAGATGCCCAAGGTGAAATGCCAAGTTCAGCATGCC 676
Qy 231 --GC-----GGAGATG---CC-----ACCTTCCCAAGCT-----AT- 258
Db 677 TGGCTTCAAGGAGAGGGCCACAGATGTGGATGTGAACC-TGCCCAAGGCTGACCTTGATG 735
Qy 259 -----GGA--CAACGT-GAC-----GGTCC-----GGC---AGGG-- 282
Db 736 TCTCAGACCCAAAGGTGGACATTTGATGTTTCCAGATGTGAATATCGAAGGCCACAGAGGAA 795
Qy 283 -----GG-----AGA-GC-----GCCACC-----CT-CA 299
Db 796 AGTTGAAAGGTCCCAATTCAGATGCTTGAGATGAACATCAAGCCCCCAAGATCTCCA 855
Qy 300 GTGCACT---ATTGA-C-AACC-G---GGTCACCC-----GGGTG----- 331
Db 856 --TGC-CTGACATTTGATCTTAACCTGAAAGG--ACCCAAAGTGAAGGTGATGATGT 910
Qy 332 G-C-CTGGCTAAACCG-----CA-GCACCA--TCCTCTATG-CTGGGA-ATGA----- 372
Db 911 GTCTCTGCAAAAGTGAAGGTGACATGCA--AGTTCC-----TGACTTGGATTTAAAGG 964
Qy 373 --CA-AGTGG-----TGCC-----TGATCTCTCGG-----TGTCCTTCG 406
Db 965 CCCCAGTGGATTTAATGCCCCAGATGTGATGTTGAGGCCCAAGCTGG--CACCTG 1022
Qy 407 A-----GC-----AACA--CCCAACG--CAGTACA-----GCATC---GAGA--- 437
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Db 1373 AGATGTGATGTTCTATGCCACAGCTGACCTGAAGATGCCAAGGTGAATAATGCCCAA 1432
Qy 630 -----C-GGTACTT--GGAGA-----CA-----CATCTCT-----CCCAA 657
Db 1433 ATTCAGATGCCAGG--ATTTAAGGAGAGGCCCAAGTGGATGT-TAATTTGCCCAA 1489
Qy 658 AGCGTTGGCTTG-TG-----AGTGAAGACGAAT-----ACT--TG-----G 692
Db 1490 AGC---TGACATGATGCTCAGGACCCCAAGT-G-GAC--ATTGACACTCTGATATTG 1542
Qy 693 AAATTC-----AGGCAATC-A-----CCC-----G-GGA---GCA-G 718
Db 1543 ATATTTCATGGTCCAGAGGGAACCTGAAGGGCCCAAAATTTAAATGCTGACCTGCACC 1602

QY 719 TCAGGAGTACG-AG-----TGC-----AG-TG-CC-----TCCA---AT 748
Db 1603 TCAGGAC--CGAAGATCTATGCTGAGTGTGACCTGAATCTGAAGGTCCTCAAGAT 1660
QY 749 -----GACGTGGCCG-----C-GCCC-----GTGCTACGAGA-GTAAAGGTCAACGTGA 791
Db 1661 GAAGGCGAGTGGAGTCTCTCTGCTCCCAAGTGG-AAGCGACCTCAAGGGC-CC-TGA 1717
QY 792 ACTATCCACCAT-ACATTTTCAGAG--CC-AAGGTTACA--GGTGTCCCGG-TG-GGA 841
Db 1718 AGT-----TGACA--TC--AAGGCCCCCAAGTGGACATTTGATGTCCAGATGTGA 1765
QY 842 C--AAAGG-----GGACAC-----TGC-----AGTGTAA--GCC-----TCAGCA 874
Db 1766 CGTTCAGGCCCAAGCTGG-CACCTTAAATGCCCCAAGTGAATATGCCCAAGTTCAGCA 1824
QY 875 GTCC-----CCTC--AGCAGATTC--A-GTG-----GT--A-----CAAGGTGA-----909
Db 1825 TGCCTGGCTTCAAGGAGAGGGCCAGATGTGGATGTGAACCTGCCCAAGGCTGACCTTG 1884
QY 910 -----CA--A--AA--GAC--TGAT-----TGAAG-GAA-A--GAAAG--GGT 939
Db 1885 AGCTCTCAGGCCCAAGGTGGACATTTGATGTTCTCTGATGTGAATTCG-AAGTCCAGAT 1943
QY 940 G-----AAAGTGG--AAA--ACAGACCTTTCT--C-TCAAAATC-----973
Db 1944 GCGAACTAAG-GGCCCTAAATTC-A--AGA--TGCCTGAGATGAACATCAAGCCCCCA 1998
QY 974 --ATCT-----T--CTTCAATGT-C-TCTGAA-----TA-----TT--TGTGTTCA--GGC--1075
Db 1999 AGATCTCCATGCTGACATTTGATTTGATCTGAAAGTCCCAAGGTGAAGGTGATGTGG 2058
QY 1007 A-ACTACACTTGC-----GTGG-----CCTCCAAACAAGCTGGGCC-----ACACC 1045
Db 2059 ATGTTTCCCTTCTTAAAGTGAAGGTGACCT--CAA--GGGCCCAAGAGTTGACATC 2111
QY 1046 AATG--CCA-----G-CATC-ATGC-----TA-----TT--TGTGTTCA--GGC--1075
Db 2112 AAGGCCCAAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2171
QY 1076 -----GCCGTGAGCAGGTGA--GC--AA--CGGCACG-----TC-----GAG 1107
Db 2172 CTGAAGATGCC--CA--AGTGAATGCTCCCAATTCAGATGCGAGGATCAAGGA--2225
QY 1108 GAGGG--CAGCTGCTGCTGCTGCTGCTT-CT--GGTCTTGCACCT--G-GTCTT 1158
Db 2226 GAGGCCCA--GATG-----TGGATGTTACC-CTTCTAAGG-C-TG-ACATTTGATTTCT 2276
QY 1159 -----CAAAAT--TTGATG--TGAGTGCCACT-TC-----CC-----ACC 1189
Db 2277 GGCCCCAAGTGGACATTTGATGCCCCCTGA-TGTGATGATGAGGTCCAGATGCAAACT 2335
QY 1190 C--GGG--AAAG-----GCTGCC-----G-CCACCA--CCACCA-----CCA---1219
Db 2336 CAAGGTCCAAAGTTCAAGATGCGAGAGATGAACATCAAGGCCCCCAAAATCTCCATGCC 2395
QY 1220 --AC--AC--AAC--AG-----CAA-----TGG-----1234
Db 2396 TGACATTTGACTTTAACTTTGAAGGTGCTCCCAAGTGAAGGTGATGTGCTCTCTGCC 2455
QY 1235 CAA-----CA-----CC-----GACGCAA-----CCA-----AT 1254
Db 2456 CAAAGTGAAGTGTATCAAGGCCCTGAAATTTGACATAAAGGCCCAAGTTTGGACAT 2515
QY 1255 -----CA--GAT--ATAT--A--C-----AAAT-----G--AAAT--A 1276
Db 2516 TGACACACTGTGATCAATTTGAAGTCCGGAAGGAATTTGAAGGCCCAAAATTTAA 2575
QY 1277 GA-----AGA--ACA-C--AGC-----CTC-ATG--G-----GA-----CA---1300
Db 2576 GATGCTGATGAACATCAAGCTCCCAAAATCTCTATGCTGATTTGATTTGACCT 2635
QY 1301 GAAA--T-----TTG-AGGG-----AGG-GGAA-----C-1320

Db 2636 GAAGGTCCCAAGGTGAAGGGTGAATGTGATGTTTCACTACTTAAGTGGAAAGTGTCT 2695
QY 1321 --AA-----AGA--ATAGTTTG--GG-----GGGA-----AAAG-----AGTTT--1348
Db 2696 GAAGGGCCAGAGGTAGACATTTGAAGTCTCTGAAGGGAAGCTCAAGGTCCCAAGTTTAA 2755
QY 1349 -----TA-A--AAAAG-----AAAT-----TGA--AAATGCTTTCAGAT 1379
Db 2756 GATGCTGATGTACATTTCAAAAGGCCCAAAATCTCCATGAGTGACATTTGATTT--GA-2811
QY 1380 ATTT--AGG-----TACA-----ATCGAGTTTCTTTTCCCAAC--GGGA-1416
Db 2812 ATTTGAAGGACCTAAGATTAAGGAGATATGACATTTTCCGTTCTTAAACTGGAGGAG 2871
QY 1417 A--GAA-----CACAG-----CACA--CCC-----GGC-TTG-----1438
Db 2872 ATCTGAAGGTCCCAAGTGGATGTCAAGGCCCTTAAGTGGCATTTGACACTCTCTGATA 2931
QY 1439 --GAC-----CC-----ACTG-----CAA-----G-CTG-----C 1455
Db 2932 TTGACATTTCAATGCTCCAGAGGGAAGTGAAGGGCCCCCAAAATTTAAATGCTGACTTAC 2991
QY 1456 A--TC--GTGCA-----ACCTCT-----TTG--G-----TG-----CC--AG 1479
Db 2992 ACCTCAAG-GCACCGAAGATCTTATGCTGAGTTGACCTGAATCTGAAAGGTCCAAAG 3050
QY 1480 TGTGGCAAGGCC-TCA--GCC--TCTGCCCCACAG-----AGTGCCC 1518
Db 3051 -GTG-----AAGGGCGACATGACATTTCTCTGCCCAAGTGAAGGCGACCTCAAGGGCCC 3106
QY 1519 CCAGTGAACATTTGAGAGTGGCATTCCTCCAAAT--CAATCA-GTCCATAGA--G 1570
Db 3107 CGAAGTTG-ACA-TC--AG--GG--ACCCCAAGTGACATTTGATGTCC--CAGATGTG 3156
QY 1571 ACG--AA--CAGAAATGAGACCT--T--CC--G-----GCCCA--AGCG 1601
Db 3157 ACGTTCAGGCCCAAGTGGACCTTAAATGCCCCAAGTGAATGCCCCAAGTTCAGCA 3216
QY 1602 TGGC--GCT-----GCGGGCAC--TTTGG-----T-----AGACTG--1628
Db 3217 TGCCTGGCTTCAAGAGGAGAGGGCCAGATGTGATGTGAACCTGCCCAAGCTGACATTG 3276
QY 1629 -TG-C-CA--CCA--CGG-CG-TG-TGT--TGTA-----AACTG--1656
Db 3277 ATGCTCAGGACCCCAAGTGGAGCTTGTGATGTCTGATGTGAATATCGAAGTCCAGATG 3336
QY 1657 -GAAA-TAAA-----AA-----GAGCA--AAA-----AAAA 1678
Db 3337 CGAACTAAGGGCCCCCAAGTTCAGATGCTGAGATGAGCATCAAGCCCCCAAGA 3393

RESULT 11

US-08-619-198-8

; Sequence 8, Application US/08619198

; Patent No. 5885831

; GENERAL INFORMATION:

; APPLICANT: Young, Michael W.

; APPLICANT: Sehgal, Amita

; APPLICANT: Vosshall, Leslie B.

; APPLICANT: Price, Jeffrey L.

; APPLICANT: Myers, Michael

; TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED

; WITH CIRCADIAN RHYTHMS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-128A CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-08-619-198-8

Query Match 41.6%; Score 698.6; DB 2; Length 5192;
Best Local Similarity 39.1%; Pred. No. 0.00023;
Matches 1432; Conservative 0; Mismatches 169; Indels 2060; Gaps 426;
2 TTGTGCTCTTCA--GCA-A-AACAG--TGGA--TTTAA--ATCTCTT--TGCAAGC 47
3 TT---T-CATCAGTGCATTAACAGCACTGAACCTAATACACGATCTATTCTG--CAA-- 54
48 TTGAGAGCAACAA--T-CTATCAGGAAG--AA-----AGAAAGA-AAAAAACC 92
55 ---AGA--AACCCAAAAAGTGC--TCAGAAAAGCTCAATTGCTTAGAATAAACAATC 107
93 GAACC-----TGA--CA-----AAAA--AGAA-GA-AG--AA-----119
108 --AGCTTTAATTGTTGATTCGAATTCGGCTAAAACTAAAACTAAAAACAGTAAATGTCT 165
120 --GA-AGAAAA--AAATCAT-----GA-----AA--ACC--142
166 GCGATAGAAAAAATTTAATAATTTTACAGATACCGCGCAATAGGCTAAGAAATACCTC 225
143 -A---TC-CAGCAAAAATG-----CACAT--TCT-----ATC 169
226 AATGTTGCGAGTCGACATAGAGAGAGTTAGGCGAGCTCCACATCACAATCTGGAATAATC 285
170 ---TCTT-----GGGCAATC--TTTCAGG--GG--CTGGCTGCTC-----TGT-- 203
286 AGAATCTTTGATAAAGTGAATCGTT-ATGACTGGTTTACTAGCAACTCCGAGTTGTAC 344
204 -----G-TCTCTTCC-----AAGG-----A-GTG-----CCCG--TGC- 227
345 AGCGGCTTCTCTCTCTTGGGTTGCTTGGAGGCGATACCTATGTTGTTCAACCCGAATGCA 404
228 ---G-CA-----GCGAGATGCACTTCCCAAG-----CTAT--GGAC--AAAC-----265
405 TTGGCCATTTCTGGAGAGAT--CAACTAC-----AAGCTCACCTATGAGGACCAACACTG 458
266 -G-----T-GACGGTCC-----GGC-----AGG-----G 282
459 CGCAGCTTTCGAGGGGCCATTCGATTTGGCCAGAAATGTGAGGTGACAGCTGATACCGCTG 518
283 ---GGAGAGGCCACCTCAGG---TGC---ACT--ATT--GACAAACGG---GTC- 322
519 CTGGAGATGCCA-----AGGATGATCGGCTCTGGAGTCTGATCTCGGATCTGCTCA 573
323 ---AC-----CCGGGTG-----CC-TGG-C-TAA-----ACCGCA-----347
574 ATCTACGGTGCC--GGTGGAGTGCTCTTCTCCGTGGAGCGTATGTATGTCGCGACGATGTG 632

QY 348 ---G---CACATCTCTC-----TA---TGCTG-----GGAA-----T--- 370
Db 633 GGTGCGCCACACCACTTTGAGCTGAATAAGCTGCTGTACACAGCAAGAGCAATTTACC 692
QY 371 -----GA---CAA---GTGGTG-----C---CTGGA--TC----- 389
Db 693 GAGGCCAGGAGCACCAAGAGCGTGTGGAGTACATGAACAACATCTGGAGTCGGACCT 752
QY 390 ---C---TCG-CG-----TG-----GTC-----CTTCTGAGCAA--- 411
Db 753 AAGCTGTGCGCGCACAAATGCAATCAACAACTGTCTGCTGCTGCTGCTGAGAAATATC 812
QY 412 ---CAC---CCA-A-ACGCA-----GT-A---CA---GCA--TCCA----- 435
Db 813 CTGCACATTCAGAGACGCATGCCCATTGGCTGATGCCATGATGCACTGATGCCGCAT 872
QY 436 -G-ATC-----CAGAAC-----GTGGA----- 450
Db 873 GGCATCTCCATGCAGAACACGATCTTGTGGAATCTTTCATCCAGAGCATCGACAAGTTA 932
QY 451 ---TGTGT---ATGAC-----GAGGCGC--CT-----TACACTG 477
Db 933 CTCTGTATCTGATGACCTGTCCGAGAGAGCTTCTGCGGAGTGACCATGTGTCACACTG 992
QY 478 -----CT-C-GG-T---GCA-GACA--GACAA--CCA--CCCA--AAGACCTCT 511
Db 993 ATTGCTTTGATCTACAGGATGATGCGCATGCGAGTGGGGAITTCAGGCCCATGTGACCTCT 1052
QY 512 AGGCT-CCACTC--ATT-----G-TGCAA-----GT---AT---C---TCCCA 542
Db 1053 --GATCCACCTCCGATTCTCGGACAAACGGCAGCAATGGCCGTGGCATGGCGGTGGCA 1110
QY 543 -----AA-----A--TTGTAGAGATTTTC-----TTCA-GA-TAT--- 567
Db 1111 TCGGGAAGAAACAGCGGCACTTTGTCAG--GAGTTCAGCGCAAGGTCAGGATATCAG 1169
QY 568 --CTCCAT-----TAA-----T---GAAG-GG--AACATAT- 591
Db 1170 AAGCCATGGCCAGAGTGCAGCGGATAAGCCGATGGCTCCGAAGAGCCAGCGATATG 1229
QY 592 -----TAGC-CTCA-CCTGCAT-----AGCAA-----C 612
Db 1230 ACGGGAACGACAGCGAGCAGCTGTGATCGCGAGCAATCCAGCCCGCGGAGTCC 1289
QY 613 -----TGG---TA---GACAGA-----GC--CT----- 628
Db 1290 ATGGATGATGGAGATTACGAGACCGAGACACAGGCAACTGAACGAGCATGGCGAAGAG 1349
QY 629 -----ACG-----GT---TAC--TT-----GGAG 642
Db 1350 GATGAAGATGAGGACGAAGTGGAGGAGGAGATGATACCAATTTGGGCCAGCTTCGGAG 1409
QY 643 -----ACACA-----T-----CTCT-----CCCAA----- 657
Db 1410 CCCCTTAATTAACACAAACACAGCTGCAAGGTCAACACACTTACCACCCACGTC 1469
QY 658 A--GCG-----GTTGGCTTTG---TGAG---TGAAG--ACGA-ATPACT-TG--GAA 694
Db 1470 AGTGGCCCAAGAGTGTCTGGGCAATGAGCCATTCAAGCACCACCACTCTCTGCGAG-- 1527
QY 695 ATTGAGGGCAT-CAAC-CCGGA-----GCAG--TCAGGGA-----CTACGA 732
Db 1528 --TCAGAGCTCCACCTCGGACACGCTCAATGCAAGTTCAACGAATCTCTCTACGC 1585
QY 733 GT-----GC-----AGT-----GC-----CTCCA-AT 748
Db 1586 GTCCACGATCTCGGTCAAAATTTGGGCCAAAAGTCCCCACATCGCGCCAGCTCCAGCT 1645
QY 749 GAC-----GTG--G-CC-----GCG-----CCC-----GT-GG--TA-C 770
Db 1646 GACCAAGGCAAGTGTGTCCACAGAAAGCGGAATGCCCCCTCTCTCGAGTCGGAGCTATC 1705

QY 771 GGA---GAGTAAAGTCCACC---GTG---AACT---ATCCA---CCA---T-----803
Db 1706 GGATTCGG-GTTATGG-CACCCAGGTGGAATAATCAGAAATCCATTTCCACCTCCAGCAAC 1763
QY 804 -AC-AT-T-----TCAGAAGCC-----AAG-----820
Db 1764 GACGATGATGGCGCAGGCGAGCGAGCGAGCAGACAGAGCCTCCGCTGTAACAGCAAGCCA 1823
QY 821 -GG-TA-CA-GG-----TGTCCTCGGTGGACAAAAAGG-----GAC-----A 853
Db 1824 CGGAATAAACACCGGACGAGTATGTCGCAATGAGCAAAAAGAGGCTTAGACGCAAAAAA 1883
QY 854 CTGCACTGTAAGCCTCAGCA---GTCC---CCTCAGCA---GAA---TTCCAGTGTATCA 902
Db 1884 CTG---GTCAAG-CGCAGCAAAAG---CAGCCTCATCAACATGAAGGGTCT---TGGTACA 1933
QY 903 -----AGGATGACA-----AAAGACTGATTAAGGAA---A-----GA---932
Db 1934 GCACACCCCCCGGATGATGATCTCCAA---TCTG-CTGAAGGAATTCACCGTGGATTT 1990
QY 933 -----AAGGGTGAAA-----GTGGA-AA-----ACA-G-AC---CTTTCTCT- 965
Db 1991 CTTCTCTCAA-GGGTTACAGCTATCTGGTGAGGAACTGCACATGCACATCTGTTTCCAATG 2049
QY 966 CAAA-----ACTCAT---CTTCTT---C-----AATGT-CT-CTGAA-----994
Db 2050 CGAAGTGCCCATGACACATCGCACTTCTTTTGGCTGTGTACTTCTCTGAAAGTTTG 2109
QY 995 -----CA-T-GA-C---TATGG-----GA-ACTA---CAC-----TTG- 1017
Db 2110 CGGCCCAACTGGAGTGTGATATGAGACATCGACACTATTCTCACCTACGATGTTTGA 2169
QY 1018 -----CGTGGCCT-----CC-----AACAAAGCTGG-----GCC-ACA- 1043
Db 2170 GCTACTTGACCTATGAGGGTGTGTCCTATGTGAGCAA-CTGGAAGTGAATGCCGACAG 2228
QY 1044 -----CCATG-CC---AGC---ATC-----ATGCTATTGG-----1068
Db 2229 GAGGCACTGACCTGAAGCCCTATCTAAGCGCAATGC-ACITGGTGTGAGCGGCATCCG 2287
QY 1069 -----TCCAGGCGC-----CGT-CAGCGAGGTGAGC-----AAGC-GCAGC- 1102
Db 2288 GGAGTTCTCCAGGC-CATTGATAGTACACAAAGTGA-CTCATCTGAACGAGACGAC 2345
QY 1103 -----TCGAGG-AG-----G-GCAG-----GC-----TG---CG-TCTG-GCTGC- 1130
Db 2346 AAAGCCCATTTGAGCGCAGCTTCAGCTGCAGATTAGCGAAATGTCCGATCTCAGGTGCTT 2405
QY 1131 -----TGCTCTCTG-GTC-TTGCA---CCTGC-TTC-T-CAA-----ATTTT---GAT 1169
Db 2406 TTTGTGCTTCTGAGGCGTTTCAATCCAGCAATTCATTCAGCAGTATCTTTCAGGAT 2465
QY 1170 GTGAGTG-----C---CACTTCC-CC-AC-----C-----CGG-GAAA-----GG 1198
Db 2466 CTG-GTGGTTACCAATCACAATCTCTTCTACTTCTTGACAGATTTCGGCCAACTTGTGG 2524
QY 1199 CTG-----C---CGCC-----AC-CA-----CCAC-----CA 1216
Db 2525 ATGTCAAAACCATTCGCTCTCGGAGCACATAACAGATTTTCCAGCTGGAGGTGATGCA 2584
QY 1217 C-----CAAC-ACAAC-----AG-----CAATG-----1233
Db 2585 CTACTATGGCAATCTGTGGAGGACTTCAACAAACAGCGAGATTTCATGACTGCAT 2644
QY 1234 -----GCAACAC-----CGA-----CAG-----CAAC 1251
Db 2645 CTTCCACCATGATGATCACAATCGGTGGGATCTGGCCAGATTGGGTTTCTATTTCAACC 2704
QY 1252 AATCA-----GATA---TATCAAAATGAAT-AGAAG-----A---AAC-----AC 1286
Db 2705 AATTATTTGAAAACCTATTCAA---GAATTTGGAAGCGGACTATGAATGTCGATGAC 2762
QY 1287 AG-C-C---TC---ATGGGA-----CA-----GAA-----1303

Db 2763 TGGTCGATCTTATCGAGTATGTGATTCACAAGTTCTCAAGTACTCTCCGAGTGCACA 2822
QY 1304 -----AT-----TTGAGGA---G-----GGGAACA-AA-----GA---ATAC- 1329
Db 2823 CTCACCATTCCTFACAACTTCCTTTGACGGAATGACCAGGACACACACGAGGATACC 2882
QY 1330 -TTTG-----GG-G-GGA-AAA-GA-----GTTTTA-----AAA 1353
Db 2883 GTTTCCTCTGTGTCGAGGAGGAAATGGACACACTTTTATTTGTTATTTGTCAGAGCAAG 2942
QY 1354 AAGAA-----ATT-----GAAA---A-TT---GC-CTTGCAG---ATATTTA---GG-TACAA 1391
Db 2943 AAGAACACAGTATTTGTGGGAAAGATGATTAGTCTCTT-CAGCAACA---ACGGCAACAA 2998
QY 1392 -TGGA-----GTTTTCT-TT-TCCCAAGCGGAA-----G-AACACAG-CA-----CAC 1430
Db 2999 GCTGAAAACACGAGGATTTCTATTATCC---AAC---AATTTTTCACA-AGACATTTATCAC 3052
QY 1431 CCGGCTTGG---AC-----CC-----A-C-----TGC-----AA---GC 1452
Db 3053 CCTG-TTGGAAATGAGTACCTGATGAAGTTTCGAGGATGCGAGTATCAGAGAACTTTGC 3111
QY 1453 TG-CA-T---CGT---GCAAC---C---TCT---TTG-----GTGC-----1476
Db 3112 TGACAACTCCCACTTCCGCAACACAGAGTCTGGAAITGAGATTAAAGGAGTGGCCTAG 3171
QY 1477 -----CAG-----TG-TGGGC-----AAG-----GGCTC 1494
Db 3172 GCAAAACCTCAGATGATGTTTCAGATCCTCTGACCTGATCATTTAAGGAAACAAAGCGC 3231
QY 1495 AGCCTCT-----CTGC-----CCACA---GAGTGC-----CCC---1519
Db 3232 AGCATTTGTTATGCTGCAAGAGATCCTCATTTGAGTGTCTCTGTTAAACTGACCCCTGC 3291
QY 1520 -----CACG---T---GGAA---C-AT---TC-TGGAGC---TGGCCATCCCA---1551
Db 3292 GGAGTGTCTCAAGTTCCGGAAGCGATCATCATGAGGCGGTGGCC-TACCACCTGC 3350
QY 1552 AT-T-CAATC---AGTCCAT-----AGAGACGAACA---GA-----A 1580
Db 3351 ATCTGAAGCAGAGTCCATTCCTGCTGCTGAGTGTCTCTGTTAAACTGACCCCTGC 3408
QY 1581 TG-----AGACCT-----TCCGG---CC-CAAGGTGC-----C-GCT-----1608
Db 3409 TGCTGTACAG-CCTTTTGTCTCTGCTCCCAAGC-TGGGCATTGAGTGGCGGCGGA 3466
QY 1609 -GCGGGC---A-CTTTGTTAG-----ACTGTGCCACC-----ACGG---1639
Db 3467 CGGGGCTCGATCTTCCGAGAAATTCGGGACTACTG-GACACGGAGACAATGTACGGAC 3525
QY 1640 CG-----TGTC-----TTGTGAACGTGAATAAA---AA---AGAGCAAAAAA 1678
Db 3526 TCGCCAAAAAGCTGGGACCGCTGGACAAACGTGAGTTAAAGTCAACACAGAAAAAACA 3585
QY 1679 A 1679
Db 3586 A 3586

RESULT 12

US-08-619-198-1
; Sequence 1, Application US/08619198
; Patent No. 5885831
; GENERAL INFORMATION:
; APPLICANT: Young, Michael W.
; APPLICANT: Sehgal, Amita
; APPLICANT: Voshall, Leslie B.
; APPLICANT: Price, Jeffrey L.
; APPLICANT: Myers, Michael
; TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
; WITH CIRCADIAN RHYTHMS
; NUMBER OF SEQUENCES: 8

/ CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Klauber & Jackson
 / STREET: 411 Hackensack Avenue
 / CITY: Hackensack
 / STATE: New Jersey
 / COUNTRY: USA
 / ZIP: 07601
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent in Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/619,198
 / FILING DATE: 20-MAR-1996
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Jackson Esq., David A.
 / REGISTRATION NUMBER: 26,742
 / REFERENCE/DOCKET NUMBER: 600-1-128A CP1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 201 487-5800
 / TELEFAX: 201 343-1684
 / TELEX: 133521
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 5198 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / DESCRIPTION: tim cDNA sequence wherein R at position 1575
 / HYPOTHEICAL: NO
 / ANTI-SENSE: NO
 / ORIGINAL SOURCE:
 / ORGANISM: Drosophila melanogaster
 / US-08-619-198-1

Query Match 41.6%; Score 698.6; DB 2; Length 5198;
 Best Local Similarity 39.1%; Pred. No. 0.00023;
 Matches 1432; Conservative 0; Mismatches 169; Indels 2060; Gaps 426;
 QY 2 TTGTGCTCTCA-GCA-A-AACAG---TGGA---TTTAA---ATCTCCT-TGCACAGC 47
 Db 1 TT---T-CATCAGTGCATATAACAGCACTGAACTATAACACGATCTATCTG---CAA-- 52
 QY 48 TTGAGAGCAACACAA---T-CTATCAGGAAG---AA-----AGAAAGA-AAAAAAC 92
 Db 53 ---AGA--AACCCAAAAGTGC--TCAGAAAAGCTCAATTGCTTAGAAAACATAAACAATC 105
 QY 93 GAACC---TGA---CA-----AAAA--AGAA-GAARA-AG---AA-----119
 Db 106 --AGCTTTAATTGTTGCAATTCGGCTAAACTAAACTAAACTAAACATAAAATTTGTCT 163
 QY 120 --GA-AGAAAA---AAATCAT---GA-----AA--ACC--142
 Db 164 GCGATAGAAAAAATTTAAATAATTGTTACAGATACCGCGCAATGCTTAAGAGTACCTC 223
 QY 143 -A---TC-CAGCAAAAATG-----CACAAT---TCT-----ATC 169
 Db 224 AATGTTGCAGTGCACAATGAGCAGAGTTAGCAGCTCCACAATCACATCTGGAATAATC 283
 QY 170 ---TCTT-----GGGCAATC--TTACCGG---GG---CTGGCTGCTC-----TGT-- 203
 Db 284 AGAATCTTGATAAAGTGAATCGGTT-ATGAGTGGTACTAGCAACTCCGAGTTGTAC 342
 QY 204 -----G-TCTCTCC-----AAGG-----A-GTG-----CCCG--TGC- 227
 Db 343 ACGCGGTTCTCTCTCTTGGGTTGCTTGGAGGCGGATACCTATGTGTTCAACCCGATGCA 402
 QY 228 ---G-CA-----GCGGAGTGCACCTTCCCCAAG-----CTAT--GGAG--AAC----- 265
 Db 403 TTGGCCATCTGGAGGAGAT--CAACTAC-----AAGCTCACCATATGAGGACCAACACTG 456

QY 266 -G-----T-GACGGTCC-----GGC-----AGG-----G 282
 Db 457 CGCACCTTTTCAGACGGGCCATTGGATTTGGCCAGAATGTGAGGTGAGAGCTGATACCGCTG 516
 QY 283 ---GGAGAGCGCCACCCCTCAGG---TGC---ACT---ATT---GACAAACGG---GTC- 322
 Db 517 CTGGAGAATGCCA-----AGGATGATCGGTCTCGGAGTCGGTTCATCCGATACTCGTCA 571
 QY 323 ---AC-----CCGGGTGG-----CC-TGG-C-TAA---ACCGCA-----347
 Db 572 ATCTGACGGTGCC--GGTGGAGTGCTCTTCTCCGTGGACGTGATGATACCGCAGGATGTG 630
 QY 348 ---G-----CACCATCTCT---TA---TGCCTG-----GGAA-----T---370
 Db 631 GGTGCGCACACCATCTTTCGAGCTGAATAAGCTGCTGTACACACAGCAAGGAAGCATTTACC 690
 QY 371 -----GA-----CAA-----GTGGTG-----C---CTGGA-TC-----389
 Db 691 GAGGCCAGGAGACCAAGACGCTGGTGGAGTACATGAACAACATATCTGGAGTCGGACCT 750
 QY 390 ---C---TCG-CG-----TG-----GTC-----CTTCTGAGCAA---411
 Db 751 AAGCTGTGCGCGCACAAATGCGATCAAAATCAACAACCTGTCTGCTGCTGCTGAGAATATC 810
 QY 412 ---CAC---CCA-A-ACGCA-----GT-A---CA---GCA-TCGA-----435
 Db 811 CTGCACATTCAGAGACGATGCCCATTCGCTGATGCCATGATGATGATGATGATGATGATGAT 870
 QY 436 -G-ATC-----CAGAAC-----GTGGA-----450
 Db 871 GGCATCTCCATGCAGAACACGATCTGTGTGAATCTTCTTCATCCAGAGCATCGACAAGTTA 930
 QY 451 ---TGTGT---ATGAC-----GAGGGCC--CT-----TACACCTG 477
 Db 931 CTCCTGTATCTGATGACCTGTCCGACAGAGCCTTCTGGGGAGTGACCATGTGCAACTG 990
 QY 478 -----CT-C-GG-T-GCA-GACA-GACAA---CCA---CCCA---AAGACCTCT 511
 Db 991 ATTGCTTTGATCTACAGGATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1050
 QY 512 AGGGT--CAACCTC--ATT-----G-TGCAA---GT---AT---C---TCCCA 542
 Db 1051 --GATCCCACTCCGATCTCCGACAAACGGCAGCAATGCGCTGGCATGGCGGTGGCA 1108
 QY 543 -----AA-----A-TTGTAGAGATTTC-----TTCA-GA-TAT---567
 Db 1109 TCGGGAGGAAGAACCGGCGCACTTTTCAG-GAGGTGACGCGCAAGGTCAGGATATCAG 1167
 QY 568 --CTCCAT-----TAA-----T---GAAG-GG--AACATAT- 591
 Db 1168 AACGCCATGGCCAGAGTCCAGCGGATAGCCCGATGCTCGAAGAGCCAGCGATATG 1227
 QY 592 -----TAGC-CTCA-CTTGCAT-----AGCAA-----C 612
 Db -228 ACGGGGAACGACAGCAGCAGCTGATCGCGGAGCAATCGCAGCCCGCGGAGTCC 1287
 QY 613 ---TGG---TA---GACCAG---GC---CT-----628
 Db 1288 ATGATGATGAGATTTCAGGACCAAGAGACACAGGCAACTGAACGAGCATGGCGAAG 1347
 QY 629 -----ACG-----GT---TAC---TT-----GGAG 642
 Db 1348 GATGAAGATGAGGACGAAGTGGAGGAGGAGAGTAGTACCTACATTTGGGCCCGCCGCTCGAG 1407
 QY 643 -----ACACA-----T-----CTCT-----CCCAA-----657
 Db 1408 CCCCTTAACCTTAACACCAACACAGCTGACAAAGTCAACACACTTACCAACCCACCTCC 1467
 QY 658 A--GCG-----GTGCTTTG---TGAG---TGAAG--ACGA-ATACT-TG---GAA 694
 Db 1468 AGTGGCCACNAGGCTGCTGGGCAATGAGCCATTCAGGCCAACCCACTCTCTCTCCAG--1525

QY 695 ATTGAGGAT-CACC-CGGG-----GCAG-----TCAGGGG-----CTACGA 732
Db 1526 --TCAGAGCTCCACCTCGGCACACGCTCAAATGCGAGAGTTTCAACGAATCTCTACGC 1583
QY 733 GT-----GC-----AGT-----GC-----CTCCA-AT 748
Db 1584 GTCCACGATCTGCGGTCAATGCGCCAAAGTCCCCACATGCGCGGCGAGCTCCAGCT 1643
QY 749 GAC-----GTG--G--CC-----GGG-----CCC-----GT-GG--TA-C 770
Db 1644 GACCAAGGCGAGTGTGTCCAGAGCGGGAATGCTCCCTCTCGCAGTCGAGGTATC 1703
QY 771 GGA-----GAGTAAGGTACCC-----GTG--AACT-----ATCCA--CCA--T-----803
Db 1704 GATTCGG--GTTATGG--CACCCAGGTGGAATATCAGGAATCCATTTCCACCTCCAGCAAC 1761
QY 804 -AC-AT--T-----TCAGAGCC-----AAG-----820
Db 1762 GACGATGATGGGCGCAGGCGAGCGGACGACACAGAGCTCCGTGTAAACAGAGCCA 1821
QY 821 -GG--TA--CA--GG-----TGTCCTCGTGGGCAAAAGGG-----GAC-----A 853
Db 1822 CGGAATAAACACGAGCAGATTTATGTGCGCAATGGACAAAGAGCTTAGACGCAAAAAA 1881
QY 854 CTGCAAGTGAAGCTCAGCA--GTCC--CCTCAGCA-----GAA--TTCCAGTGTATCA 902
Db 1882 CTG-----GTCAAG--CGCAGCAAAAG--CAGCCTCATCAACATGAAGGCTC--TGGTACA 1931
QY 903 -----AGGATGACA-----AAGACTGATTTGAAGGAA--A-----GA-----932
Db 1932 GCACACCCCGCAGATGATGATCTCCAA--TCG--CTGAGGAATTCACCGGTGATTT 1988
QY 933 -----AAGGGGTGAAA-----GTGGA--AA-----ACA-G--AC--CTTTCCTCT- 965
Db 1989 CCTCCTCAA--GGGTACAGTATCTGTGGAGGAACTGCACATGCAACTGCTTTCCAAATG 2047
QY 966 CAAA-----ACTCAT-----CTTCTT--C-----AATGT-CT--CTGAA-----994
Db 2048 CGAAGGTGCCCATGACATCGGCATCTCTTTGGCTGGTAACTACTTCTCTGAAAGTTTG 2107
QY 995 -----CA--T--GA--C-----TATGG-----GA-ACTA-----CAC-----TTG- 1017
Db 2108 CCGCCCACTGAGCTGGATGATGAGCAGCATCTGACATCTTCTCACCTACGATGTTTGA 2167
QY 1018 -----CGTGGCT-----CC-----AACAGCTGG-----GCC--ACA--1043
Db 2168 GCTACTTGACCTATGAGGCTGTGTCTCTATGAGCAA--CTGGAACGTAATGCCGACAG 2226
QY 1044 -----CCAATG--CC--AGC--ATC-----ATGCTATTGG-----1068
Db 2227 GAGGCGAGTCACTGAAGCCCTATCTTAAGGCGAATGC--ACTTGTGGTGGCGCCATCCG 2285
QY 1069 -----TCAGGCGC-----CGT--CAGCGAGGTGAGC-----AACG--GCAG--1102
Db 2286 GGAGTTCTCTCCAGC--CAITGATACGTATCAACAAGTGA--CTCATCTGAACGAGGAGAC 2343
QY 1103 -----TCGAGG--AG-----G--GCAG-----GC-----TG--CG--TCTG--GCTG--1130
Db 2344 AAGGCCATTTGAGGAGCTTACGCTGCAGATAGCGMAATGTCGATCTGAGGTGCTT 2403
QY 1131 -----TGCCTCTCTG--GTC--TTGCA--CCTGCG--TTC--T--CAA-----ATTTT--GAT 1169
Db 2404 TTTGTGCTCTGCTGAGCGCTTCAATCCAGCATTCATCCAGCATTCATTCGAAGCATCTTCAGGAT 2463
QY 1170 GTGAGTG-----C-----CACTTCC--CC--AC-----C-----CGG--GAAA-----CG 1198
Db 2464 CTG--GTGGTTTACCAATCACATCTCTCTACTCTTCTGAGCATTTGCGCCAACTTGGTG 2522
QY 1199 CTG-----C-----CGCC-----AC-CA-----CCAC-----CA 1216
Db 2523 ATGTCAACCATTCGCTCTGCGAGGACATACACAGATTTGCCACGCTGGAGGTGATGCA 2582
QY 1217 C-----CAAC--ACAA-----AG-----CAATG-----1233

RESULT 13

Db 2583 CTACTATGCAATCTGTGTTGGAGGACTTCAACAAACGAGAGATTGTCAATGACTGCAT 2642
QY 1234 -----GCAACAC-----CGA-----CAG-----CAACC 1251
Db 2643 CTTTCACTGATGATCATCATCGGTGGCATCTGGCCAGATTTGGGTCTTATTTCAACC 2702
QY 1252 AATCA-----GATA-----TATACAAATGAAT--AGAAG-----A--AAC-----AC 1286
Db 2703 AATTATTTTGAACCTATTCAA--GAATTTGGGAAGCGGATCATGAATCTGTGCGATGAC 2760
QY 1287 AG--C--C--TC--ATGGG-----CA-----GAA-----1303
Db 2761 TGGTCTGATCTTATCGATGTGATTCACAAAGTTTCATGAATCTCTCCGAAGTCGCCA 2820
QY 1304 -----AT-----TTGAGGA--G-----GGGAACA--AA--GA--ATAC--1329
Db 2821 CTCACCATTCCTACAACTTCTTGACGGAATGACCAAGGAACAACAACAGAGCATACC 2880
QY 1330 -TTTG-----GG--G--GGA--AAA--GA-----GTTTTA-----AAA 1353
Db 2881 GTTTGCTCTTGGTCGAGGAGGAATGACACACTTTTATTGTTATGTTGTCAGAGCAAG 2940
QY 1354 AAGAA-----AAT-----GAAA--A--TT--GC--CTTGCAG--ATATTTA--GG--TACAA 1391
Db 2941 AAGAACACGATATTTGGGAAGAGATAGTTAAGCTCTT--CAGCAACA--ACGGCAACA 2996
QY 1392 --TGGA-----GTTTTCT--TT--TCCAAACCGGAA-----G--AACACAG--CA-----CAC 1430
Db 2997 GCTGAAAACACGAGATTTCTATTATCC--AAC--AACTTTGCAACA--AGACATATTAC 3050
QY 1431 CCGCTTGG--AC-----CC-----A--C-----TGC-----AA--GC 1452
Db 3051 CCTG--TTGGAATACGATGACCTGATGAATTCGAGGATTCGGACTATCAGAGAACTTGC 3109
QY 1453 TG--CA--T--CCT--GCAAC--C-----TCT-----TTG-----GTGC-----1476
Db 3110 TGACACTCCACTTCCGCAACACAGAGTCTGGAATTTAGATTAGGAGTGGCCTACG 3169
QY 1477 -----CAG-----TG--TGGGC-----AAG-----AAG-----GGCTC 1494
Db 3170 GCAAAACCTCAGATGATGTTTTCAGATCTCTGCTGGACCTGATCATTAAGGAACAAAGCGC 3229
QY 1495 AGCTCTC-----CTGC-----CCACA--GAGTGC-----CCC-----1519
Db 3230 AGCATTTGTTAGGCTGCAAGGATCTCTATTGAGTCTGCTTAAACTGACCTGC 3289
QY 1520 -----CAGC--T--GGAA--C--AT--TC--TGGAGC--TGGCATCCCAA--1551
Db 3290 GGAGTGGTCTCAAGGTTCCGGAAGGCGATCATATGAGGCGGTGGCC--TACCACTGC 3348
QY 1552 AT--T--CAATC--AGTCCAT-----AGAGACGAACA--GA-----A 1580
Db 3349 ATCTGCAAGCAGAACTCCATTCGGTGGTGCAGTG--GAACACGAGCAATCCACTACGA 3406
QY 1581 TG-----AGACCT-----TCCGG--CC--CAGCGTGG-----C-GCT-----1608
Db 3407 TGTGTACAG--CCTTTTGTCTCTGCTCCACAAGC--TGGGCAATTCAGCTGCGGCGGA 3464
QY 1609 -GCGGCGC-----A--CTTTGTAG-----ACTGTGCCAC-----ACGG--1639
Db 3465 CCGGCGCTCGATCTTCGCCCAAGATTCGCGACTACTG--GACACCGGAGCAATGTACGGAC 3523
QY 1640 -CG-----TGTG-----TTGTGAACGTGAATAA-----AA--AGAGCAAAAAAA 1678
Db 3524 TCGCCAAAAGCTGGGACCGCTGGCAACAACTGAGTTAAAGTCAACCAAGAAAAACA 3583
QY 1679 A 1679
Db 3584 A 3584

US-09-566-921-109
; Sequence 109, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 109
; LENGTH: 4792
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 369213.15
US-09-566-921-109

Query Match 41.6%; Score 698.4; DB 4; Length 4792;
Best Local Similarity 40.1%; Pred. No. 0.0002;
Matches 1399; Conservative 0; Mismatches 194; Indels 1892; Gaps 395;
QY 1 GTTGTGTCCTTC-AGC-----AA--A-CAGTGGATTTAAAT-C-TCCTTG----- 40
Db 378 GCTGTGTCCTTCAGCTACCTGATGAGACAGTGAAGTGAAGTCTTCTTGGAGTCTG 437
QY 41 -C-----ACA-AGC---T---TGA-----GA-GC---AA-----CAC----- 60
Db 438 TCAGGGGAACAGAGGCTCTCACTGACCTGAGGCGGAGATGACGTACTCCACTGTG 497
QY 61 -----AA-TCT-ATC-----AGGAAGAGAG-----A-----AAG 83
Db 498 TCGCCTTCGTGTCCTCCAAAGTCTTCATCCATGAGGAAGTATGTTCTCCTCACTGTCNAAG 557
QY 84 -AAAAAACGACCTGACAA-AA---AAGAAG-----AAA-----AAGAA- 119
Db 558 TGAAGGAGCC-AACC---CAAGAATTTAAGAGCGGACACAGTATGTTAAGACGAG 613
QY 120 GA-----AGA-AAAAAATCA---TGAACCCA-TCAGGCA-AAAA 155
Db 614 GACAGTCTGCTTTGTTCAGACAGACAAATCAATCTCAAAACCGAGGAGACAGTGA 673
QY 156 TGCACAAATC-----TATCT-CTTGG--GCAATC-TTCAC-----G---GGGCTGGTGT 199
Db 674 T-----TTCGTGTTCTCTCCATGGATGAATCACTTTCACCCCTGATGAGTTGATTCA 727
QY 200 CT-GTGT-C--TC-----TTCC-AAGGAGTCCCGTGCAG-----GCGGAGATGCCA--- 242
Db 728 CTAGTATACATTGAGATCCCAAGGAATCGCAT-CGCACAATGCGAGATTTCCAGTT 786
QY 243 -----CC-----TTCCC-----CAAAGC---T-ATGG----- 260
Db 787 AGAGGGTGGCCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGCTCT 846
QY 261 ACAAGTGAAGTCCCGG-----CAGGGG-----AGAGGCGCACCTC-----C----- 298
Db 847 ACAAGTGGTGTGTCAGAGAAGAAATCAGTGGAGGACAGAG---CACCTTTTCACCGTGG 903
QY 299 AGG-----TG-----CACTA--TTG---AC-----AACCGG-----TCACC--C- 326
Db 904 AGGAATTTGTTCTTCCCAAGTTTGAAGTACAAAGTAAACAGTGCACAAAGATAATCACTCT 963
QY 327 -GG-----GNG-GCCTGG-CTAAAC-C-----GCAGCACCATCC 356
Db 964 TGAAGAAGAGATGAATGTATCAGTGTG--TGGCCTATACATATATGGGAAGC-CTGTCC 1020
QY 357 TCT-----ATG-----CTGGGA--AT-----GACAAG--TGGTG-----CCTGGA-T-CCTC 392
Db 1021 -CTGACATGTGACTGTGAGCATTTGCGAGA-AAGTATAGTACCGTTCC--GACTGCCAC 1076

QY 393 GCGTG--G--TC-----C-TTC--TGAG-----CA-----ACACCAAAAC-----GCAG 424
Db 1077 G-GTGAAGATTCAAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGCTG 1135
QY 425 -----TA-CAGCA-T-----CGAG---ATCCA---GAAGTGG-ATGTGTATG----- 458
Db 1136 CTTCTATCAGCAAGTAAAAACCAAGGTCTTCCAGCTGAA--GAGAAAGGAGTATCAATGA 1194
QY 459 -----AC-GAGGGCCCTTACA-CC-----TG-----CT----- 479
Db 1195 AACTTCACACTGA-GGCCC---AGATCCAAGAAGAAGACAGTGGTGGAAATGACTGGAA 1251
QY 480 --CGGTGCGAG-----ACAGACAAC--ACCCAAA-----GAC--- 507
Db 1252 GGCAGTCCAGTGAATCACA-AGAACCATAACCAAACTCTCATTTGTGAAAGTGGACTCA 1310
QY 508 --CTCT---AGGG---TCCACCTCATTGCGA-----AGTA-----T 536
Db 1311 CACTTTCGACAGGGAATTC-CTTCTTTGGGCGAGGTGCGCCTAGTAGATGGGAAGCGCT 1369
QY 537 C-----TCCAAAATTTGAGAG-AT-TTCTTCAGA-----TAT--CTCC- 571
Db 1370 CCTATACCAAA---TAAAGTCATATTTCATCAGAGGAATGAGCAAACTATTACTCCA 1425
QY 572 AT--TA-----ATGA--AGGG-----AA-----CAATATTA----- 593
Db 1426 ATGCTACCACGATGAGCATGGCCTTTGTACAGTTCTCTATCAACACCAACCAATGTTATGG 1485
QY 594 G--CCTCAC--CTGCATAG---CAACTGGTAGACAG---AG--CC--TAGGGTT 634
Db 1486 GTACCTCTCTTACTG--TTAGGGTCAATT---ACAAGATCGTAGTCCCTGTTAGGGCT 1539
QY 635 AC--T---TG-----GAGACACATC-----TCTCC 655
Db 1540 ACCAGTGGGTGTGAGAGAACAAGAGAGGACATCAGCTCTTATCTTGTGTTCTCC 1599
QY 656 AAGC--GTTGGCTTTG---TGAG-----TGAAGACGA-----A 685
Db 1600 CAAAG--AGCTTTGTCCACCTTGAGCCCATGTCTCATGA--ACTACCTGTGGCA 1654
QY 686 TACT-----T--GG---AAATTCAG-----GSCA----- 704
Db 1655 TACTCAGACAGTCCAGGACATATATTTCTGATGAGGACCCCTGTGTTGGGCTGAAGAA 1714
QY 705 --TCACC-----C---GGGA-GCA--GTGAG---GGGACTAC--- 730
Db 715 GCTCTCTTCTATTATCTGATAATGGCAAGGGAGGCATTTGCGAACTGGGACT-CATG 1773
QY 731 GA-----GT---GCAG-----TG-----CC-TC-CAAT----- 748
Db 1774 GACTGCTGTGAGCAGGAAGACATGAAGGGCCATTTTTCATCTCAATCCCTGTGAAGT 1833
QY 749 --GAGTGGC-----CGC-----GC-----CCGTGGTAC--- 770
Db 1834 CAGACATTTGCTCTGCTCGTGGTGTCTCATCTATGTGTTTACCTACCG-GGACGTG 1892
QY 771 -----GGA-----GA-GT---AAA-----GGTCACC---GTGAATC--A-- 795
Db 1893 ATTGGGATTTCTGCAAAATATGATGTTGAAATTTGTCTGGCCAAACAGGTGATTTGAGC 1952
QY 796 TCCA--CCAT-ACA---T-T-----TCAGAACCAA-----GGGT-ACAG----- 827
Db 1953 TTGAGCCCATCACAAGTCTCCAGCCCTCACAGCCACCTGCGAGTCAACAGCGGCTCT 2012
QY 828 --GT--GT-----CC--CCGTG---GGACAAG--GGGACACTGC-----AGTGTGA- 864
Db 2013 CAGTCCCTCTGGCCCTCCGTGCTGTGTGACCAAGCGTG---CTGCTCATGAAGCCTGAT 2069
QY 865 ---AGC-CTCAGCAGTCC-----CCT-C-AGCAGAA-----TT 891
Db 2070 GCTGAGCTCTCGGC-GTCCCTCGGTTTACAACTGCTACCAGAAAGGACCTCACTGCTT 2128

QY	892	CCAGTGG-----T-ACAAG-----GATGACAAAGACTG-----AT--TG--	923
Db	2129	CC-CTGGCCCTTTGAAATGACCAGGACGATG-----AAGACTGCATCAATCGTCAATAATGTC	2183
QY	924	-----AA-GCA-----AAG-----AAGGGGTGAAGTGGAAA-----	950
Db	2184	TATATTATGGAATCACATATACTCCAGTATCAAGTATCAAA-----TGAAAA--GGATATGT	2238
QY	951	ACAGACCTTTCCCT-----CTCAAA--ACTCA-----TC-----TTCTTT-----	981
Db	2239	ACAG--C--TTCTTAGAGACATGGGCTTAAGGCAATTCACCACTCAAGATTCGTAAAC	2295
QY	982	CAA--TGTC-----TC-----TGAA--CATG-----AC-----	1000
Db	2296	CCAAATGTGTCCACAGCTTCAACAGTATGAAATGCAATGGACCTGAAGGCTACGTGTAG	2355
QY	1001	-----T-ATGGGAA-----C-TACA--CT--TGGGTG-----GC	1023
Db	2356	GTTTTATAGTCAAGTATATGGAAGAGGCCATGACCGCTGGTNGCATGTTGAAGAGC	2415
QY	1024	CTCCAACAAGCTG--GGCCACACCAA-----TGCC--AGCATCATG--CT--ATTTGG	1068
Db	2416	CTC--ACA--CGGAGACCGTACGAAAGTACTTCCCTGAG-A-CATGATCTGGGATTTGG	2469
QY	1069	TCCAGGCGCCG-----TCAGC-----GAGGT--GAGCAACGG-----	1098
Db	2470	T-----GGTG--GTAAACTCAGCAGGTGTGGCTGAGGTAGGAGTAACAGTCCCTGCACCAT	2524
QY	1099	CAGTCCA--GGAGGGCAGG-----CTGC--GTCTG-----GCTG-----	1129
Db	2525	CAC--CGAGTGGAAAGCAGGGGCTTCTGCTGTCTGAGATGTGGACTTGGTATCTCT	2582
QY	1130	-----CTGCCCTT-TCGT-GTCTTGCA--CCTGCTT-----CTCA-AAT--TT-----	1165
Db	2583	TCCACTGCCCTCTCCGAGCCTTCCAGCCCTCTTGTGTGGAGTCACAATGCTTACTCT	2642
QY	1166	TGAT--GT--GAG-----T--GCCA-----CTTCCC-----C	1186
Db	2643	GTGAATCGTGGAGAGGCTTTCACACTCAAGGCCACGGTCTCTAAACTACCTTCCCAATGC	2702
QY	1187	ACCGGGAAAG-----GCTG-----CGCC--ACC-A-----CC-----AC	1214
Db	2703	ATCCGGTCACTGTGCAGCTGGAGCCTCTCCCGCCTTCTCTAGCTGTCCAGTGGAGAA	2762
QY	1215	CACCAA-----CACAACA-----GCAA-----TGGCAACA-----CC--GACACAA-	1249
Db	2763	GAACAAGCGCCTCACTGCATCTGTGCAACGGCGCGCAA-CTGTGCTCTGGGCATTAAC	2821
QY	1250	CCAATCAGATATATA-CAAA--TGAATTT-A--GA--AGAAACAC--AGCCTCA	1293
Db	2822	CCCAA--AGTCAT-TAGGAAATGGAATTTCACTGTGAGCGCAGAGGCCTAGAGTCTCA	2878
QY	1294	-----TGGGACAGA-----AATT--TGA-----GGGAG-----	1314
Db	2879	AGAGCTGTGTGGACTGTGAGTGCCTTCAGTTCTGAAACCGGAAGGAAGACACAGTCAT	2938
QY	1315	-----GG--GAAC--AA-----AGAA-----TACT	1330
Db	2939	CAAGCCTCTGTGTGTTGAACTCAAGGACTAGAGAAGGAACAACATTCACCTCCCTACT	2998
QY	1331	TTG-----GG-GG-GA-----AAAGATT-T--TAAAA-----AAGAAAT-----T	1361
Db	2999	TTGTCCATCAGTGTGTGAGGTTTCTGAAGAAATATCCCTGAAACTGCCACCAATGTGTGT	3058
QY	1362	GAA-AAT-TGCC-----TT-GCAGATAT-TTAGG-----T-----	1387
Db	3059	AGAAGAACTGTGCCGAGCTTCTGTCTCAGTTTGGGAGACATATTAGGCTCTGCCATGCA	3118
QY	1388	-----ACAA-----TGAG-----TTT-----TCTT	1403
Db	3119	AAACACACAAAATCTTCTCCAGATGCCCTATGCTGTGGAGAGCAGATATGCTCTCTT	3178
QY	1404	T--TCCCAA-----ACGGG-----AA-G-A-CACACAGCA-----CA-----	1429

RESULT 14
US-09-911-842A-3
; Sequence 3, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11230
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-911-842A-3

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Query Match      41.6%; Score 698.3; DB 4; Length 11230;
Best Local Similarity 37.7%; Pred. No. 0.0011;
Matches 421; Conservative 0; Mismatches 152; Indels 2195; Gaps 412;

QY      2 TTGTGTCCT---TCA-----G--CA--AAACA-----GTG-----24
Db      2806 TTAT-TCCTACGATCACTCTCTGGATGTGTGACGAAACACCCACCGATGTGGCAAG 2864
QY      25 ---GAT-----TTAAA-----TCTCC---TTG-----CACAAGCTTGAGAC---55

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Db 2865 CCAGATGCTCAGGATTAAGAAAGCTGTCCTCAATGTCGTGACCCCAAAATT--CAGCTAAT 2922
QY 56 ---AACA-CA-ATCTA---TC---AGGAAGAA---GAA---A 82
Db 2923 TTTTAAACATCACAGTACGCTAGCGGCCACTCCACAGAGAAAGAACGATACCCCTTGAATGGA 2982
QY 83 GAA---AA---AAAC---AAAC---CGAA---CCTGA---CA--- 102
Db 2983 GAATCAGCAGGACTCATTAAGACATTGGAACAATCACCAATCGCTTGAAGACACCTT 3042
QY 103 -AA-AAAGA---A---GAAAA---GAAAA---GA-AG-AA 122
Db 3043 GAATAAGAGACCCATGATTTCTTCAGCTCGCTCGAACAACAGTGGTGGCTGACACAA 3102
QY 123 ---GAAA-A-AAAA---TCATGAACACCA---TC--- 145
Db 3103 TTCCCTCGAAACAGAAAGGCTTTCTCTTC-TGACACACAGGCTCTGTGCTGAGGGGGC 3161
QY 146 -CA---GCCAA---AA---A---TG---CAC---AA 162
Db 3162 GCATGTGTCAACTGCCCCCTGGGAACCTTACTCTCTGGAGCAATTCACCTGTGAAA 3221
QY 163 -T---TC-T---ATCTCT---TGG---GCAA---TCT--- 182
Db 3222 GCTGCCTCATGGGATC-CTACCAAGATGAAGAGGGCAGCTGGAATGCAAGCTCTGTCCC 3280
QY 183 ---TCACGGGG---CTG---GC---TG---CAC--- 205
Db 3281 CCRAAGACTCAGCGGAATACCTCCATCAAGAGCGTCTCTGNAATCAAGCTCAGTGT 3340
QY 206 ---CTCTTCA---AGAG---TGC---CGTG---CGCAG--- 231
Db 3341 AAGCAAGGACCTACTCTCTCAGTGGGCTGGAGACCTCGAAATCGTGTCCGCTGGGTACT 3400
QY 232 ---CGGAGATGCCACT-T-CGC---CAA--- 252
Db 3401 TATCAACCGGAATTGGATCCGGAGCTGCTCTCTATGCCCGAAGAACCAACAAAGGTG 3460
QY 253 ---AGCTATGGACAAC---GTGACG-GT---CCGG---CAGGGGGAGA--- 287
Db 3461 AAAAGAGGAGCGGTGACATCTCTGCTGTG---GAGTGCCTTGCCTAGTAGGAGATCT 3518
QY 288 ---GGC---CACCTCAGG---TGC---ACTATTGCAACC--- 317
Db 3519 CCGCTTCTGGGCTAACACCTT---GCTACCTTGGCTTGCCTCGAGACTATTACCAACCAATG 3575
QY 318 ---GGG---TC-ACC-CGGGTGGCC---TGG---GTA-AACC---GCAGCA 350
Db 3576 CAGGGAAGTCTTCTGCTGCTGCTTGTCCCTTTATGGAACCTACACCATCACTGGGCGCCA 3635
QY 351 ---CCATC---CTCTA---TGCT--G--G--GAATGACAAG--T 377
Db 3636 CGTCCATCACAGACTGCTCAAGTTTATAGCTCTACTCTTCAGCAGCAGAA-GR-AAGCAT 3693
QY 378 GGTGCTGGATCTCTCGGTGCTCTCTGACACACA---CCCA-AAC---G 421
Db 3694 AGTGCC---CCT--CGTGCCCC--CTG-G--ACATTCGACGAACAGTACGAGTCAG 3741
QY 422 CAGTACAG---CATCGAGAT---CCAGAAC-GTGA--- 450
Db 3742 CAGT-CAGGCTTTTCA-CGA-ATGCTTCTTAACCCCTGGCCACACAGTGGAACTGGCCA 3798
QY 451 ---T---GTG---TATGACGAGG---GC---CCT---TACACCTGCT---CG-GT 483
Db 3799 ACAGCTTGGGCGTGTGTATGTC---TGCTCTGCGCCACCTGGATACACAGGCTTAAAGTGT 3856
QY 484 G---CAGACA---GA---CAAC-CAC---CC---AA---AGAC 507
Db 3857 GAACAGATATGATGAATGACGCTCTCTGCTTTCCTCAATGGTGGAAATTTGTAGAGAC 3916
QY 508 C---TCTAGGG---TCCAC---C---TCATTGTGCAAGTATCTC---CCAAA-AT-TG 548

Db 3917 CAAGT-TGGGGGATTCAGCTGCGAATGTTTCATTGGGC---TAT-TCAGGTCAATATGTG 3971
QY 549 TAGAGATTTCTTCA--GA---TATCTCCA---TAAATGAAGGAA---CAAT-A 590
Db 3972 AAGAAAAAT--ATAAATGAGTGTATCTCCAGCCCTTGCTTAAATAAAGAAACCTGCACTGA 4029
QY 591 ---TT---AGC---CT-CACCT---GCATAGCA---ACTG--- 614
Db 4030 CGGCTTGGCAAGCTACCGCTGTACCTGTGTGAAGGATA-CATGGGTGCTCATGTGAAA 4088
QY 615 ---GT--A-GA---CCAG---AGCC---T---ACG---GTTACTTG---GAGACA 645
Db 4089 CAGACGTCAATGAATGACCTCAAGCCCTGCTTAAACAACGCACT---TTGTAAGAC- 4144
QY 646 CA---TCTC-TCCCAAAG---CGG---TTGG---CT--- 668
Db 4145 CAAGTTGGGGGGTCTCGTGCAAAATGCCACCCCGATTTTGGGTACTCGGTGTGAAAA 4204
QY 669 --T-TG--TGAGTG---A---AG---ACG---AAT---ACTT---GGA--- 693
Db 4205 AATGTGATGAGTGTCTCAGTCAGCCATGCCAAATGGAGCCACTTCTAAGGATGGTGCC 4264
QY 694 AA---TTCAGG-GCATCA---CCCGGAGAGCAG---TCA-GGGGACTAGA---GTGCAG 738
Db 4265 AACAGCTTCAGGTG--TCAATGTCC---AGCAGGCTTCACAGGAC-AC-ACTGTGAAC 4316
QY 739 TG--CCTCAATGACGTGGCG--C-GCCGCTGGTACGGAGAGTAA--AGGTCAAC--- 787
Db 4317 TGAACAT-CAACGA-GTGTGAGTCCAAACCGT-GTA-GG---AACGAGGCCACCTGTG 4367
QY 788 --G-TGAACATATCCAC-CATACA-TT---TCAGAAAGCCA---AGGGTACAG 827
Db 4368 TGGATGAACATA--AACTCATACAGTTGTAATGTC--AGCCAGGATTTTCAGGCCACAG 4422
QY 828 GTGT---CC-CGG---TGG---GA---CA--AAAG 848
Db 4423 GTGTGAGACAGACAGCCCTTCCGGTTTAACTGGATTTTGAAGTTTCTGGCATCTACGG 4482
QY 849 GAGAC--ACTGTC---AGTG-TG--AAGCCT-CA-GCAGTCCCTCAGCA--- 886
Db 4483 GTACGTCTCTGATAGTGGAGTGTGCTGCCAACCTTCCATGCCGTAACTCGCATCTGGAT 4542
QY 887 GAATTC---A-GT---GG---TA---CA---AGGATGACAA 912
Db 4543 GAAATCTCTGATGTCATCAACTACGCGACGCCCATCTCTATGCACTTGAGGATGACAA 4602
QY 913 A-----A-----GACTGATTGAAGGAAGAAAGG-----GTGAAATGGA 948
Db 4603 AGAACACACCTTCCCTCCTGACTGATTT--A-CACGCTGGGTCTTTTATGTGAA--TGGA 4657
QY 949 A---AACAG---ACC---TTTCTCTC---AAA-----ACT---CATCTTCTT-CAATG 986
Db 4658 AAGGAAAAGATCACCAACTGCCCTCCGTAATGATGGCATTTGGCATCATATGCA-- 4715
QY 987 TCTC-TGAACA-----T-GA---CTAT-----GGGAACATA-CAGTTG 1017
Db 4716 TCATATGACACAGTATTGGTGGAGCCTGGAGGCTCTATATAGATGGGAATATC---TG 4772
QY 1018 -CG---TGSCCTC---CAA-----CA-AG--C-TG 1036
Db 4773 ACAGTGTACTGCGCTCTCCATTTGGCAAGCCATACCTGGTGGCGGTGCTAGTTCTTG 4832
QY 1037 GGC-----CA-----CA-----CCA 1046
Db 4833 GGCAAGACGACGACAAAAAAGGAGGGGTTCACCCGGCTGAGTCTTTTGTGGGTCCA 4892
QY 1047 -ATGCCAGATCA---TG---CTATTT--GGTC---CAGGCGCGT-----C 1081
Db 4893 TAAGCCAGC-TCAACCTCTGGGACTATGCTCTCTCCACAGCAGGTGAATGCTGGCC 4951
QY 1082 AGC-----GAGG---TGAG-C-----AAGC-----GCA-----C-GTGG 1105
Db 4952 AGCTCTGCCAGAGAACTGAGTGGGGAACGCTGTAGCATGGCCCGATTTCTGTCTCG 5011

QY	1106	----	AGG	----	AGG	----	GCAG	----	GC	----	TG	CGCT	1121
Db	5012	GGAAATC	CGGGAAGT	GAAAGT	TGATTC	CAGACG	ATGTTCT	GCTCT	GTGATT	GTCCGCT	5071		
QY	1125	----	GG	----	CTG	----	CTGC	----	CTC	----	CTC	1136	
Db	5072	TTAGAAG	GATCCGT	GCCTC	CACCT	GAGACCT	GCATC	CAGAAAT	CAGAAAT	CAGAAAT	5131		
QY	1137	T	----	TC	TGCT	TGAC	CC	TGCTT	CTCAAT	----	TG	1172	
Db	5132	GTCACT	CTGTTCT	GTGAT	CCGGCTTC	CAGAT	GTTGGGAAT	CCTGT	GCAGTAT	TGCT	5190		
QY	1173	----	AGTG	----	CCACT	TCCCCA	----	----	----	----	1187		
Db	5191	GAAACCA	GGGAGT	GGACAC	AACAC	TCCCCA	CTGTG	GAACG	CAATCG	CTGTGGG	5250		
QY	1188	CCCG	----	GG	AA	GGCT	----	GGCG	----	CCA	C	1214	
Db	5251	TCCCG	CCTTG	AAGAT	GCTTCT	ACT	CAGCC	AGGACTT	CCATCG	GGGAC	CGGTG	5310	
QY	1215	----	CACCA	----	AC	----	----	----	----	AAAA	1225		
Db	5311	CTATCAG	TGCAC	AGTGG	CTACT	ACCTG	TGGGT	GAATCC	CGAAT	TTCTG	5370		
QY	1226	C	----	AGC	----	AA	GGCA	ACACC	----	----	1241		
Db	5371	CGGAG	CTGGA	ACGGCAT	TTT	CACCAT	CCTGT	CTCGAT	GTG	CGAGT	5430		
QY	1242	GAC	----	AGCA	----	AAAA	TT	AGCA	TTCA	----	1261		
Db	5431	GGACT	GTAGT	GAGC	ACGCT	CCTG	CTGGA	CAACCA	CGGAT	CCTAGT	5489		
QY	1262	----	ATACA	----	A	ATG	----	AAAA	TT	AGCA	1280		
Db	5490	ACCCAC	ATAC	CGG	AGAT	GGGAA	AACTGT	GCAGAA	CACTG	TAAAT	5549		
QY	1281	AAA	----	CACA	----	GCC	----	TC	----	A	1305		
Db	5550	AAAAT	CAGAAA	ATGCG	CTCT	TGCG	AGATTT	TACAC	CGTGGG	TACTG	5609		
QY	1306	T	----	TGA	----	GG	----	GAG	----	GGCA	1325		
Db	5610	TTTCT	GTG	CGAAG	GGC	ACGAG	CTGTG	GGGAGT	GAAC	CACTAC	5669		
QY	1326	----	AT	----	AT	----	A	----	CTTTGGG	----	1337		
Db	5670	CGGAGT	GGGAT	CGCCT	CAGCG	CTCTG	TGA	AGCCAT	TTTCT	GTTGGT	5729		
QY	1338	----	GA	----	GT	----	TT	----	TAA	----	1351		
Db	5730	CTGAAA	ATG	TGTTG	TGAC	GGT	TGGCAT	TGCAGT	TAAGT	TGGT	5789		
QY	1352	----	AAAA	GAAT	----	TCGA	AAAT	----	TGCCT	TGC	1377		
Db	5790	GTGATA	AAGGAT	ATCTT	GTCT	GGGGAT	TGAAG	AGT	CAGAT	CTGCT	5849		
QY	1378	A	T	----	ATT	----	TAG	----	GT	----	1392		
Db	5850	GGAGT	CAT	CTCT	CTGTG	CGGGCT	AGT	GAAGT	TTCC	CAGCT	5909		
QY	1393	----	GG	----	AGT	----	TTTTCT	TT	----	TC	1410		
Db	5910	ACGGCA	AAAT	ATAT	CTTAA	GTGGG	CTCAC	TACCT	TTTCT	TATG	5969		
QY	1411	ACGGGA	----	AG	----	AACA	----	CA	----	GCACA	1441		
Db	5970	AC	GGAT	AC	AGTT	TAC	AGG	CCCAT	CCCT	CCTTGA	6028		
QY	1442	----	CCA	----	CTG	CAA	----	G	----	CTGC	1460		
Db	6029	AGAG	CGCC	CTAG	CTGT	CACT	TTG	TCT	CTCTG	GGAG	6088		

QY	1461	-----GGAACCTC--TTTGGTG--C-CAGTGTG-----GGCA---AGG	1499
Db	6089	GTCACTACTGGGAGCAACTTTCACCTTTTGG-GAACACAGT-TGCTTACACATGCAAGAGG	6146
QY	1491	GCT-CAGCCT--CT-----CTG-C-CCA-CAGAGTGCC---CCACAG-----TGGAA---	1528
Db	6147	GCTACACCTTGTCTGGGCGCTGACACCATATA-TGCCAGGCCAACGCCAATGGAATCA	6205
QY	1529	-----CA-----TTCTG-----GAGC-----TGG-CCA---TC-	1547
Db	6206	AGTAACCAACAGTGCCTGGCTGTCTCCTGTGACGAGCCCCCAATGTGGACCAAGCCTCT	6265
QY	1548	CCA---AAT--TCAATCAG--TCCATAGAGAC-----	1574
Db	6266	CCAGAGACTGCTCA--CAGGCTCTTTGGAGACACCGCGTTTACTACTGTGCGGATGGCT	6323
QY	1575	ACAG-----AATG---AG-----AC---CTTC-----	1590
Db	6324	ACAGCCTGGCTGATAATTCCAGCTCATCTGCAATGCCAGGGGAACTGGGTTTCCCCCG	6383
QY	1591	CGGCCCCAAGC-GTG--CGCGTGC---GGGCACTTTGGTAGACHTGT-----CCA---	1633
Db	6384	CGGCCCCAGGCTGTGCGCGCTGTGATAGCTCACTT-----CTGTGAAAAACCCCATCT	6436
QY	1634	----CC-ACGGCGGTGTCTTGAAAC-GTGA--AATAAAAAAGAGCAAA	1673
Db	6437	GTTTCTCTCAGC--ATCTTG-GAATCTGTGAGCAA-----AGCAAA	6474

RESULT 15

US-08-841-349-3

; Sequence 3, Application US/08841349B

; Patent No. 5955594

; GENERAL INFORMATION:

; APPLICANT: MISHRA, LOPA

; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .

; FILE REFERENCE: XX/PO4470USO

; CURRENT APPLICATION NUMBER: US/08/841,349B

; CURRENT FILING DATE: 1997-04-30

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 6960

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (333)..(6794)

US-08-841-349-3

Query Match 41.5%; Score 697; DB 2; Length 6960;
Best Local Similarity 36.7%; Pred. No. 0.00044;
Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;

QY		1	GTTG----	TGTCTTCA--GCA-----AAACA-----G---TG---GATTT---	29
Db		903	GATGGCATGCCCTTCATGCACCTGATACATAAATCGGCTGACCTGATAGATTTTTGGAT	962	
QY		30	-----AAAATCT-----C-CT-----TGACAA-GC--TT-----G-AGACGA	57	
Db		963	AAACTGAAGAATCTTAATGCACACTACATCTGCAGNATGANTTTAACCTGGCCGAGCAG	1022	
QY		58	CAC-----AAATCT-----ATCA-----GGA-----A--AG	75	
Db		1023	CACCTTGGCCTCACTAAACTGTTAGACCCTGAAGATATCATGCTGGCACCCCTGATGAG	1082	
QY		76	AA-----A-----GA-----AA--GAA-----	85	
Db		1083	AAGTCTATCATCATACGTGGTGACTTACTACCCTACTCTTCCAAGATGAAGGCCCTTG	1142	
QY		86	-----AA--AAACCG-----AA-----CCTGACAA-----AAA-AGAGAAAAA	116	
Db		1143	GCTGTGAGGAAGCGCATTTGGAAGGTCCTTGATAATGCTATAGAACAG--AGAAAT	1201	

117 GA---AGAGAA---AAAAA---A---TC---A-TGA---AAACATC--- 145
1202 GATTGAGAGTACAGACACTTGTCTTGACCTTCTGGAGTGGATTGAACAACCATCAT 1261
146 CAGCC-AAA-AA-TGCACAAAT-CTA-TCTC---TTGGG---CAA---TC--- 181
1262 CATCTAAACAAACCGCA-AAATTTGCTAATTCACCTGTTGGGTTCCACAGAGCTCCAG 1320
182 -TTCA---CG---GG---G---G---CTG--- 193
1321 CATTTACACGTACCGCACAGTGGAGAAACACACTAAGTTTACTTGAGAGGGGAATTTGG 1380
194 -GCTGCTCTGTCTC-TTC---CAAG---GAG---TGC 221
1381 AGGTGCTCTCTTTTCGCGATTTCAGAGCAAGATCGCGAGCAATATCAGAAAGTCTACATGC 1440
222 CCGTGGCCAGGGAGATGC-CACCT---TC-C---CC---AAAG-CT--- 256
1441 CC---CGC-GAGGGGAAGCTCATCTCTGACATCAACAAGGCTTGGGAAAGACTGGAAAA 1496
257 -ATG---GACAAC-G---TGACGG---TC---CGGAGG--- 281
1497 GCAGACATGAGAGAACTTGGCTCTG-CGGAATGAGCTCATACGGCAGGAAAAACTGGA 1555
282 -AC---AAC-CG-GG---TC---GAGAGA---GC---G--- 290
1556 ACAACTCGCCCGAAGATTTGATCGCAAGCGAGCTATGAGGGAGACATGGCTGAGTGA 1615
291 CCACC---CTCAGG---TG---CACTATTGA--- 312
1616 CCAGCGTCTTGTCTCAGGACAACTTTGGATTGACCTTCCCGCTGTTGAGGCTGCTAC 1675
313 C---AAC-CG-GG---TC---AC--- 327
1676 CAAAAACACAGGCGCATTTGAGACAGACATCGCTGCATATGAAGACGAGTTGAGCGCT 1735
328 GGTGGC-CTGGC---T-AAACCGAG-C-ACCAT---CCTC---TAT---G 362
1736 GGTGGCTGTGGCCAGGGAACCTTGAAGCG-AGAATACCATGACATCAAGCGCATCACAG 1794
363 CTGGGAATGAAA-GTGGT---GC-CTGG-ATCCTCGGTGCTCTCT- 406
1795 CGAGGAGGACAAATGTCATCCGGCTCTGGGAATACTTGC-TGGAATCTGCTCAGGGCCAGG 1853
407 A-GCAAC---ACC---CAAACG---CAGTACA-GC--- 430
1854 AGGCAGGCTCTTGAGATGAACCTGGGATTCGAAGAGATATTCAGGAATGCTTTATATT 1913
431 ATCGA---GATCCA---GAACGTG---GATGTGT-ATGACGAGGC---C-CTTA 471
1914 ATGGACTGGATGATGAAATGAAGGTGCTATTGCTGTCTCAAGACTATGGCAAACTTA 1973
472 C---ACCTG---CTCGGT---GCAGACA---GACAA-CC 497
1974 CTTGGTGTGAAGACCTGTTACAGAAGCATGCCCT-GGTTGAAGCAGACATTG-CAATCC 2031
498 ACCCA---AAGA---CCTCT---AG-GGT---CCAC--- 520
2032 AAGCAGAGCGGTGAAGAGGTGTGAATGCTCTGCCAGAGATTGCAACAGATGGGGAAG 2091
521 -CT---CATTTG---CHAFTA---TC---T-CCCA-A---AATTGT--- 549
2092 GCTACAGGCA-TGTGACCCCGAGGTAAATTCGAGACCGGTGTTGCCACATGGAGTTCTGC 2150
550 -AGAGATTCTTCAGATATCT-CCATTATGA---AGGGAAC---ATA-T- 591
2151 TATCAGAGCTTT-GTCAGTGTGCTGCC---GAGCGTAGGGCTCGCCTGGAAGATC 2203
592 -TAGCCTC---A---C-CT---ATAGCAA---CTGGTAGACACAGAG- 625
2204 CCGTCGCTCTGGAAGTTCTTCTGGGAGATGGCAGAAGGAAGGCTGG-ATACGAGAGA 2262

QY 626 ---CCT---ACGTTACTTGG---AGA---CA---CAT---CT 650
Db 2263 AGGAAAAGATCCTGTCTCTCTGATGATTAC---GGGAAAGACTTGACCACTGTCTAGCGCT 2320
QY 651 -CT---CC---CA---A---A---GGGT---TGGC---TTTG--- 671
Db 2321 GCTGAGCAAGCACCGGCACTTTGAGGATGAGATGAGTGGCCGTAGTGGCCATTTGAGCA 2380
QY 672 ---T---GA---GTGAAGAC---GAATACTT---GSA---AT--- 696
Db 2381 GGCCATTAAAGAGGTGAAGACATGATTGCAGAGGAACACTTTTGGATCGGAAAGATCCG 2440
QY 697 TCAGGCGATC---ACCGGAGCAG---TCAG---G 723
Db 2441 TGAGAGATCATTTATATCCGGAGCAGTGGGCAACCTTGGAAACAGCTCTCAGCCATTAG 2500
QY 724 G---GA---CTACGAG---TG---CAG--- 738
Db 2501 GAAGAGCGCTTA-GAGGAAGCCTCATTACTGCACCAGTTCCAGGCTGATGCTGATGATA 2559
QY 739 ---TGC---CTC---CAATGACGT-GGCC--- 757
Db 2560 TTGATCTTTGGATTTAGATATATACTCAAGATTGTTCTCCAGCAATGATGTGGCCATGATG 2619
QY 758 -G---CGCC-CG---TGCT-ACG-G---AGA-CTA---AAG-G-TCACC---CT 789
Db 2620 AGTACTCCACGAGTCTCTGGTCAAGAACATTAAGATGTAGCAGAAGAGATCACCACCT 2679
QY 790 G-A---ACTAT---C-CAC-CAT---A---CA---TTTCAGAAAGC-CA---AG 820
Db 2680 GCAGGCCCACTATTGACACACTGCTGAGCAAGCCAGTCCCTTCCACAGCAGATGAG 2739
QY 821 GG---TACAGTCT---CC---CG---TG-GGA---CAA--- 844
Db 2740 AGTCTCAGATGTGAAGGCGCGCTGGCAGGAATTGAGGAGCGCTGCAAGAGATGGCAG 2799
QY 845 ---AAG---GACAC---TG-CA 858
Db 2800 AGTTAACCGCTAAGGAGCAGGCTCTGCAGGACACCTTGCCCTGTACAGATGTTCA 2859
QY 859 GTG---TGA---AGC---CTCA---GC 873
Db 2860 GTGAGCTGATGCTGTGAGCTCTGATTTGAGAGAGGAGCAGTGGCTCAACAACATGC 2919
QY 874 AG-TCC---CCT---CAG--- 884
Db 2920 AGATCCGAGAGAGCTGGAGGACCTTGAAGTCAATCCAGCAGATTGTGAGACCTTAGAAC 2979
QY 885 CAGAA---TTC---CAGTGGT---ACAAG---GA 906
Db 2980 CAGAAATGAACAACCAAGGCTTCCCGGTTGCTGTGTGTAACCCAGATTGCACGGCAGCTGA 3039
QY 907 TG-ACAAAG---AC---TGATTGAAGAA---AGA---AAG--- 935
Db 3040 TCACAATGGCCACCCCAAGTGA---AAAGGAAATCAGAGCTCAGCAAGACAAACTCAACAC 3097
QY 936 G-GGTGA---AGT---GGA--- 951
Db 3098 GAGGTGGATCAGTTTCAGAGAACTGCTGACAGGAAAGAGATGCTCTTCTGTCTGCCCT 3157
QY 952 ---CAG---ACCT---T---TCCT-C-TC---AAAA 971
Db 3158 GAGCATCCAGAACTACCACTCGAGTGCATGAACCAAAATCCTGCATCCCGGAGAGAC 3217
QY 972 ---TCATC---T---CAA---TGTCT-T---CTGAA 994
Db 3218 CAAGTCTCATCGAGTCTACCAAGACCTTGGCAATGACCTGGCAGGTGTCTATGGCCCTGCA 3277
QY 995 ---CA---TGACT---ATGGGAACCTACACTT---GC---GTGGCC 1024
Db 3278 GTGCAAGCTGACTGGCAT-GGAACGAGACTTTGGTAGCCATTTGAGGCGAAGCTGATGACC 3336
QY 1025 TCCA-----ACAACTGG-G-CC-A-CACCAATG-CCAGCATCATGCTAT--TT 1066

Db 3337 TCAGAAAGAGCTGAGAGCTGGAGTCGAGCACC-CTGACCAAGGCTCAAGCTATCCT- 3394
QY 1067 GGTCCAGGC-GCCG-TGACGAGGTG-----AG-CAAC-G-GCAGC 1102
Db 3395 -GTCTGGGTGCGCCGAGATCACTGATGTGTGGGAGGAATGAAGCAACCCCTGAAGAAC- 3452
QY 1103 TCGAG-----GAGG-GCAGGCTGC-G-TCT-GG-CT-G- 1129
Db 3453 -CGAGAGGCTCCCTGGGAGAGCCAGCAGCTGAGCAGATTTCTGGGGAATTCGACGA 3511
QY 1130 TCGCC-TCTT-----CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCCAGTCTTGCTCTCCAGGACCCAGACTCTATCGCTCAGAGGACATGCCCAATAC 3571
QY 1151 -----CT-----GCTCTCA-----AATTT-----TGA----- 1169
Db 3572 CTTCACTGAGGAGAGAGCTTCTCACAGCAGCAGAAATATCAAAATGAGATCGACAA 3631
QY 1169 -TGTGAG-----TGC-----CA-----C-----T-TC-CCCA----- 1187
Db 3632 TTATGAGGAAGACTACCAAGATCGGGACATGGCGGAGATGGTCAACCCAGGGCAGAC 3691
QY 1188 -----CC-----CGGAAAGGCTGC-CGCC-----ACCCAC----- 1211
Db 3692 TGATGCCAGTATATGTTTCTGCGGCGAGCGGTGCGAGCCTTAGA-CACTGGCTGGAATG 3750
QY 1212 -CACCAC-----CAACA-CAA-----CAG-CAATG-----GC 1235
Db 3751 AGCTCCCAAAATGGGAGAGACAGGCAAAACCTCTCTCCAGTCCCATACCAGC 3810
QY 1236 A-----ACACC-GAC-AGC-AAACC-----AAT-----CA-GA-TAT----- 1261
Db 3811 AGTTCTTTAGGACACCAACAAAGCTGAAGCTTTTCTTAATACCAAGAGATGTTTGG 3870
QY 1262 -ATAC-AAATG-----A-----AATTA-GAAG-----AAACA-CAG----- 1288
Db 3871 CTCATACTGAATGCCACCACCTGGAAGAGCTGAAGAGCCCATTAATAAAGCAGGAGG 3930
QY 1289 -CTCATG-----GGA-CA-----GA-----AAT-----TTGAGG----- 1311
Db 3931 ACTTCATGACCATGATGCCACGAGGAGAAATCAATGCTGTGTGGAGAGTGGCC 3990
QY 1312 -----GAG-----GGGAACA-----A-AGAA-T-ACT----- 1330
Db 3991 GAAGACTGGTGAGCGATGGGAACATCACTCCGACCGCATCCAGGAGAGTGCACCTA 4050
QY 1331 TTG-G-G-----GG-GAA-----AAG-----AGT-----T-----TTAAA- 1352
Db 4051 TTGACGACAGACACAGGAGAAATCGAAGAGCAGCCAGTGAACCTTCTGATGAGGTTAAAG 4110
QY 1353 -AA-----AGAA-----ATTG-AA-----AAT- 1367
Db 4111 ACAACCGTATCTACAGAGTTCTGCGAGATGTCAGAGCTGTCCCTCTGGATCAATG 4170
QY 1368 -----TGCCTT-GC-AGATAT-TTA-----G-----GTACA 1390
Db 4171 AAAAGATG-CTTACAGTCAAGACATGCTTATGATGAAGCCAGAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG-TTT-T-----CTT-TTCC-CAA-----AC- 1412
Db 4229 ATGTTAAAGCATCAAGCATTTATGGGGAACCTTGATCCAAAGAAATGGCTTGACAA 4288
QY 1413 -----G-GAA-GAA-CA-----CAGCACACC-----G-GCT-TGG----- 1439
Db 4289 AATTGAGAGGAAGATGACGCTTATTTGAGAAAGCCAGAAACAGAGCTGGGTAA 4348
QY 1440 -----ACCACTG-----C-----AAG--C-TGCATC-----GTGCAA 1464
Db 4349 GGAATAACTCACTGGTTTACATAAAATGTGGGAAGTCTTGAATCCACACCCAGACAA 4408
QY 1465 -----C-CTCTTTGGTGCA-----G-TG-----TGCGC----- 1486

Db 4409 GGCACAGCGGCTCTTTGATGCAATAAGCTGAGCTTTTTCACAAAGCTGCGAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC-TCTGCC-----CACAGAGTG 1515
Db 4469 TGACAAATGGCTACATGCGCTGGAGAGCCAGATTCAATCTGACGACTATGGCAAGA- 4525
QY 1516 CCC-----CCACGTG-GAACATTTCT-----G-----GA-GCTGG-CAATCCCA-AA 1552
Db 4526 -CCTTACCA-GTGTCAATATTTCTTTGAAAAAGCAACAGATGCTGGGAATCAGATGAA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA--G 1570
Db 4584 GTTGGGAAGAAGATCGAGAACTGCAGAGCCAGCCAGGCGCTGAGTCAGAGGGG 4643
QY 1571 ACGA-ACAGAAATGAG-----A-CTTT-CCG-GC-----CCAG--CGTGGCGCT 1608
Db 4644 AAGAGCAG-ATGAGGTGGAGCAACAGCGCTTACTGTGCGAGCCAGATTCATGGAGCT 4702
QY 1609 GC-GG-GCAGTTTGT-AGA-----CTGT-G-----CCA-----CC----- 1635
Db 4703 TCTGGAGCCCTTGAGTGAGGAGGAGCATAACTGTGTAGCTTCCAGGAGATCCATCAGT 4762
QY 1636 -AC-----GG-CG-----TGTGTTG-----T-GAAACCT- 1656
Db 4763 CAACAGGATGTGGAGGAGCAATCCTATGGGTTGGCGAGGATGCCCTTGGCAACTTC 4822
QY 1657 -GA-A-----ATTA-----AAA-----G-AGC-----AAAAAAA 1679
Db 4823 CACAGATCATGGCCATACTTCAAACTGTGCAGCTGTTAATAAGAAAA 4873

RESULT 16
US-09-431-184A-3
; Sequence 3, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P04470051/BAS
; CURRENT APPLICATION NUMBER: US/09/431,184A
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 6960
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (333)..(6794)
US-09-431-184A-3

Query Match 41.58; Score 697; DB 4; Length 6960;
Best Local Similarity 36.74; Pred. No. 0.00044;
Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;
QY 1 GTTG---TGTCCTTCA-GCA-----AAACA-----G--TG---GATTT--- 29
Db 903 GATGGCATGGCTTCAATGCACTGATACATAAATCGGCTGACCTGATAGATTGAT 962
QY 30 -----AAATCT-----C-CT-----TGCACAA-GC--TT-----G-AGAGCAA 57
Db 963 AAATGAAGAAATCTAATGCACTACACTCAATCTGCAGATGCAATTAACCTGGCAGAGCAG 1022
QY 58 CAC-----AATCT-----ATCA-----GGA-----A--AG 75
Db 1023 CACCTTGGCCTCACTAACTGTTAGACCTGGAAGATATCAGTGTGGACCACTGATGAG 1082
QY 76 AA-----A-----GA-----AA-----GAA----- 85

Db 1083 AAGTCTATCATCATACGTCGGTGACTTACTACCACTACTTCTCCAGAGTGAAGCCCTTG 1142
Qy 86 -----AA-AAACCG-----AA-----CCTGACAA-----AAA-AGAGAAAAA 116
Db 1143 GCTGCGAAGGAAAGCGCATTTGGAAGAGTGCTTGATATGCTATAGAAACAG-AGAAAT 1201
Qy 117 GA--AGAAGAA--AAAA--A--TC-----A-TGA-AAACCATC-- 145
Db 1202 GATTGAGAGTACAGACACTTGCTTCTGACCTTCTGGAGTGGATTGAACAAACCATCAT 1261
Qy 146 CAGCC-AAA-AA-TSCCAAT--CTA--TCTC--TTGGG--CAA-----TC----- 181
Db 1262 CATCTAAACAACCGCA-AAITTCCTAATTCACCTGTTGGGTCACACAGCTCCAAG 1320
Qy 182 --TTCA-----CG-----GG-----G-----CTG----- 193
Db 1321 CATTTCAACAGTACCGCACAGTGGAGAAACCCACTAAGTTTACTGAGAAGGGAAATTGG 1380
Qy 194 -GCTGCTCTGTGCTC--TTC--CAAG--GAG-----GAG-----TGC 221
Db 1381 AGGTGCTTCTTTTCGCAATTCAGAGCAAGATGCGAGCGAATATCAAGAGGTCTACATGC 1440
Qy 222 CCGTGCGCAGCGGAGATGC-CACTC-----TC--C-----CC-----AAAG-CT----- 256
Db 1441 CC--CGC-GAGGGGAAGCTCATCTGTGACATCAACAAGCGCTGGGAAAGACTGGAAAA 1496
Qy 257 -----ATG--GACAC--G--TGACCG-----TC-----CGGCAGG----- 281
Db 1497 GCAGAACATGAGAGAACTGGGCTCTG-CGGAATGAGCTCATACGGCGGAGAAAACTGGA 1555
Qy 282 -----GAGAGAA-----GGGAGA-----GC--G----- 290
Db 1556 ACAACTCGCCGAAGATTTGATCGCAGCAGCTATCAGGAGGACATGCGTGTAGTGA 1615
Qy 291 CCACC-----CTCAGG-----TG-----CACTATTGA----- 312
Db 1616 CCAGCGCTTGTGTCTCAGACAACTTTGGATTGACCTTCCCGCTGTTGAGGCTGCTAC 1675
Qy 313 C-----AAC-CG-GG-----TC-----AC-----CCG- 327
Db 1676 CAAAAACACAGCGCCATTGACAGACATCGCTGCATATGAAGAAGAGTTTCAGGCCGT 1735
Qy 328 GTGGC-CTGGC-----T-AAACCGCAG--C-ACCAT--CCTC-----TAT--G 362
Db 1736 GTGGCTGTGCCAGGGAAGTGAAGCG-AGAATACCATGACATCAACCGCATCACAG 1794
Qy 363 CTGGGATGACAA-GTGGT--GC-CTGG--ATCTCGGTGGTTCCTTCT-- 406
Db 1795 CGAGGAAGGCAATGTCTATCCGCTCTGGGAATCTTGC-TGGAACTGCTCAGGGCCAGG 1853
Qy 407 A-GCAAC-----ACC-----CAAAAG-----CAGTACA-GC----- 430
Db 1854 AGCAGCGTCTTGATGATGACCTGGGATTCCAAAGATATTCAGGAATGCTTTATATT 1913
Qy 431 ATCGA--GATCCA-----GAACGTG--GATGTGT-ATGACGAGGSC--C-CTTA 471
Db 1914 ATGGACTGGATGATGAATGAAGGTGCTATTGCTGTCTCAAGACTATGCGCAAACTTA 1973
Qy 472 C-----ACCTG-----CTCGGT-----GCAGACA--GACAA-CC 497
Db 1974 CTTGGTGTGAAGACCTGTTACAGAAGCATGCGCCT-GGTTGAAGCAGACATTC-CAATCC 2031
Qy 498 ACCCA-----AAGA-----CCTCT-----AG--GGT--CCAC----- 520
Db 2032 AAGCAGAGCGTGAAGAGGTGTGAATGCCCTCTGCCAGAGTGTGAACAGATGGGGAAG 2091
Qy 521 -CT-----CATTGTG-----CAAGTA--TC-----T-CCCA-A--AATTGT-- 549
Db 2092 GCTACAGGCA-TGTGACCCCGGAGTAAATTCGAGACCGTGTGCGCACATGGATTCTGC 2150
Qy 550 -----AGAGATTTCTCAGATATCT-CCATTATGA-----AGGGAAC-----ATA-T- 591

Db 2151 TATCAAGAGGCTTT-GTCAGCTGCTGCTGCC-----GAGCGTAGGGCTGGCTGGAAGAGTC 2203
Qy 592 ---TAGCCTC---A---C---CT-----GC---ATAGCAA---CTGGTAGACCAAGAG- 625
Db 2204 CCCTGCGCTCTGGAAGTCTTCTTGGGAGATGGCAGAGAGGAGGCTGG-ATACGAGAGA 2262
Qy 626 -----CCT---ACGTTACTTGG---AGA-----CA-----CAT---CT 650
Db 2263 AGGAAAAGATCTCTGCTCTCTGATGATTAC--GGGAAAGACTTGACCACTGCTATGGCCT 2320
Qy 651 -CT-----CC---CA-----A--A--GGGT--TGSC--TTTG--- 671
Db 2321 GCTGAGCAAGCACCGGCTATTTGAGATGAGATGAGTGGCCGCTAGTGGCCATTTTGA 2380
Qy 672 -----T---GA--GTGAAGAC-----GAATACTT-----GGAA---AT--- 696
Db 2381 GGCCATTAAAGAGGTGAAGACATGATTGCAGAGGAACACTTTTGGATCGGAAAGATCCG 2440
Qy 697 TCAGGCGATC-----ACCGGGAGCAG-----TCAG-----G 723
Db 2441 TGAGAGATCATTTATATCCGGAGCAGTGGGCCAACCTTGAACAGCTCTCAGCCATTAG 2500
Qy 724 G--GA-----CTACGAG-----TG-----CAG----- 738
Db 2501 GAAGAGCGCCTA-GAGGAAGCCTCATTTACTGCACCAAGTTCAGGCTGATGCTGATGATA 2559
Qy 739 ---TGC-----CTC---CAATGACGT-GGCC----- 757
Db 2560 TTGATGCTTGGATTTAGATATATCAAGATTGTCTCCAGCAATGATGTGGGCCATGATG 2619
Qy 758 -G--CGCC-CG-----TGGT-ACG-G-----AGA-CTA-----AAG-G-TCACC--GT 789
Db 2620 AGTACTCCACGCGAGTCTCTGGTCAAGACATTAAGATGTAGCAGAGAGATCAACCACT 2679
Qy 790 G-A-----ACTAT--C-CAC-CAT-----A--CA-----TTTCAGAAGC-CA---AG 820
Db 2680 GCAGGCCCACTATTGACACACTGCTGATGACCAAGCCAGTGCCTTCCACAGCACTGCGAG 2739
Qy 821 GG--TACAGGTGT---CC-----CCG---TG-GGA-----CAA----- 844
Db 2740 AGTCTCCAGATGTGAAGGCGCGCTGGCAGGAATTTAGGAGCGCTGCAAGAGAGATGGCAG 2799
Qy 845 -----AAGG-----GGACAC-----TG--CA 858
Db 2800 AGTTAACCGCTTAAGGAAGCAGGCTCTCCAGGACACCTTGGCCCTGTACAGATGTTCA 2859
Qy 859 GTG-----TGA-----AGC-----CTCA-----GC 873
Db 2860 GTGAGGCTGATGCTGTGAGCTCTGGATTGACGAGAAGGAGCAGTGGCTCAACACATGC 2919
Qy 874 AG-TCC-----CCT-----CAG----- 884
Db 2920 AGATCCACAGAGAGTGGAGACCTTGAAGTCAATCCAGCAGACAGATTTGAGAGCTTAGAAC 2979
Qy 885 CAGAA-----TTC-----CAGTGT--ACAAG-----GA 906
Db 2980 CAGAATGAACCAACGAGCTTCCCGGTTGCTGTGTGTGACCAAGATTGACGCGAGCTGA 3039
Qy 907 TG-ACAAAG--AC-----TGATTGAAGAA--AGA-----AAG----- 935
Db 3040 TGCACAATGGCCACCCAGTGA--AAAGGAATCAGAGCTCAGCAAGACAAACTCAACAC 3097
Qy 936 G-GGTGAA--AGT-----GGAAAA----- 951
Db 3098 GAGGTGGAGTCAATTGAGAGAACTGGTGGACAGGAAAGGATGCTCTTGTCTGCGCCT 3157
Qy 952 -----CAG-----ACCT-----T-----TCCT-C-TC-----AAAAC 971
Db 3158 GAGCATCCAGACTACCACTCGATGCAATGAACCAAAATCTCTGATCCGGGAGAGAC 3217
Qy 972 -----TCATC---T-----CTT--CAA-----TGTC-T-----CTGAA 994
Db 3218 CAAGGTCAATCGAGTCTACCAAGACCTTGGCAATGACCTGGCAGGTGTCATGGCCCTGCA 3277

QY	1440	-----ACCCACTG-----C-----AAG--C--TGCATC-----GTGCAG	1464
Db	4349	GGAAAACTCACTGGTTTACATAAAATGTGGGAAAGTCTCTTGAATCCACACCCAGACCA	4408
QY	1465	-----C--CTCTTTGGTGCCA--G-TG-----TGGGC-----	1486
Db	4409	GGCCGAGGGCTCTTTGATGCARATAGGCTGAGCTTTTACACAAAGCTGCGCAGATCT	4468
QY	1487	-----AAGGGCT-----C-----AGCC--TC--TCTGCC-----CACAGAGTG	1515
Db	4469	TGCARAAATGGCTACATGCGCTTGGAGAGCCAGATTCAATCTGACGACTATGGCAAGA	4525
QY	1516	CCC---CCACGTG-GAACATCTCT-----G--GA-GCTGG-CCATCCCA---AA	1552
Db	4526	-CCTTACCA-GTGTCAATATCTTCTGAAAAGCAACAGATGCTGGAGATCAGATGGAA	4583
QY	1553	-TTC-----A-ATC-----AGTCCA-----T-A-GA--G	1570
Db	4584	GTTCCGGAAGAAAGATCGAGGAACCTGCAGAGCAAGCCAGGCGGTGAGTCAGAGGGG	4643
QY	1571	ACGA--ACAGAAATGAG-----A--CCTT-CCG-GC---CCAAG--CGTGGGCT	1608
Db	4644	AAGAGCACAG-ATGAGGTGGACAGCAACGCCTTACTGTGCAGACCAAGTTCATGGAGCT	4702
QY	1609	GC-GG-GCACTTTGGT-AGA-----CTGT--G--CCA-----CC-----	1635
Db	4703	TCTGGAGCCTTGAGTCAGAGGAAGCAATACCTTGTTAGCTTCCAAGGAGATCCATCAGTT	4762
QY	1636	--AC-----GG-CG-----TGTGTTG-----T-GAACGT--	1656
Db	4763	CAACGAGGTGGAGAGCAAGAAATCCTATGGTGTGGCGAGAGGATCCCTTGGCAACTTC	4822
QY	1657	----GA--A-----ATAA-----AAA---G-AGC-----AAAAAAAA	1679
Db	4823	CACAGATCATGGCCATAACCTTCAACTGTGCAGCTGTTAATAAGAAAAA	4873

RESULT 17
 US-08-841-349-5
 ; Sequence 5, Application US/08841349B
 ; Patent No. 5955594
 ; GENERAL INFORMATION:
 ; APPLICANT: MISHRA, LOPA
 ; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT.
 ; FILE REFERENCE: XX/P0470US0
 ; CURRENT APPLICATION NUMBER: US/08/841,349B
 ; CURRENT FILING DATE: 1997-04-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 8176
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-08-841-349-5

Query Match 41.5%; Score 697; DB 2; Length 8176;
 Best Local Similarity 36.7%; Pred. No. 0.00061;
 Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;

QY	1	GTTG--TGTTCCTTCA--GCA-----AAACA-----G--TG--GATTT-----	29
Db	903	GATGGCATGCGCTTCAATGCACTGATACATAAACATCGCGCTGACCTGATAGATTGAT	962
QY	30	-----AAATCT-----C-CT-----TGCACAA-GC--TT-----G-AGAGCAA	57
Db	963	AAACTGAAGAAATCTAATGCACTACAACTCTGCAGAAATGCAATTAACCTGCGAGAGCAG	1022
QY	58	CAC-----AATCT-----ATCA-----GGA-----A--AG	75
Db	1023	CACCTTGGCCTCACTAAACTGTTAGACCTGAGATATCAGTGTGGACCAACCTGATGAG	1082
QY	76	AA-----A-----GA-----AA-----GAA-----	85


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QY 995 ---CA---TGACT---ATGGGAACCTACACTT---GC---GTGGCC 1024
Db 3278 GTGCAAGCTGACTGCGAT---GGAAACGAGACTTGGTAGCCATTGAGCGAAGCTGAGTGACC 3336
QY 1025 TCCA-----ACAAGCTGG-G-CC-A-CACCAATG-CCAGCATCATGCTAT--TT 1066
Db 3337 TGCAGAAAGAAAGCTGAGAAGCTGGAGTCCGAGCACC-CTGACCAGGCTCAAGCTATCT- 3394
QY 1067 GGTCCAGGC--GCG--TCACGAGAGTG-----AG-CAAC--G-GCAG 1102
Db 3395 -GTCTCGGCTGGCCGAGATCAGTGATGTGTGGAGGAAATGAAGAACACCCCTGAAGAAC- 3452
QY 1103 TCGAG-----GAGG--GCAGGCTGC--G-TCT---GG-CT---G- 1129
Db 3453 -CGAGAGGCTCCCTGGGAGAGCCAGCAGCTGAGCAGGTTTCTGCGGACTTGGACA 3511
QY 1130 CTGCC--TCTTT-----CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCCAGTCTTGGCTCTCCAGGACCCAGACTGCTATCGCTCAGAGGACATGCCCAATAC 3571
QY 1151 ---CT-----GCTTCTCA-----AATTT-----TGA----- 1168
Db 3572 CTTCACTGAGCAGAGAAGCTTCTCACAGCAGCAGAAATATCAAAAATGAGATCGCAA 3631
QY 1169 -TGTGAG-----TGC-----CA-----C--T--TC-CCCA----- 1187
Db 3632 TTATGAGGAAGACTACCAGAGATCGGACATGGCGAGATGGTTCACCCAGGGCGCAGAC 3691
QY 1188 ---CC-----CGGAAAGGCTGC-CGCG-----ACCAC----- 1211
Db 3692 TGATGCCAGTATATGTTTCTGCGCAGCGGCTGCAGGCTTAGA-CATGCTGGAATG 3750
QY 1212 --CACCAC-----CAACA-CAA-----CAG--CAATG-----GC 1235
Db 3751 AGCTCCACAAATGTGGAGAAACAGCAAACTCTCTCCCGTCCCATGCTTACCAGC 3810
QY 1236 A-----ACACC-GAC-AGC-AAACC-----AAT---CA-GA-TAT----- 1261
Db 3811 AGTTCTCTTAGGCACACCAACAACTGAAGCTTTTCTTAATAACCAAGAGTATGTTTGG 3870
QY 1262 --ATAC--AAATG-----A-----AATTA--GAAG-----AAACA-CAG----- 1288
Db 3871 CTCATCTGAATGCCACCACTGGAAGGAGCTGAAGCAGCCATTAATAAGCAGAGG 3930
QY 1289 -CCTCATG-----GCA--CA-----GA-----AAT-----TTGAGG----- 1311
Db 3931 ACTTCATGACCACATGATGTCACAGGAGAGATCAATCTGTTGTGGAGACTGGCC 3990
QY 1312 -----GAG-----GGGAACA-----A-AGAA--T--ACT--- 1330
Db 3991 GAAGACTGGTGAAGCGATGGGAACATCAACTCCGACCGCATCCAGGAGAAGGTGGACTTA 4050
QY 1331 TTG-G--G--GG-GRA-----AAG-----AGT-----T-----TTAAA-- 1352
Db 4051 TTGACGACAGACAGGAAGAAATCGAGAAGCAGCCAGTGAATCTCTGATGAGGTTAAAGG 4110
QY 1353 --AA-----AGAA-----ATTG-AA-----AAT- 1367
Db 4111 ACAACCGTGATCTACAGAAGTTCTTGCAGAGATTGTCAAGAGCTGTCCCTCTGGATCAATG 4170
QY 1368 -----TGCTTT--GC--AGATAT--TTA-----G-----GTACA 1390
Db 4171 AAAAGATG-CTTACAGCTCAGACATGCTTATGATGAAGCCAGAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG-TTT-T-----CTT--TTCC-CAA-----AC-- 1412
Db 4229 ATGGTTAAGCATCAAGCATTTATGGGGAATTTGCGGAATCTGCATCCCAACAAAGAATGCTTGCAA 4288
QY 1413 -----G-GGAA-GAA--CA-----CAGCACACCC-----G-GCT-TGG----- 1439
Db 4289 AATTGAGAAGGAGGAATGCAGCTTATTTCAGAAAGCCAGNAACAGAGCTGTGGTAAA 4348
QY 1440 -----ACCCACTG-----C-----AAG--C-TGCATC-----GTGCAA 1464
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Db 4349 GGAATACTCACTGCTGTTTACATAAAATGTGGGAAGTCTCTTGAATCCACAACCCAGACAA 4408
QY 1465 -----C-CTCTTTGGTGCCA-----G-TG-----TGCGC----- 1486
Db 4409 GCGCCAGCGGCTCTTTGATGCAAAATAGGCTGAGCTTTTCACACAAGCTGCGCAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC--TCTGCC-----CACAGAGTG 1515
Db 4469 TGACAAATGGCTTACATGGCTCGAGAGCCAGATTCAATCTGACGACTATGGCAAGA-- 4525
QY 1516 CCC---CCACCTG-GAACATTTCT-----G-----GA-GCTGG-CCATCCCA--AA 1552
Db 4526 -CCTTACCA-GTGTCAATATTCTTCTGAAAAAGCAACAGATGCTGGAGAAATCAGATGAA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA---G 1570
Db 4584 GTTCGGAAGAAAGAGATCGAGGAACTGCAGAGCCAAAGCCAGGGCGCTGAGTCAGGAGGG 4643
QY 1571 ACGA--ACAGATGAG-----A--CCTT-CCG-GC--CCAAAG--CGTGGCGCT 1608
Db 4644 AAGAGCAG-ATGAGGTGGA-CAGCAAAACGCTTACTGTGCAGACCAAGATTTCATGGAGCT 4702
QY 1609 GC-GG-GCCTTTGCT-AGA-----CTGT--G--CCA-----CC----- 1635
Db 4703 TCTGGAGCCTTGAGTGAGAGGAAGCATAACTGTGTAGCTTCCAAGGAGATCCATCAGTT 4762
QY 1636 --AC-----GG-CG-----TGTGTTG-----T-GAAACGT- 1656
Db 4763 CAACAGGATGCGGAGGACGAAATCTATGGTTTGGCGAGAGGATGCCCTTTGGCACTTC 4822
QY 1657 ---CA-A-----ATRA-----AAA-----G-AGC-----AAAAAAA 1679
Db 4823 CACAGATCATGGCCATACCTTCAAACTGTGCGAGCTGTTAATAAGAAAAA 4873

RESULT 18
US-09-431-184A-5
; Sequence 5, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P044700S1/BAS
; CURRENT APPLICATION NUMBER: US/09/431,184A
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8176
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-431-184A-5

Query Match 41.5%; Score 697; DB 4; Length 8176;
Best Local Similarity 36.7%; Pred. No. 0.00061;
Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;

QY 1 GTTG---TGCTCTCA-GCA-----AAACA-----G---TG---GATTT----- 29
Db 903 GATGGCATGGCTTCATATGCACTGATACATAAAACATCGGCTGACCTGATAGATTTGAT 962
QY 30 -----AAATCT-----C-CT-----TGCAAA-GC--TT-----G-AGAGCAA 57
Db 963 AAACCTGAAGAAATCAATGACACTCAAACTGCAGATGCAATTAACCTGGCAGAGCG 1022
QY 58 CAC-----AATCT-----ATCA-----ATCA-----A-AG 75
Db 1023 CACCTTGGCTCTCACTAAACTGTTAGACCTTGAAGATATCACTGTGGAGCCACCTGATGAG 1082
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QY 76 AA-----A-----GA-----AA-----GAA-----85
Db 1083 AAGTCTATCATCATAGTGGTCACTTACCACTACTTCTCCAAAGATGAAGCCCTTG 1142
QY 86-----AA-----AAACCG-----AA-----CCTGACAA-----AAA-AGAAAGAAAA 116
Db 1143 GCTGTCGAAGGAAAGCGCATTTGGAAGAGTGCTTGATTAATGCTATAGAAACAG-AGAAAT 1201
QY 117 GA---AGAGAA---AAAA-----A---TC-----A-TGA---AAACCATC---145
Db 1202 GATTGAGAAGTACGAGACACTTGCTTCTGACCTTCTGGAGTGGATTGAACAAACCATCAT 1261
QY 146 CAGCC-AAA-AA-TGCACAATT---CTA---TCCTC---TTGGG---CAA-----TC-----181
Db 1262 CATCTTAACACCGCA-NAITTCCTAATTCACCTGGTTGGGTCACACAGCTCCAAG 1320
QY 182---TTCA-----CG-----GG-----G-----CTG-----193
Db 1321 CAITCAACAGCTACCGCACAGTGGAGAAACCACTAAGTTTACTTGAGAAGGGGAATTTGG 1380
QY 194 -GCTGCTCTGTCTC---TTC---CAAG-----GAG-----TGC 221
Db 1381 AGTGCTCTCTTTTCCGGAATTCAGACGAAGTGGAGCGAATAATCAGAAGGCTCTACATGC 1440
QY 222 CCCTGCGCAGCGGAGATGC-CACCT---TC-C---CC---AAAG-CT-----256
Db 1441 CC---CGC-GAGGGGAAGCTCATCTTGACATCAACGAAGCCCTGGGAAGAACTGGAAAA 1496
QY 257-----ATG---GACAAAC-G---TGACGG-----TC---CGGCAGG-----281
Db 1497 GCAGAACATGAGAGAGAACTGGCTCTG-CGGAATGAGCTCATACGGCAGGAAAAAATCGGA 1555
QY 282-----GAGAG-----GGAG-----GC-----G-----290
Db 1556 ARACTGCCCGAAGATTGATGCGAAGCGAGCTATGAGGGAGACATGGCTGAGTGAATA 1615
QY 291 CCACC-----CTCAGG-----TG-----CACTATTGA-----312
Db 1616 CCAGCGTCTTGCTCAGGACAACTTTGGATTGACCTTCCCGCTGCTGAGGCTGCTAC 1675
QY 313 C---AAC-CG-GG-----TC-----AC-----CCG-327
Db 1676 CAAAAACACGAGGCCATTTAGACAGACATCGCTGCATATGAAGAACGAGTTCAGGCCGT 1735
QY 328 GTGGGC-CTGGC-----T-AAACCGCAG-C-ACCAT--CCTC---TAT---G 362
Db 1736 GTGGCTGTGGCCAGGAACTTGAGCCG-AGAACTHCCATGACATCAAGCGCATCACAG 1794
QY 363 CTGGGAATGACAA-GTGGT---GC-CTGG---ATCCTCGCGTGGTCTTCT------G 406
Db 1795 CGAGGAAGGACAAATGTCTCCGGCTCTGGGAATACTTGC-TGGAACCTGCTCAGGCCCAGG 1853
QY 407 A-GCAAC-----ACC-----CAAACG-----CAGTACA-GC-----430
Db 1854 AGGACGGCTTGGATGAAACCTGGGATGCAAAAGATATTCAGGAAATGCTTTATATT 1913
QY 431 ATCGA---GATCCA-----GAACGTG-----GATGTGT-ATGACGAGGSC---C-CTTA 471
Db 1914 ATGACTGGATGATGAATGAGGTGCTATTGCTGTCTCAAGACTATGGCAAACTTA 1973
QY 472 C-----ACCTG-----CTGGT-----GCGAGACA---GACAA-CC 497
Db 1974 CTTGGTGTGAAGACCTGTTACAGAAGCATGCGCT-GGTTGAAGCAGACATTG-CAATCC 2031
QY 498 ACCCA-----AAGA-----CCTCT---AG---GGT---CCAC-----520
Db 2032 AAGCAGAGCGTGAAGAGGTGTAATGCTCTGCCAGAGATTGCAACAGATGGGGAAG 2091
QY 521 -CT-----CATTTG-----CAAGTA---TC-----T-CCCA-A---AATTGT--549
Db 2092 GCTACAGCCA-TGTAGCCCCAGGTAAITTCGAGACCGTGTGCCCAACATGGAGTTCTGC 2150

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QY 592-----TAGCTC---A---C---CT-----GC-----ATAGCAA---CTGGTAGCCAG-625
Db 2204 CCCTGCGCTCTGGAAGTTCTTCTGGGAGATGGCAGAGAGGAAGGCTGG-ATACGAGAGA 2262
QY 626-----CCT---ACGGTTACTTGG---AGA-----CA-----CAT---CT 650
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QY 651 -CT-----CC-----CA-----A---A---GGGT---TGGC---TTTG---671
Db 2321 GCTGAGCAAGCACCGGCATTTGAGGATGAGATGAGTGGCCGTAGTGGCCATTTTGAGCA 2380
QY 672-----T---GA---GTGAAGAC-----GAATACCT-----GGAA---AT---696
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QY 697 TCAGGGATC-----ACCGGGAGCAG-----TCAG-----G 723
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QY 724 G--GA---CTACGAG-----TG-----CAG-----738
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Db 2560 TTGATCCTTGGATTTAGATATATCAAGATTGTCTCCAGCAATGATGTTGGCCATGATG 2619
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QY 859 GTG-----TGA-----AGC-----CTCA-----GC 873
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QY 907 TG-ACAAAAG--AC-----TGATTGAAGGAA---AGA-----AAG-----935
Db 3040 TGCACAAATGGCCACCCCACTGA--AAAGGAATCAGAGCTCAGCAGACAACTCAACAC 3097
QY 936 G-GGTGAA---AGT-----GGAATA-----951
Db 3098 GAGGTGGAGTCACTTTCAGAGAACTGGTGACAGGAAAGAGTGTCTTCTGTCTGCCCT 3157
QY 952-----CAG-----ACCT-----T-----TCCT-C-TC-----AAAC 971
Db 3158 GAGCATCCAGAACTACCTCCTCGATGCAATGAACCAAACTCCTGATCCGGGAGAGAC 3217
QY 972-----TCATC---T-T-----CTT---CAA-----TGTC-T-----CTGAA 994

Db 3218 CAAGGTCTAGTCTACCCAGACCTTGGCAATGACCTGGCAGGTGTCTATGCGCCCTGCA 3277
QY 995 ---CA---TGACT---ATGGGAACACTT-----GC---GTGGCC 1024
Db 3278 GTGCAAGCTGATGGCAT--GGAAAGAGATCTGGTAGCCATTGAGGCGAAGCTGAGTGACC 3336
QY 1025 TCCA-----ACAAGCTGG--G-CC-A--CACCAGTG--CCAGCATCATCTAT--TT 1066
Db 3337 TCCAGAAAGAACTGAGAACTGGAGTGGAGTCGAGCACC--CTGACAGGCTCAAGCTATCCT- 3394
QY 1067 GTTCAGGC--GCCG--TCAGCGAGGTG-----AG-CAAC--G--GCACG 1102
Db 3395 -GTCTCGGCTGCCGAGATCAGTGATGTGTGGAGGAAATGAAGACAACCCCTGAAGAAC- 3452
QY 1103 TCGAG-----GAGG--GCAGGCTGC--G--TCT--GG-CT-----G- 1129
Db 3453 -CGAGAGGCTCCCTGGGAGAGCCAGCAAGCTGACGAGTTTCTGCGGGACTTGGACGA 3511
QY 1130 CTGCC--TCTT-----CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCCAGTCTTGCTCTCCAGGACCCAGACTGCTATCGCTCAGAGGACATGCCCAATAC 3571
QY 1151 ---CT-----GCTTCTCA-----AATTT-----TGA----- 1168
Db 3572 CCTCACTGAGGAGAGAACTTCTCACAGCAGCAGAGAAATCAAAAATGAGATCGACAA 3631
QY 1169 -TGTGAG-----TGC-----CA-----C--T--TC-CCCA----- 1187
Db 3632 TTATGGAAGACTACCAAGATCGGAGATCGGAGATGGTCAACCCAGGGGCAGAC 3691
QY 1188 ---CC-----CGGAAAGGCTGC--CGCC-----ACCAC----- 1211
Db 3692 TGATGCCAGTATATGTTTCTGCGCAGCGCTGCGAGCCTTAGA--CACTGCTGGAATG 3750
QY 1212 --CACCAC-----CAACA--CAA-----CAG--CAATG-----GC 1235
Db 3751 AGCTCCAAAATGTGGGAGAACAGGCAAAACCTCTCTCCAGTCCCATGCTTACCAGC 3810
QY 1236 A-----ACACC--GAC--AGC--AACC-----AAT--CA-CA-TAT----- 1261
Db 3811 AGTTCCTTAGGACACCAACAAGCTGAAGCTTTTCTTAATAACCAAGGAGTGTTTTG 3870
QY 1262 ---ATAC--AAATG-----A-----AATTA--GAAG-----AAACA-CAG----- 1288
Db 3871 CTCATCTAAATGCCACCCCTCGAAGAGCTGAAGCAGCCATTAAGAAGCAGGAG 3930
QY 1289 -CCTCATG-----GGA--CA--GA-----AAT-----TTCAGG----- 1311
Db 3931 ACTTCATGACCACCATGGATGCCAACGAGGAGAGATCAATGCTGTGTGGAGACTGGCC 3990
QY 1312 -----GAG-----GGGAACA-----A-AGAA--T--ACT--- 1330
Db 3991 GAAGACTGTGTAGCGATGGGAACATCACTCGGACCGCATCCAGGAGAGGTGCACTCTA 4050
QY 1331 TTG--G--G-----GG--GAA-----AAG-----AGT-----T-----TTAAA-- 1352
Db 4051 TTGACGACAGACACAGGAAGATCGAAGACGAGCCAGTGAATCTCTGATGAGGTTAAGG 4110
QY 1353 --AA-----AGAA-----ATTG--AA-----AAT- 1367
Db 4111 ACAACCGTGATCTACAGAAAGTTCCTGCAAGATTGTCAAGAGTGTCTCTGGATCAATG 4170
QY 1368 -----TGCCCTT---GC---AGATAT---TTA-----G-----GTACA 1390
Db 4171 AAAGATG--CTTACAGCTCAAGACATGTCTTATGATGAAGCCAGAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG--TTT-T-----CTT--TTCC--CAA-----AC-- 1412
Db 4229 ATGGTTAAAGCATCAAGCATTTATGGCGAACTTGCATCCCAACAAGAAATGCTTGACAA 4288
QY 1413 -----G--GGAA-GAA--CA-----CAGCACCC-----G--GCT-TGG----- 1439

Db 4289 AATTGAGAAGGAGGAATGACGCTTATTTCAGAAAGCCAGAAACAGAGCTGTGTGTA 4348
QY 1440 -----ACCCACTG-----C-----AAG--C--TGCAATC-----GTGCAA 1464
Db 4349 GGAATAACTACTGTGTGTACATAAAATGTGGGAAGTCTTGAATCCACAACCCAGACCAA 4408
QY 1465 -----C--CTCTTTGTGCCA-----G-TG-----TGSGC----- 1486
Db 4409 GGCCAGCGGCTCTTTGATGCAATATAGGCTGAGCTTTTTCACAAAGCTGGCAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC--TCTGCC-----CACAGACTG 1515
Db 4469 TGCAAAATGGCTACATGSCCTGGAGAGCCAGATTCATCTGACGACTATGGCAAGA-- 4525
QY 1516 CCC---CCACGTG--GAACATTTCT-----G-----GA--GCTGG--CCATCCCA---AA 1552
Db 4526 -CCTTACCA--GTGTCAATATTCTTCTGAAAAAGCAACAGATGCTGGAGAATCAGATGGA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA---G 1570
Db 4584 GTTGGRAAAGAGATCGAGAACTGCAGAGCCAGCCAGGCGCTGAGTCAGAGGGG 4643
QY 1571 ACGA--ACAGAAATGAG-----A--CCTT--CCG-GC---CCAG--CGTGGCGCT 1608
Db 4644 AAGAGCACAG--ATGAGGTGGACAGCAACGCTTACTGTGCGAGACCAAGTTTCATGGAGCT 4702
QY 1609 GC-GG-GCAGTTTGGT-AGA-----CTGT--G--CCA-----CC----- 1635
Db 4703 TCTGGAGCCCTTGAGTGAGAGGAAGACATAACCTGTGTAGCTTCCAGAGGAGATCCATCAGTT 4762
QY 1636 --AC-----GG-CG-----TGTGTTG-----T-GAAACGT- 1656
Db 4763 CAAAGGATGTGGAGGAGCAAAATCCTATGTTGGCGAGAGGATGCTTTGGCACTTC 4822
QY 1657 ---GA--A-----ATAA-----AAA-----G-AGC-----AAAAAAA 1679
Db 4823 CACAGATCATGCCATAACCTTCAAACTGTGCAGCTGTTAATAAGAAAA 4873

RESULT 19

US-09-620-312D-343
; Sequence 343, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
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; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
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; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 343

Db 2433 GCGCCAAATCTATACATGGTCCCGAGGGGATCAGGCCCTGTGGTCCAGCTCACTGCCAT 2492
QY 717 --AG--TC--A--GGGG--ACT--AC-- 730
Db 2493 TGAAGATTCTAGCTTGGGGTTAAGAAATATGAAAACTTCCAGATGGCTTCTATCACATC 2552
QY 731 -----GAGTG-----CAGTG-----CCT 743
Db 2553 CCCCAGCTCTTGTGTGGAGTGTGGAGGAGAAAGGTGGAATCGGTGGTGTATCAAAAACCT 2612
QY 744 -----CCAA-----TG-----ACGTGGCGCGCC--GT 765
Db 2613 TAAGAAGACACCCCACTTCCAAAGTCTGTCTCTCTCATGAAAGTGTCTTGGCCCAAGGA 2672
QY 766 G-----GTAC-----GGAGAGTAAAGTC--ACC--GT-----GA 791
Db 2673 GGAATTGTATACGCCCCCACTGGTGA--TCAAGGTATCGACCACAGGAGTTTGGCGGA 2731
QY 792 A--CTATC-----CACCAT--A--C--AT-----TT-- 809
Db 2732 AGCCTGTCTAGGCCAGTGCACCATCGAGCGCTGGATGGCTTTCGTGTGACCCTTATG 2791
QY 810 CAG--AAGCCAAG--GT--ACAGGT--G--TCCC--C--GT----- 837
Db 2792 CAGGGAAG--AGGACATCGTCCACACAGCTCAAGCCCTCCCTTCTGTGCGCCCAACCAT 2848
QY 838 -----GGACA-----AAAGG--GAC-----ACTG--C--AGTG--TGA 865
Db 2849 GCGGGACATCGTTATCGAAATGGAAGACACCAACCATTACTGGCTTCTAAGTCTTAA 2908
QY 866 GC-----CTCAGCAGTCCCTCAGCAGAT--TCCAGTG--GT-----AC-- 901
Db 2909 GCAGTATGTCAACG--CACTCAGCAAAATGGCTTCTCCAGGACAGTGCATCTGACAGA 2966
QY 902 --AAGATGACAAA--GACTG-----AT-----TGA 924
Db 2967 AAGAGGAGAAATCGTGGACTGTGTGAGTAAATTTATGCTTCCCTCAGGGGAACATGA 3026
QY 925 A-----GGA-----A--AGAAAG--GGT--GA--AA--GTG-- 946
Db 3027 AAAATGCGACAGTATATTCAGAAAGGCTATTCCAGGCTCAAGATATATTAATGTGAAC 3086
QY 947 -GAAA--CAGACCTTT--CCTCTCAA--ACTCATCTTC--TTCAA--TGT-- 987
Db 3087 AGAAATGTAGCAGA--ATTGTAGGCGCTGACAGACTTCTCAGATAGTTCAAGTTGTACC 3145
QY 988 --C--TC--TGAACATGA-----CTATG----- 1004
Db 3146 GAGGCAAGTCGATGAAATGAGATCCTTCTGTGTGGAGAGTTTAAGGCTCCTTTC 3205
QY 1005 GGAATCACT--T-----GCGTG--G--CCTCCACA--AGCT--GGGCA 1041
Db 3206 GGATCTACCTCTGCGGATGATCCCGAGCGTCCAGCCCTCCAGACAGTTTCCGG--A 3263
QY 1042 --CACCATGCCAGATC--ATGC-----TA-----T--TTGGTCCAGC-- 1075
Db 3264 ATTACC--TGACAGCTCCACAGGAATGCAGGTAGGATTTACATTTGTTCCAGGCTTA 3321
QY 1076 --GCCGT--CAGC-----GA-----G--GTGAGC--AAC--G 1097
Db 3322 GAGC--TCCAGCCCGAGACACATATGGCTGTGTGACCTTACATATAAATAACACTGG 3379
QY 1098 GC-----AGCT--G--AG--GAG-----G 1111
Db 3380 GCAAAAAGTCAATTGAAGACCGAGATCACTACATTTCCCAACACTCTCAACCCAGTCTTTG 3439
QY 1112 CGAGGCTG--CG--TCTG--GCTG--TGCCTC-----TTCTGGTC 1144
Db 3440 GCAGGATGTACAACTGAGCTCTACTTACCTCAAGAAAAGACCTGAAAATTTCT--GTC 3498
QY 1145 T-----TG--CACCTGCTT--CTC-----A--AATT--TTGATG-- 1172
Db 3499 TATGATTATGACCT--TTACCCGGATGAAAAAGTAGGAGAAACAATTTATGATCTGG 3556

QY -173 --A--G-----TGCCACTT--CCGCAC--COGGA--A--AGG----- 1198
Db 3557 AAAACCGATTCCTTTCCCGCTTTGGGTCCGCATACCCAGAGGAGTACTGTGTTT 3616
QY 1199 CTGCGGCC--ACC-----ACCACC-----ACCAACACAAACAGC--AATG--GCAA 1237
Db 3617 CTGGAGTCAATACCTGGCGGAGATCAACTGAGACCAACACAGCTGCTTCAAAATGTGCCA 3676
QY 1238 --CA-----CGACAGCAACC-----AATCAGATAT-- 1261
Db 3677 GATTCAAAAGGCTTCC--CA--CAACCCATCTTTCGAAAGATGGGAGTAGATCATATATG 3733
QY 1262 --A--TACA-----AATGAATTTAGAG--AAA----- 1283
Db 3734 GAGGACGAGACTACAGCTTGGATG--AATTTGAGCCAAACAAATCTCGACACGACCTC 3792
QY 1284 -----CACAGCTCA-----TGS-----GA-- 1298
Db 3793 GGGGCCCTGAAGAGCGGCTTGTCTCTTCACTCTCTCAGGACTCAGGGGCTGGTCCCTGAG 3852
QY 1299 CA-----GAAA-----TTTG--AG-----G-----GA-- 1313
Db 3853 CAGTGGAAACAAGGACTTTGCACAGCACCCTTCCAGCCCAACATTTCCAGATACTACCTG 3912
QY 1314 --G--G-----GGAACA--AAGAA--TACTTTGG-----GG--G 1337
Db 3913 CGTGTATCATCTGGAACACCAAGGACGTATCTTGGACGAGAAAGCATCACAGGAGAG 3972
QY 1338 GAAAGAGT-----TT-----T--AA--AAAGAAATTTGAA 1365
Db 3973 GAAATGAGTACATCTACGTCAAAGGCTGGATTCCTGGCAATGAAGAAACAAACAGAAA 4032
QY 1366 A--TTG--CC--TTGCAGATATT-----AGG-----TACATG--GA--GTTTT 1400
Db 4033 ACAGTGTCCGTACAGATCTTGGATGGTGAAGGAAATTTTA--ACTGGCATTTGTTTT 4091
QY 1401 C-----TT-----TTCC-----CAA-----A--CG--G--GAAGACACAGCA--C-- 1428
Db 4092 CCCGTTTGACTACCTTCCAGCGCAACACTCTGTATCTGTGGAA--AAAGAGCATTTCT 4150
QY 1429 -----ACC--CGG--CTTGA--CCCACTGCAAGCTG--CA--TC--G--TG--C 1462
Db 4151 GGAGTATTGACAAACGGAATTCGAATCCAC--CCAGGCTGATCATTCAGATATGGAC 4209
QY 1463 A--AC-----CTCT-----TTGG----- 1473
Db 4210 AATGACAGTTTTCTCTGGATGACTACTTTGGGTTTCTTAGAACTTGACTTCGTCACACG 4269
QY 1474 -----TG-----CCAG-----TG-----TGGCAAG-----GG----- 1491
Db 4270 ATCATCTCTGCAAAATCACAGAGAATGCAGATTTGGACATGATTCGGACCTCAAAGCC 4329
QY 1492 -----CT-----CAGCCT--CTCT--GC----- 1505
Db 4330 ATGAACCCCTTAAAGCCCAAGCAGCCTCCCTCTTTGAGCAGAAAGTCCATGAAGAGATG 4389
QY 1506 --CCA-----CAGAG-----T--GCCCCACCT--GSAACATTTCTGAGCTG 1541
Db 4390 TGGCATCTAGGACAGAAAGATGGCGCCCGGTATATGGCTGGAA--A--GTGAGAT-- 4445
QY 1542 GCCATCCCAAT--TCAATC-----AGTCC-----ATAG-----A-----G 1570
Db 4446 GACATTGGAATCTCTAA--CGAGAAGGAGGCCGAGAGAGCCAGCCGAGAGGGCGGG 4504
QY 1571 ACGAAC-----AG-----AAT--G--AGA-----CCTTCC-- 1591
Db 4505 ACGAACCAACATGAACCCCAAGCTTGAATTTACAAATCGACAGAAACCTCTCTCTCT 4564
QY 1592 GG-----CCCAAGC-----GTGGCGCTGC-----GGG-- 1613
Db 4565 GTTCAACCAACCCATGCAAGACCATGAAGTTTCATCTGTGTGGCGCGCTTTAAGTGGGTCA 4624

QY 475 --CTGC--TC-----GGTGC-----AGACAGCAACACCCCA-----502
Db 1839 AGCTGCATCTTTAACTTTGAAGGTGCTCCCTTGGGGCAGAC-ACTACCGAAGATGGGGATG 1897
QY 503 --AAGA-CCT-----CTAG-G-G--GT-CCACC-----T-----C 523
Db 1898 AGAAGAGCCTGGAGAAC-AGAAGCACAGTGGCCACCACTGTGTTGGGAGCAACACCCCC 1956
QY 524 ATTG-----TGCAAGT-----ATCTCCCA-----542
Db 1957 ATTGTTCTGCAATTTTGCAGAGACTACATCTACCATCTGCGTCTATGTCTATCAA 2016
QY 543 ----AAA---TTG---TAGA---GAT---TTCTTCAGAT-----565
Db 2017 GCCAGAACTCTTGGCTTTAGTAAGGATAGCTT-TTCAGATCCATTTGGTCTCATCTG 2075
QY 566 -----ATC-TCCATT-AA---TGAA-----GGG- 583
Db 2076 TTTCTCCATCGAGCAAAACCACTGAGATCATCCATTCAACCTGGAATCCACAGTGGGA 2135
QY 584 ---AACA---ATATT---AG-----CC-----596
Db 2136 CCAACAAATTATTCGATGAAGTTGAATCTATGCGGGAACCCCAACAGTCTCTACAGAA 2195
QY 597 T-CACC-----TG---C-----AT-AGCAACTGG-----T 616
Db 2196 TCCACCAAGTATATCATGGAATTTTTCAGATGACCAAGTGGGCAAGATGAATTTT 2255
QY 617 A-GACAGAGC-----CTAC---GGT---T---ACT-----TGGAGA-CACA-----647
Db 2256 AGGACGA-AGCATTTTCTCTCTGTGGTGAACCTGAACTCAGAAATGGACATCACAACCA 2314
QY 648 ----TCTCT-----CC-----CAGAGC-----GG-----TTG-----665
Db 2315 AACTTCTTGGCACCACCAAGTAATGAATGGAGACAAAGCCTGCGGGGATGTTCTGTAAC 2374
QY 666 ----GCT---TTGTGAGTG--AAGACGA-----ATACTT-----690
Db 2375 CAGAGCTGATTCTGAGGGCAAG--GATGGCTCCAACTTCCCATTTCTCCCTCAAG 2432
QY 691 GG-----AAT-----T-----CAGGGCATCA-CCCG-GG---AGC-----716
Db 2433 GCGGCCAAATATATACATGTCCTCCCGAGGGGATCAGGCTGTGGTCCAGCATCACTGCCAT 2492
QY 717 --AG-TC-AG--GGGAC-TAGCA-----G-----TGCAAG-TGCCTCCATGACGTG 754
Db 2493 TGAGATCTAGCTTGGGGCTTTAAGAAATATGAATACTTCCAGATGGCTTCTATCACAT- 2551
QY 755 GCGGCGCC-----GTG--GTACGGA-GAGTAAAGG-----TC--784
Db 2552 -CC---CCAGTCTTGTGTGGAGTGTGGAGGAG-AAAGGGTGAATCGTGGTGTATCAA 2606
QY 785 --ACCGT--G-----AATATCCA-----CCATACATTTCA-GAA-----G-C 816
Db 2607 AAACTTAAAGAACACACCAACTTTTCCAAAGTTCTGTCTCTTTCATGAAAGTGTCTTGCC 2666
QY 817 CAAGG-----GTACAGGTGTCCTC-GTGG-GA-CAAAAGGG-----GA-CAC-TGCAG 859
Db 2667 CAAGGAGGAATGTATCA--TGCCCCCACTGGTGTATCAA--GGTCAATGCCACAGGCAG 2721
QY 860 TGT-----GAAGCC-TC-AG--CAGT-----C-----877
Db 2722 TTTGGCGGAAGCTGTCTGTGAGCCAGTGCAACATCGAGCGCTGATGCTTTTCGTGT 2781
QY 878 --CCCT---CAG-----CAG---AA-----TT-----891
Db 2782 GACCCCTATGCGAGGGAAGAGGACATCGTCCACAGCTCAAGACCTCCCTCTGTCTGCC 2841
QY 892 ---CCAGT---GGTAC-----AA-GGATGACA-AAA-----G-----A 916
Db 2842 CCACCA-TGCCGGGACATCGTTATCGAATGGAAGACACCAACCACTACTGGCTTCTAA 2900

QY 917 -CTGATTG--AAGGA--AAGAA-----GG-----GTTG-----AAA-----943
Db 2901 GCTGACAGAAAGGAGGAAGAAATCGTGACTGGTGGAGTAAATTTTATGTCTTCCTCAGG 2960
QY 944 -G-----TGAAAA-----CAGA---CCT--TTCC--TCTCAA-----968
Db 2961 GGAACATGAAATAATCGGACAGTATATTTCAGAAAGGCTATTCCAAAGCTCAAGATATATA 3020
QY 969 -----AACT-----CA-----T-----CTTC-----TTCAA 984
Db 3021 TTGTGAACCTAGAAAAATGTAGCAGAAATTTGAGGCGCTGACAGACTTCTCAGATACGTTCAA 3080
QY 985 --TGT-----C--TC--TGAACATGA-----CTATG-----1004
Db 3081 GTTGTACCGAGCAAGTCTGATGAATAATGAAGATCTTCTGTGGTGGAGAGTTTAAGGG 3140
QY 1005 -----GGAACTACACT-----T-----GCGTG--G--CCTCCAACA-AGCT 1035
Db 3141 CTCCTTTGGATCTACCTCTGCGGATGACCCAGCGTGCAGCCCTCCAGACAGTT 3200
QY 1036 --GGGCCA--CACCAATGCCAGATC-----ATGC-----T---ATT---GGTC 1070
Db 3201 TCGGG--AATTACC--TGACAGCGTCCACAGGAATGCACGGTTAGGATTTACATTTGTT 3256
QY 1071 CAGGC--GCGGT-CAGC--GA-----G-CTGAGC-----1093
Db 3257 GAGGCTTAGAGC--TCCAGCCCCAGGACAAACATGGCTGTGTGACCTTACATATAAAT 3314
QY 1094 AAC-----GCG--ACGTC--G-AG--GAG-----1110
Db 3315 AACACTGGGCAAAAAGTCAATTGAAGACCGAGATCACTACATTCCCAACACTCTCAACCC 3374
QY 1111 -----GGCAGGCTG--CG-TCTG-GCTGC--TGCCTC-----1136
Db 3375 AGTCTTTGGAGATGTAGAACTGAGCTGTCTACTTACTCTCAAGAAAAGACCTGAAAT 3434
QY 1137 TTCTGCTCT-----TG-CACCTGCTT-CTC-----A-AATT-T 1165
Db 3435 TTCT-GTCTATGATTATGACACT--TTACCGGGATGAAAAGTAGGAGAAACATATAT 3491
QY 1166 TGATGTG--A-G-----TGCCACTT---CCCCAC-CCGGGA---A-AGG---1198
Db 3492 TGATCTGAAAAACCATTTCTTTCGGCTTTGGGTCCCATCGCGCATACACAGAGGATGA 3551
QY 1199 -----CTCGCGC--ACC-----ACCACC--ACCAACACACAGC-----AA 1231
Db 3552 CTGTTTCTGGAGTCAATACCTGCGGAGATCACTGAGACCAACACAGCTGCTTCAAAA 3611
QY 1232 TG--GCAA--CA-----CCGACAGCAAC-----AAT 1254
Db 3612 TGTGCGCAGATTCAAAGGCTTCC--CA-CAACCCATCTTCCGAGATGGGAGTAGAAT 3668
QY 1255 CAGATAT--A-TACA-----AATGAATTTAGAAG-----AAA-----1283
Db 3669 CATATATGGAGCAGAGACTACAGCTTGGATG-AATTTGAAGCCCAACAAAATCTCTGCACC 3727
QY 1284 -----CACAGCTCA-----TGG 1296
Db 3728 AGCCTCGGGGCCCTCGAAGAGCGGCTTGTCTTTCATCTCTCAGGACTCAGGGGCTGG 3787
QY 1297 ---GA-CA---GAAA-----TTTG--AG-----G-----GA- 1313
Db 3788 TCCCTGACACGTGAAACACAGGACTTTGCACAGCACCTTCCAGCCCAACATTTCCAGAT 3847
QY 1314 -----G-G-----GGAACA--AAGAA--TACTTTTG-----1334
Db 3848 ACTACCTCGGTGTATCATCTGGAACACCAAGGAGCTTATCTTGGACGAGAAAGCATCA 3907
QY 1335 --GG--GGAAGAGT-----TT-----T-AA-AAAAA 1357
Db 3908 CAGGAGAGAAATGAGTGACATCTACGTCAAAGGCTGGATTCCTGGCAATGAAGAAAAA 3967
QY 1358 AATTGAAAA--TTG-CC-TTGCAGATATTT--AGG-----TACAATG--GA 1395

Db 2619 GCGCAGGACACCTACACGATGCGAAACCGGATATAA--GCAGCATCACCCAGCGAGTTG 2676
Qy 354 ----TCCTCTATGCTGGGAATGACAG--TGCTGCTGGATC-----C-----TC--GC 394
Db 2677 ACTTGTCTCCAGGTTGGGAATGGGAAGATGATCATG--TCCTATGACATAAATCGAGC 2735
Qy 395 G-----TGG-----TCCTCTG----- 406
Db 2736 GGTGATGAGAAAGCTGGGAATATGGAATCACCATTCTCTCTGATCATAGCCCAATC 2795
Qy 407 ----AGCA-----ACAC-----CC--AAACG 421
Db 2796 CTGGTTGACGAGAGAAATGTACACACTCATAGACGGGAGGCTGGTCCGAAACG 2855
Qy 422 C-----AG--T--ACAG-----CATCGAG--AT----- 438
Db 2856 CAAGAAAGATTAAACACAGACTGCTTCAAGCACCGAAGGCCATGGAGGAATTCGAAGA 2915
Qy 439 CCA-----GAA-----C-----G--TGG-----T-----GT--G 454
Db 2916 CCAAGAGGCTGGGAATATGCTTCTTAATTGGCTGGAATTTCACTGGAACAACGATG 2975
Qy 455 T-----AT-----GAC-----GAG-----GGC--CCTT-----ACAC----- 474
Db 2976 TTCAGATACCTTCGCCCGCAGACGCTGGAGGAGAGAAATGGCTCTTCAGAAACACATGG 3035
Qy 475 ----CTGC--TC-----GGT-----GCAGACA----- 490
Db 3036 TGCAGTCCCATCTTTAACTTGAAGTGGCTTGGGCGAGACACTACCGAAGATGGGGA 3095
Qy 491 ----GACAA-----GACCC-----CCACC-----CAAAGACC-- 508
Db 3096 TGAGAAGAGCCTGGAGAAACAGNAGCACAGTGCACCACTGTGTTCGGAGCAAAACACCCC 3155
Qy 509 ----TC-----T-----AGGTC--CACCT--CAT--TG-----TGC--AAGTATCTC- 539
Db 3156 CATGTTTCTGCAATTTGACAGAGTCTACATCTACCATCTGGCCTGCTATGTCTATCA 3215
Qy 540 --CCA-AAA-----TTG-----TAGA-----GAT-----TCTTTCAGAT----- 565
Db 3216 AGCCAGAAACCTCTTGGCTTTAGATAAGATAGCTT--TTCAGATCCATATGCTCATATCT 3274
Qy 566 ----TCTCTCCATCGGAGCAAAACCACTGAGATCATCCATTCAACCTGAATCCACGTGGG 3334
Db 3275 GTTTCCTCCATCGGAGCAAAACCACTGAGATCATCCATTCAACCTGAATCCACGTGGG 3334
Qy 584 ----AACA--ATATT-----AG-----CC----- 596
Db 3335 ACCAAACAAATTATTCGATGAAGTTGAAATCTATGGGGAACCCCAACAGTTCTTACAGA 3394
Qy 597 -T-CACC-----TG-C-AT-AGCAACTGG----- 615
Db 3395 ATCCACCCAAAGTTATCATGAACTTTTGGACATGACCAAGTGGGCAAGATGAAATTTT 3454
Qy 616 TA-GACCAGAGC-----CTAC-----GGT-----T--ACT-----TGGAGA-CACA-- 647
Db 3455 TAGACGA-AGCAATTTCTCTCTCTGTGTGTAATCTGAACTCAGAAATGGACATCACACC 3513
Qy 648 ----TCTCT-----CC-----CAAAGC-----GG-----TTG----- 665
Db 3514 AAACTTCTCTGCCACCCCAAGTAATGATGGAGACAAAGCCTCGGGGATGTTCTTGTAACT 3573
Qy 666 ----GCT--TTGTGAGTG--AAGACGA-----ATACTT----- 690
Db 3574 GCAGAGCTGATTCTTGAGGGCAAG--GATGGCTCCAACCTTCCCATCTTCCCCCTCAA 3631
Qy 691 --GG-----AAAT-----T-----CAGGGATCA--CCCG--GG-----AGC----- 716
Db 3632 GGGGCCAAATCTTATACATGTTGCCCGAGGATCAGGCTGTGGTCCAGCTCACTGCCA 3691
Qy 717 --AG--TC-AG-----GGAC--TACGA-----G-----TGCAG--TGCCTCCAATGAGT 753
Db 3692 TTGAGATTCTAGCTGGGGCTTAGAAATATAGAAATATGAAAACTTCCAGATGGCTTCTATCAT 3751

Qy 754 GGCCTGGCCC-----GTG--GTACGGA-GAGTAAAG-----TC- 784
Db 3752 --CC--CCAGTCTTGTGTGGAGTGTGGAGGAG-AAAGGGTGAATCGGTGTGTGATCA 3805
Qy 785 ----ACCGT--GA-----ACTATCCA-----CCATACATTCA-GAA-----G- 815
Db 3806 AAACCTTAAAGAGACACCCAACTTTCGAGTTCGTTCCTTCATGAAGTGTCTTTCG 3865
Qy 816 CCAAGG-----GTACAGTGTCCCC-GTGG-GA-CAAAAAGG-----GA-CAC--TGCA 858
Db 3866 CCAAGGAGGAATTGTACA--TGCCCCACTGGTGATCAA--GGTCAATCGACCAACAGCA 3920
Qy 859 GTGTG-----AAGCCT-----CAG-----CA-----G--TC----- 877
Db 3921 GTTTGGGCGGAAGCCTGTCTCGGCCAGTGCACCATCGAGCGCTTTCGCTG 3980
Qy 878 ----CCCT-----CAG-----CAG--AA-----TT----- 891
Db 3981 TGACCTTATCGAGGAAGAGGACATCGTCCACAGCTCAAGCTCCCTCTCTGTCTGC 4040
Qy 892 ----CCAGT--GGTAC-----AA--GGATGACA--AAA-----G----- 915
Db 4041 CCCACCA--TGCCGGGACATCGTTATCGAAATGGAAGACACCAACCATTTACTGGCTCTA 4099
Qy 916 A-CTGATTG--AAGGA--AAGAAA--GG--GGTG--AAA----- 943
Db 4100 AGCTGACAGAAAGGAGGAGAAATCGTGGAGTGTGGAGTAAATTTTATGCTTCTCTCAG 4159
Qy 944 --G-----TGGAAAA-----CAGA--CCT--TTCC--TCTCAA----- 968
Db 4160 GGAACATGAAATGCGGACAGTATATTCAAGAGCTATTCGAAGTCAAGATATATA 4219
Qy 969 ----AACT-----CA-----T-----CTTC-----TTCA 983
Db 4220 ATTGTGAACCTAGAAATGTAGCAAAATTTGAGGCGCTGACAGACTTCTCAGATACGTTCA 4279
Qy 984 A--TGT-----C--TC--TGACATGA-----CTATG----- 1004
Db 4280 AGTTGTACCGAGGCAAGTCGGATGAAATGAAGATCTCTCTGTGTGGAGAGTTTAAAG 4339
Qy 1005 ----GGAATACACT--TGC-----GTG-----G--CCTCC-A-ACA-- 1031
Db 4340 GCTCTTTGAGTCTACCTCTCGCGGATGACCCCGGTCGACGCTCCAGCCCTCCAGACAGT 4399
Qy 1032 ----AGCTG--G-G--CCACCAATGC-C--AGCAT--CAT----- 1059
Db 4400 TTCCGGAATTACCTGACAGCGTCCACAGGAATGACGGTTAGGATTTACATTTCTCGAG 4459
Qy 1060 GCTATTTG-G-TCCAGCGGCC--GTCA-----CGAG-GTGAGC-----AA 1095
Db 4460 GC--TTAGACTCA--GCCCAGGACAACTATGCGCTGTGTGACCTTACATATAAATAA 4516
Qy 1096 C-----GSC-----ACGTC--G-AG--GAG----- 1110
Db 4517 CACTGGGCAAAAGTCAATTGAAGACCGAGATCACTATATCCCAACACTCTCAACCCAG 4576
Qy 1111 ----GGCAGGCTG--CG-TCTG-GCTGC-----TGCCTC-----TT 1138
Db 4577 TCTTTGCGAGGATGTACGAACTGAGCTGCTACTTTACCTCAAGAAAGAGCCTGAAAAATTT 4636
Qy 1139 CTGTGCT-----TG-CACCTGCTT--CTC-----A-BAAT--TTG 1167
Db 4637 CT-GTCTATGATATGACACT--TTACCCGGGATGAAAAGTAGGAGAAACAAATTTATG 4693
Qy 1168 ATGTG--A-G-----TGCCACTT-----CCCCAC--CCGGGA--A-AGG----- 1198
Db 4694 ATCTGAAAACCGATTCTCTTTCCGCTTTTGGGTCCCACTCGGCGCATACCAGAGGAGTACT 4753
Qy 1199 ----CTGCGGC--ACC-----ACACC-----ACCAACCAACACAGC-----AATG 1233
Db 4754 GTGTTTCTGAGTCAATACCTTGGCGAGATCAACTGAGACCAACACAGCTGTCTCAAAATG 4813

Qy	1234	--GCAA--CA--	CCGACAGCAACC	-----AATCA	1255
Db	4814	TCGCCAGATTCAAAGGCTTC-	CA-CAACCCATCTCTTCGAAAGATGGGAGTAGAATCA	4870	
Qy	1257	GATAT-----A-TACA-	AATGAAATTAGAAG-----AAA-	1283	
Db	4871	GATATGGAGGACGAGACTACAGCTTGATGNA-TTTGAGCCACAAATATCTTCGACCAG	4929		
Qy	1284	-----CACAGCTCA-	-----TGG--	1296	
Db	4930	CACCTCGGGGCCCTGAAGAGCGGCTTGCTCTTCACATCTCTCAGGACTCAGGCGCTGGTC	4989		
Qy	1297	--CA-CA--GAAA--TTTG-	-----AGGA	1313	
Db	4990	CCTGAGCACGTGGAAAACAAGACTTTTCACAGCACCTTCAGGCCCAACATTTCCAGGA	5049		
Qy	1314	-----GGG-	-----	1317	
Db	5050	AAACTTCAGATGTGGTGGATGTTTTCCCAAGAGTTTGGGGCCACCAGGCCCTCTTTC	5109		
Qy	1318	AACA-----NAG-AATACT-	-----	1330	
Db	5110	AACATCACCCCGAAAGCCAGAAATACTACCTGCGTGTGATCATCTCGAACAACAAG	5169		
Qy	1331	-----TTGG-	GG--GGAAGAAGT-----TTTA-----AAA	1353	
Db	5170	GAGCTTATCTTGGACGAGAAAAGCATCACAGGAGAGGAATAGTGACATCTACGTCAA	5229		
Qy	1354	-----NAG-----AAATTGAAA--TTG-CC-TTGCAGATATT--	1383		
Db	5230	GGCTGGATTCCTGGCAATGAAGAAAACAACAGAAACAGATGCCATTACAGATCTTTG	5289		
Qy	1384	-----AGG-----TACAATG--GA--GTTTTG--TT--TTCC-----	1407		
Db	5290	GATGCTGAAGGGAATTTTA-CTGGCGATTGTTTCCCGTTTGACTACTCTTCAGCCGA	5348		
Qy	1408	CBA-----A-CG--G-GAAGAACACAGCA--C-----ACC--CGG--CTTG	1438		
Db	5349	ACAACCTGTGATCGTTGCGAA-AAAAAGAGCATTTCTGGAGTATGACCAACGGAATTC	5407		
Qy	1439	GA--CCCACTGCAAGCTG--CA-TC-G--TG--CA--AC-----CTCT--	1469		
Db	5408	GAATCCAC--CCAGGCTGATCATTCAGATATGGCAATGCAAGTTTCTCTGATGAC	5466		
Qy	1470	-----TTGG-----TG-----CCAG--	1479		
Db	5467	TACTTGGGTTTCTAGAACTTGACTTGGTGCACACGATCATCTCTGCAAAATCACCAGAG	5526		
Qy	1480	-----TG-----TGGCAG--GG-----CT-----CA	1495		
Db	5527	AAATGCAGGTTGACATGATTCGGACCTCAAGCCATGAACCCCTTAAAGCCAAGACA	5586		
Qy	1496	GCCT--CTCT--GC-----CCA-----CAGAG--T	1514		
Db	5587	GCCTCCCTCTTTGACGAGAAAGTCCATGAAAGGATGGTGGCCATGCTACGCAGAGAAAGAT	5646		
Qy	1515	-GCCCCCACT-----GGAACTCTCGAGCTGGCCATCCCAAT--TCAATC-----	1559		
Db	5647	GGCCCCCGGTATGGCTGGAA-A-GTGGAGAT-GACATGGAAATCCTCAA-CGAGA	5701		
Qy	1560	---AGTCC---ATAG-----A-----GACGAAC-----AG--	1578		
Db	5702	AGGAGCCGACGAGAGCCAGCCGGAAGGGCGGAGCAACCAATGAACCCCAAGC	5761		
Qy	1579	---AAT-G---AGA---CCTTCC--GG-----CCCAAGC-----	1600		
Db	5762	TGGACTTACCAAAATCGACCGAAGAACTCTCTCTGTTTCCAAACCCATGCAAGACCA	5821		
Qy	1601	-----GTGGCGCTGC-----GGG--CA---CTT--TG-----G--TA	1623		
Db	5822	TGAAGTTATCGTGTGGCGCGCTTTAAGTGGGTTCATCATCGGCTTGCTGTTCTGCTTA	5881		
Qy	1624	GACTG-TGC-CACACGG-CGTG-----TG-----TTGTGAACGTGA	1658		

Db	5882	TCCTGCTGCTCTTCGTGGCGTGCTCCTCTACTCTTTGCCGAACCTATTTGTCAA--TGA	5938
Qy	1659	A-AT---AA---AAA-GAGCAAAAAA---AAA	1679
Db	5939	AGATTGTAAAGCCAAATGTGTACCAAGGCAAA	5971
RESULT 22			
US-09-534-638-2			
; Sequence 2, Application US/09534638			
; Patent No. 6320038			
; GENERAL INFORMATION:			
; APPLICANT: Panula, Pertti A.J.			
; APPLICANT: Brandt, Annika			
; APPLICANT: Westerlund, Johanna			
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof			
; TITLE OF INVENTION: For therapy and diagnosis			
; FILE REFERENCE: 2530-104			
; CURRENT APPLICATION NUMBER: US/09/534,638			
; CURRENT FILING DATE: 2000-03-27			
; EARLIER APPLICATION NUMBER: 09/365755			
; EARLIER FILING DATE: 1999-08-03			
; NUMBER OF SEQ ID NOS: 22			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 2			
; LENGTH: 5124			
; TYPE: DNA			
; ORGANISM: Mouse			
US-09-534-638-2			
Query Match 41.4%; Score 695.2; DB 4; Length 5124;			
Best Local Similarity 39.0%; Pred. No. 0.00026;			
Matches 1403; Conservative 0; Mismatches 181; Indels 2012; Gaps 398;			
Qy	1	GT-----TG TG-T-CCTTCA-GCAAAA-----CA-----GTG-G-----ATT	28
Db	687	GTCAAGTGTGATGCGCTGCATGCAAAAACCACTTCCCATGTTCCTGTGTGCCCCCAATA	746
Qy	29	TAAAT-----CT-----CC-----TTGCACAAG-CT-T--GAGAGCA---	56
Db	747	AAATGGTCGGTGCTGCTCAGNATCCCTGTGTTGGACAAGACTGTGAGGAGCAGGTG	806
Qy	57	--A---CA-----CAAT-----CT--A-TCAG-----G--A-----	72
Db	807	GGAGCCCAAGGGCAATAGCTGTAGCCCGCTTCACTCCACTCAGTCTCTAGCCATTCTG	866
Qy	73	-----AAGAAAGA-----AAGAAAAAAGCGAACCT-----G--ACAAAAAG	108
Db	867	TTGTTAAG---GATCCCAGAGGCTACTATGCACTTGGCTCTCTCTCGGTAAACAAAAAG	923
Qy	109	ARGA-----AAAAAGAAAGAA---A--A-----A-----AAA---TCATGAAA	140
Db	924	AACAAGGGGTTCAAAGAGGAGAACAGACTCACCATGTTTATTCCTTATACCTCATG--AC	981
Qy	141	CCA--TCC-----AGCCAAAATGCA-CA--ATTG-----165	
Db	982	CCAGGCCAGAGAGACGAGGTTTGGAGAGCCAAAGA--CGACGATTTATTTCAGGACTCCA	1040
Qy	166	-TA---TC--TC---T-----TG-GG-C-AATC---T--TCAC--GGGGC-----	191
Db	1041	ATAGATTATCCATCACCACCGAATGAGACAATCCTGTGCTGCTGGGGCCCTGTGG	1100
Qy	192	-----TGGC-----TGCT---CTGTGCT---CT---TC-CAAGG-----AGTGCCTGTGG-	228
Db	1101	TTCATGGCTCTTGGCTTGGCTGTGGCTTCCCTCAGTCTCAAGGCAGACAG-GC---TGTGT	1156
Qy	229	CAGCG---GAGATGCCACCTTC-----CCCAAGCTA---TGGACACGTGACGGTCC	275
Db	1157	CAGAGGTAGATGGCA-CTTTCGAGGGGTACAGAGCTAGGTGGA--TAC-----ATGGACC	1211
Qy	276	GGCAGGGGGAGA--GGCG-----CA---CCCTCAGGTGCA-----CT	307

Db	704	GTGAGGAAATTGTCTTCCAAAGTTTGAAGTACAAGTAACAGTGCACAAAGATAATCAACC	763
Qy	326	--C--GG--	
Db	764	ATCTTGAAGAAGAGATGAATGTATCATAGTGTG--GTG-GCTGG-CTAAAC-C-----GCAGCAACC	352
Qy	353	ATCCTCTP-----ATG---CTGGGA--AT-----GACAAG--TGGTG-----CCTGGA-T-388	820
Db	821	GTCC-CTGGACATGTGACTGTGAGCATTTGCAGA-MAGTATAGTGACGCTTCC--GACTG	876
Qy	389	CCTCGGTG-G-TC-----C-TTCT--GAG-----CA-----ACACCCAAAC-----420	
Db	877	CCAGG-GTGAAGATTACAGGCTTCTGTGAGAAATTCAGTGGACACGCTAAACAGCCATG	935
Qy	421	GCAG-----TA-CAGCA--T-----CGAG---ATCCA---GAACGTGG-ATGTGTATG--458	
Db	936	GCTGCTTCATCAGCAAGTAAACCAAGGCTCTTCAGCTGAA-GAGGAAGAGATGAA	994
Qy	459	-----AC-GAGGCCCTTACA-CC-----TG-----CT479	
Db	995	ATGAAACTTCACACTGA-GGCC--AGATCCAAGAAGAGAAACAGTGGTGAATTGACT	1051
Qy	480	-----CGGTGAG-----ACAGCAACC--ACCCAA-----GA506	
Db	1052	GGAAGGAGTCCAGTGAATTCACA-AGAACCATAACCCAACTCTCAATTTGTGAAAGTGA	1110
Qy	507	C-----CTCT-----AGGG--TCCACCTCAATTGCA-----AGTA-----535	
Db	1111	CTCACACTTCGACAGGAATTC-CTTCTTTGGCAGGTGCGCTAGTAGTGGAAAG	1169
Qy	536	---TC---TCCCAAATTTAGAG--AT--TTCTTCAGA-----TAT--C568	
Db	1170	GCGTCCCTATACAAA-----TAAAGTCAATTCATCAGAGGAAATGAAGCAAACTATTAC	1225
Qy	569	TCC-AT--TA-----ATGA--A-GG-----GAACA-----ATATTAGCTCAC--601	
Db	1226	TCCAATGCTACCAAGATGACATGCGCTTGTACAGTTCTCTATCAACCAACCAACGTT	1285
Qy	602	TGCATAGC-----AACTGGTAG-----ACCAG-----AG--CCT---ACGGTTAC636	
Db	1286	ATGGTACCTCTTACTGTGTAGGTCATTAACAAGATGTTAGTCCCTGTTAGGCTAC	1345
Qy	637	---T---TG-----GAGACAATC-----TCTCCCAA657	
Db	1346	CAGTGGGTGTGAGAAGAACACGAAGAGGACATCACATGCTTATCTTGTGTTCTCCCA	1405
Qy	658	AGC--GGTTGGCTTG-----TGAG-----TGAAGACA-----ATA687	
Db	1406	AGCAAG---AGCTTTGTCCACCTTGAGCCCATGTCTCATGA--ACTACCTGTGGCCATA	1460
Qy	688	CT-----T---GG-----AAATTCAG-----GGCA-----704	
Db	1461	CTCAGACAGTCCAGGCACATTATTTCTGATGGAGGCACCTGCTGGGCTGAAGAGC	1520
Qy	705	TCACC-----C---GGGA-GCA--GTTCAG---GGGACTAC---GA732	
Db	1521	TCTCCTTTTATTATCTGATAAATGGCAAAGGGAGGCATTTGTCGAACTGGGACT-CATGGA	1579
Qy	733	---GT---GCAG-----TG-----CC-TC-CAAT-----748	
Db	1580	CTCCTGTGAGCAGGAAGACATGAAGGGCCATTTTTCATCTCAATCCCTGTGAAGTCA	1639
Qy	749	GAGTGGC-----CGC-----GC-----CCGTGGTAC-----770	
Db	1640	GCAATTGCTCTGTGCTCGGTTGCTCATCTATGTCTGTTTTTACTACCG-GGAGCTGAT	1698
Qy	771	---GGA-----GA-GT---AAA-----GGTCACC---GTGAAC-T--A--TC797	
Db	1699	TGGGGATTCTGCAAAATATCATGTGTGAATTTGCTGGCCAAACAAGGTGATTTGACTT	1758
Qy	798	CA--CCAT-ACA---T-T-----TCAGAAGCCAA-----GGGT-ACAG-----827	

1759	DB	CAGCCCATCAAAAGTCTCCAGGCTTCCAGCCCTCACACGCCACCTCGGAGTCACAGCGGCTCTCTCA	1816
828	QY	GT---GT-----CC-CGGTG-----GGACAAAG-GGGACACTGC-----AGTGTGA---864	
819	DB	GTCGCTCTCGCCCTCGTCTGTGGACCAAGGGTG---CTGCTCATGAAGCCTGATGC	1875
865	QY	--AGC-CTCAGCAGTCC-----CCT-C-AGCAGAA-----TTCC	893
876	DB	TGAGCTCTCGGC-GTCTCGGTTTACAACTGCTACCAGAAAAGGACCTCAGCTGGCTTCC	1934
894	QY	AGTGG-----T-ACAG--GATGACAAAGACTG-----AT--TG-----923	
1935	DB	CTGGGCTTTGAATGACACGACGATG-----AAGACTGCATCAATCGTCATAATGTCTA	1989
924	QY	---AA-GGA-----AAG---AAAGGGTGAAAGTGGAAA---AC	952
1990	DB	TATTATGGAAATCACATACTCCAGTATCAAGTACAAA---TGAATA-GGATATGTAC	2044
953	QY	AGACCTTTCTC-----CTCAAA---ACTCA-----TC-----TTCTT-----C	982
2045	DB	AG--C-TTCCTAGGACATGGGCTTAAAGGCATTACCAACTCAAAGATTGTAACACC	2101
983	QY	AA-----TGTC-----TC-----TGAA---CATG-----AC-----1000	
2102	DB	AAAATGTGTCCACAGCTTCAACAGTATGAATGATGAGCCTGAAGTCTACGTAGGT	2161
1001	QY	-----T-ATGGGAA---C-TACA---CT--TGGGTG-----GCCT	1025
2162	DB	TTTTATGAGTCAGATGTAATGGGAGAGGCCATGCAGCGCTGGTGATGTTGAAGAGCCT	2221
1026	QY	CCAACAAGCTG-GGCCACACCAA-----TGCC--AGCATCATG---CT---ATTGGTC	1070
2222	DB	C--ACA--CGGAGACCGTACGAAAGTACTTCCCTGTAG-A-CATGGATCTGGGATTTGGT-	2274
1071	QY	CAGCGCGG-----TCAGC-----GAGGT--GAGCAACGG-----CA	1100
2275	DB	--GGTG--GTAAACTCAGCAGGGGTGGCTGAGGTAGGAGTTAACAGTCCCTGCACCATCA	2330
1101	QY	CGTCGA--GGAGGGCAGG-----CTGC--GTCTG-----GCTG-----1129	
2331	DB	C--CGAGTGAAGCAGGGGCTTCTGCCCTGTCTGAAGATGCTGGACTTGGTATCTCTTC	2388
1130	QY	--CTGCCCTCT-CTGTGTGCA--CCTGCTT-----CTCA-AAT--TT-----T	1166
2389	DB	CAGTGCCTCTCTCCGAGCCCTCCAGCCCTCTTTGTGGAGCTTACAATGCCTTACTCTGT	2448
1167	QY	GAT--GT---GAG-----T---GCCA-----CTTCCC-----CAC	1188
2449	DB	GATTCGTGGAGAGCGCTTCACACTCAAGCCGCTCTTAAACTAGCTTCCCAATGCAAT	2508
1189	QY	CCGGGAAG-----GCTG-----CCGCC-ACC-----ACC-----ACCA	1216
2509	DB	CCGGCTCAGTGTGCAGCTGGAGCCCTCTCCGCCCTTCTTGTGTCCAGTGGAGAAGGA	2568
1217	QY	CCAA-----CACAACA-----GCAA-----TGGCAACA-----CC--GACAGCAA--C	1250
2569	DB	ACAAGCGCCTCACTGCATCTGTGCAACGGCGGCAAA-ACTGTGTCTCTGGCAGTAACCC	2627
1251	QY	CAATCAGATATATA-CAAA--TGAAATT-A---GA---AGAAACAC--AGCCTCA--1293	
2628	DB	CAA--AGTCAT-TAGGAAATGTGAATTTCACTGTGAGCGCAGGCACTAGAGTCTCAAG	2684
1294	QY	-----TGGGACAGA-----AATT--TGA-----GGGAG-----1314	
2685	DB	AGCTGTGGGACTGAGGTGCTTCACTTCTTGAAACAGGAAGGAAGACACAGTCAATCA	2744
1315	QY	-----GG--GAAC--AA-----AGAA-----TACTTTT	1332
2745	DB	AGCCTCTGTGGTTGAACCTGAAGGACTAGAGNAGGAAACACATTCAACTCCCTACTTT	2804
1333	QY	G-----GG-GG-GA-----AAAGATT-T---TAAAA-----AAGAAAT---T-G	1362
2805	DB	GTCCATCAGTGTGAGGTTTCTGAAGATTATCCCTGAACTGCCACCAATATGTTGTAG	2864


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QY 1363 AA-AAT-TGCC-----TT-GCAGATAT-TTAGG-----T----- 1387
Db 2865 AAGATCTGCCGAGCTTCTGTCTCAGTTTGGAGACATATAGGCTCTGCCATGCAA 2924
QY 1388 -----ACAA-----TGGAG-----TTT-----TCCTT- 1404
Db 2925 ACACACAAAATCTTCTCAGATGCCCTATGCTGTGGAGACAGAAATATGCTCTTTG 2984
QY 1405 -TCCAA-----ACGG-----AA-G-AACACAGCA-----CA-----C- 1430
Db 2985 CTCCTAACATCTATGTACTGTGATTTCTAAATGAACACACAGCCTTACTCCAGAGTCA 3044
QY 1431 ---CC-GGC--TTGG--ACC-----CACTG-----CA-----AGCTGCATCTGCA-- 1464
Db 3045 AGTCCAGGCCATTTGGCTATCTCAACACTGTGTACACAGACAGTTG-AAC-TACAACA 3102
QY 1465 -----CCT-----CTTTGG-----TGCCAGTG-----TGGGCAA-----G 1489
Db 3103 CTATGATGGCTCTTACAGCACCTTTGGGGAGCGCATATGGCAG-GAACAGGGCAACACCT 3161
QY 1490 GGCT--CAGCC-----TCT-----C-----TGCCACAG--AGTGCC--C--C--CA-CG-T 1524
Db 3162 GGCTCAGGCCCTTTGTTCTGAGACCTTTTGCCCA-AGCTCAGCCTACATCTTCATCGAT 3220
QY 1525 GGA-----ACATT-CTGGAGC-----TGCCCATCCCA-----AA----- 1552
Db 3221 GAAGCACACATACCCAAAGCCCTCATATGGCTCTCCAGAGGCGAGAGGACATGGCTGT 3280
QY 1553 TTCA--A-----TCAGT-----CCAT--AGAGACGACAGA--ATGA--G 1584
Db 3281 TTCAGGAGCTCTGGGTCACTGCTCAACAATGCCATAAAGGAGGAGTGAAGTGAAGTG 3340
QY 1585 A-CCT-TCCG-----GCC-----CA-AG-----CGT 1602
Db 3341 ACCCTCTCCGCTATATCACCATCGCCCTCTGTGGAGATTCCTCTCAGTCACTCACCT 3400
QY 1603 G-----GC--GC-----TGC--GG-G-CA--CTTTGGTAGAC----- 1626
Db 3401 GTTGTCCGAATGCCCTGTTTGTGCTGGAGTCAGCCT--GGAAGACACAGCAAGAGGGG 3458
QY 1627 ---TG--TGCC-----ACCA-----C-GGCGTGTG--TTG-----A 1651
Db 3459 ACCATGCGAGCCATGTATATACCAAGCACTGTGCGCCTATGCTTTGCGCTGCGAGTA 3518
QY 1652 A-----AC-----GTGAATA--AA-----AA-GAGCAA-----AA-AAA-- 1677
Db 3519 ACCAGGACAGAGGAG-AGAGTACTCAAGTCACTTATGAGGAGCTGTGAAGAGAC 3577
QY 1678 AA 1679
Db 3578 AA 3579
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RESULT 24

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US-09-241-606-1
; Sequence 1, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; FILE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4460003
; CURRENT APPLICATION NUMBER: US/09/241.606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4577
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (44)..(112)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)..(4468)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (113)..(4468)
US-09-241-606-1
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Query Match 41.4%; Score 695; DB 4; Length 4577;
Best Local Similarity 40.1%; Pred. No. 0.00021;
Matches 1397; Conservative 0; Mismatches 197; Indels 1888; Gaps 395;
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QY 1 GTTGTGTCTTC-AGC-----AA-A-ACATGTGATTTAAAT-C-TCTTTG----- 40
Db 183 GCTGTGTCTTCTGAGCTACCTGAATGAGACAGTACTGTAACTGCTTCTTGGAGTCTG 242
QY 41 -C-----ACA--AGC--T--TGA--GA-CG--AA-----CAC----- 60
Db 243 TCAGGGGAAACAGAGCCCTTCTCAGTCCCTGGAGCGGAGAGATGAGTACTCTCACTGTG 302
QY 61 -----AA-TCT--ATC-----AGCA--AA-G-----A-----AA- 78
Db 303 TCGCCTTCGTGTCCCAAAGTCTTCATCAATGAGGAGGTAAATGTTCTCTCACTGTCCAAG 362
QY 79 -GAAAGAAAACAGCAACCTGACAA-AA--AGAAG-----AAA-----AAGA 118
Db 363 TGAAG-----GACC-AACC-----CAAGAATTTAAGAAAGCGGACCAAGTGTGTTAAGA 413
QY 119 A-----CA-----AGA-AAAAAATCA--TGAAAAACA-TCCAGCCA- 151
Db 414 ACAGAGACAGTCTGGTCTTTGTCCAGACAGACAAATCAATCTACAACCAAGGACAGACAG 473
QY 152 -AAAAATGCACAATTC--TATCT-CTTGG--GCAATC-TTCAC-----G--GGGCTGG 194
Db 474 TGAAT-----TTGCTGTGTCTCCATGATGATAAACTTTCACCCCTGAAATGAGTTGA 527
QY 195 CTGCTCT-CTGT-C--TC-----TTCC-AAGGAGTCCCTGCGCA-----GGGAGATGC 240
Db 528 TTCCACTAGTATACATTCAGGATCCCAAGGAAATGCGAT-CGCAATATGGCAGAGTTTC 586
QY 241 CA-----CC-----TTCCC-----CAAAGC--T--ATGG- 260
Db 587 CAGTAGAGGGTGGCTCAAGCAATTTCTTTCCCTCTCATCAGAGCCCTTCAGGGC 646
QY 261 -----ACAAGTACAGTCTCGG-----CAGGGG-----AGAGCGCCACCT-----C 298
Db 647 TCCTACAGGTGTGTGTACAGAAATCAGGTGGAAGGACAGAG--CACCTTTCCACC 703
QY 299 -----AGG-----TG-----CACTA--TTG-----AC-----AACCGG-----TCACC 325
Db 704 GTGGAGAAATTTGTTCTTCCCAAGTTTGAAGTACAGTAAAGTGCACCAAGATAATCACCC 763
QY 326 --C--GG-----GTG-GCCTGG-CCTAAC-C-----GCAGCACCC 352
Db 764 ATCTTTGGAAGAAGAGATGAATGATCAGTGTG--TGGCTATACACATATGGAAGC-CT 820
QY 353 ATCTCT-----ATG--CTGGGA--AT-----GACAAG--TGGTG-----CCTGA-T- 388
Db 821 GTCC-CTGGACATGTGACTGTGAGCATTTGACAGA-AAGTATAGTACGCTTCC--GACTG 876
QY 389 CTGCGGTG--G--TC-----C-TTCT--GAG-----CA-----ACACCCAAAC----- 420
Db 877 CCAGG-GTGAAGATTACAGGCTTTCTGTGAAATTTAGTGGAGCAGCTTAAAGCCATG 935
QY 421 GCAG-----TA-CAGCA--T-----CGAG-----ATCCA--GAACGTGG-ATGTATG-- 458
Db 936 GCTGCTTCTATCAGCAAGTAAACCAAGGCTTTCAGCTGAA-GAGGAAGAGTATGAA 994
QY 459 -----AC-GAGGGCCCTTACA-CC-----TG-----CT 479
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Db 995 ATGAACCTTCACTGA-GGCC--AGATCCAAAGAAAGGAACAGTGGTGAATTGACT 1051
Qy 480 -----CGGTGAG--ACAGACACC--ACCCAA-----CA 506
Db 1052 GGAGGCACTCCAGTGAATCACA-AGAACCATAACCAAACTCTCANTTTGTGAAGTGA 1110
Qy 507 C-----CTCT--AGGG--TCCACCTCATTTGTGA-----AGTA-----535
Db 1111 CTCACACTTTCCAGACGGAATTCC-CTTCTTTGGCAGGTGGCGCTAGTAGTGGAAAG 1169
Qy 536 --TC--TCCAAATTTGTAG--AT--TTCTTCAGA-----TAT--C 568
Db 1170 GGTCCCTATACCAAA--TAAAGTCATATTATCATCAGAGGAATGAAGCAAACTATTAC 1225
Qy 569 TCC-AT--TA--ATGA--A-GG--GAACA-----ATATTAGCCTCACC-----601
Db 1226 TCCATGCTACACGATGAGCATGCCCTGTGTACGTTCTCTATCAACACCACCAAGT 1285
Qy 602 -TGCATAGC-----AACTGGTAG-----ACCAG-----AG--CCT--ACGGTTAC 636
Db 1286 ATGGGTACCTCTCTTACTGTAGGTCAATTACAAGGATCGTAGTCCCTGTTACGGCTAC 1345
Qy 637 --T--TG-----GAGACACATC-----TCTCCCAA 657
Db 1346 CAGTGGGTGTCAAGAAACACGAGAGGCACATCACACTGCTTATCTTTGTGTTCTCCCA 1405
Qy 658 AGC--GGTTGGCTTTG-----TGAG-----TGAAGACGA-----ATA 687
Db 1406 AGCAAG--AGCTTTGTCCACCTTGAGCCCATGTCTCAIGA--ACTACCCTGTGGCCATA 1460
Qy 688 CT-----T--GG-----AAATTCAG-----GGCA-----704
Db 1461 CTCAGACAGTCCAGGCACATTAATTCTGAATGGAGGCCCTGTGCGGCTGMAAGAC 1520
Qy 705 TCACC-----C-----GGGA-GCA--GTCAG-----GGGACTAC--GA 732
Db 1521 TCTCCTTTTATATCTGATAATGGCAAGGGAGGCAATTGTCCGAACCTGGGACT-CATGGA 1579
Qy 733 -----GT--GCAG-----TG-----CC-TC-CAAT-----748
Db 1580 CTGCTGTGAAGCAGGAGACATGAAGGCCATTTTTCCATCTCAATCCTCTGTAAGTCA 1639
Qy 749 GACGTGGC-----CGC-----GC-----CCGTGGTAC-----770
Db 1640 GACATGTCTCTGTGCTCGTGTCTCATCTATGCTGTGTTTACCTACCG-GGAGCGTGAT 1698
Qy 771 ---GGA-----GA-GT---AAA-----GGTCACC--GTGAAT--A--TC 797
Db 1699 TGGGATTCGCMAAATATGATGTGAATAATGTCTGGCCCAACAGGTGGATTTGAGCTT 1758
Qy 798 CA--CCAT-ACA--T-T-----TCAGAAGCCAA-----GGGT-ACAG-----827
Db 1759 CAGCCCATCAAAAGTCTCCAGCCTCACAGCCCACTCGGAGTCAAGCGGCTCCTCA 1818
Qy 828 GT--GT-----CC-CCGTG--GGACAAAG-GGGAACCTGC-----AGTGTGA--864
Db 1819 GTCCGTCTGCGCCCTCGTGTGTGACCAAGCGTG--CTGCTCATGAAGCCTGATGC 1875
Qy 865 --AGC-CTCAGCAGTCC-----CCT-C-AGCAGAA-----TTCC 893
Db 1876 TGAGCTCTCGGC-GTCCCTCGTTTACACCTGTCTACCAAAAGGACCTCACTGGCTTCC 1934
Qy 894 AGTGG-----T-ACAAG--GATGACAAAAGACTG-----AT--TG-----923
Db 1935 -CTGGSCCTTTGAATGACCGAGGAGATG--AAGACTGCATCAATCGTCAATATGTCTA 1989
Qy 924 ----AA-GGA-----AAG-----AAGGGGTGAAGTGAAGAA--AC 952
Db 1990 TATTAATGAATCACATATACTCAGTATCAAGTACAAA--TGAAAA--GGATATGTATC 2044
Qy 953 AGACCTTTCTCT-----CTCAAA--ACTCA-----TC-----TTCTT--C 982
Db 2045 AG--C-TTCTTAGAGGACATGGGCTTTAAGGCAATTCACCAACTCAAAAGATTCTGTAACCC 2101
Qy 983 AA-----TGTC-----TC-----TGAA-----CATG-----AC-----1000
Db 2102 AAAATGTGTCCACAGCTTCAACAGTATGAATGCAAGCTTGAAGGCTACGTGTAGGT 2161
Qy 1001 -----T-ATGGAA-----C-TACA--CT--TGCGTG-----GCCT 1025
Db 2162 TTTTATGAGTCAGATGTAATGGAGAGGCCATGACGCTGTGTCATGTTGAAGAGCT 2221
Qy 1026 CCAACAAGGTG--GGCCACACAA-----TGCC--AGCATCATG--CT--ATTGGTTC 1070
Db 2222 C--ACA--CGGAGACCGTACGAAAGTACTTCCCTCGAG-A-CATGGATCTGGGATTTGGT- 2274
Qy 1071 CAGGCGCCG-----TCAGC-----GAGGT--GAGCAACGG-----CA 1100
Db 2275 --GGTG--GTAACHTCAGAGGGGTGGCTGAGTAGGAGTAACAGTCCCTGACACCATCA 2330
Qy 1101 COTCGA--GGAGGGCAGG-----CTGC--GTCTG-----GCTG-----1129
Db 2331 C--CGAGTGAAGGAGGGGCCCTTCTGCTGTCTCTGAAGATGCTGGACTTGGTATCTCTTC 2388
Qy 1130 --CTGCTCT-TCTG-GTCTTGCA--CCTGCTT-----CTCA-AAT--TT-----T 1166
Db 2389 CACTGCTCTCTCCGAGCCTTCCAGCCCTTCTTTGTGGAGCTTACAATGCTTACTCTGT 2448
Qy 1167 GAT--GT--GAG-----T--GCCA-----CTTCCC-----CAC 1188
Db 2449 GATTCGTGAGAGGCTTCACTCACTCAAGGCCAGGCTCTAAACTACCTTCCCAATGAT 2508
Qy 1189 CCGGAAAG-----GCTG-----CGCC-ACC-----ACC-----ACCA 1216
Db 2509 CCGGTCTAGTGTGACGTGGAAGCCTCTCCGCCCTTCTTGTCTGCCAGTGGAGAGA 2568
Qy 1217 CCAA-----CACACA-----GCAA-----TGGCAACA-----CC-GACAGCAA--C 1250
Db 2569 ACAAGCGCTCACTCATCTGTGCAACGGGGCGGCAA--ACTGTGTCTGGGAGTAACCC 2627
Qy 1251 CAATCAGATATATA-CAAA--TGAATT-A--GA--AGAAACAC--AGCCTCA--1293
Db 2628 CAA--AGTCAT-TAGGAATGTGAATTTTCACTGTGAGCGCAGAGGACTAGAGTCTCAG 2684
Qy 1294 -----TGGGACAGA-----AATT--TGA-----GGGAG-----1314
Db 2685 AGCTGTGTGGGACTCAGGTGCTTCACTTCTGAAACGGAAGGAAGACAGATCATCA 2744
Qy 1315 -----GG-CAAC--AA-----AGAA-----TACTTT 1332
Db 2745 AGCCTCTGTGTTGAACCTGAAGGACTAGAGAGGAACAAACATTCACCTCCCTACTTT 2804
Qy 1333 G-----GG-GG-GA-----AAAGAGTT-T--TAAAA--AAGAAAT--T-G 1362
Db 2805 GTCCATCAGTGTGAGGTCTTGAAGATTAATCCTGAACTGCAACCAATGTGTAG 2864
Qy 1363 AA-AAT-TGCC-----TT-GCAGATAT-TTAGG-----T-----1387
Db 2865 AAGAATCTGCCGAGCTTCTGTCTCAGTTTGGGAGACATATTAGGCTCTGCCATGCAA 2924
Qy 1388 ----ACAA-----TGGAG-----TTT-----TCITT-1404
Db 2925 ACACACAAATTTCTCCAGATGCCCTATGCTGTGGAGGACGAATATGTCCTTTG 2984
Qy 1405 -TCCCAA-----ACGGG-----AA-G-AACACAGA-----CA-----C-1430
Db 2985 CTCCTTAACATCTATGTAATGATTAATTAATGAACACAGCAGCTTACTCAGAGATCA 3044
Qy -431 --CC--GGC--TTGG--ACC--CACTG-----CA-----AGCTGATCGTGCA--1464
Db 3045 AGTCCAAGGCCATTTGGCTATCTCAACACTGTTTACCAGACAGTTG-AAC-TACAAACA 3102
Qy -465 -----CCT-----CTTTGG-----TGCCAGTG-----TGGCAA--G 1489
Db 3103 CTATGATGGCTCTACAGCACTTTTGGGAGGCGATATGGCAG-GAACACAGGCAACCT 3161
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Qy	1490	GGCT--CAGCC-----TCT-----C-----TGCCCA	CAG--AGTGCC--C--C--CA--CG-T	1524
Db	3162	GGCTCAGAGCCTTTGTTCTGAAGACTTTTGCCCA-AGCTCGAGCCTACATCTTCATCGAT	3220	
Qy	1525	GGA---ACATT-CTGGAGC-----TGGCCATCCCA-----AA-----	1552	
Db	3221	GAAGCACACATTACCCAGAGCCCTCATATGGCTCTCCAGAGGCAGAAGGACATGGCTGT	3280	
Qy	1553	TTCA--A-----TCAGT-----CCAT--AGAGACGAACAGA--ATGA--G	1584	
Db	3281	TTCAGGAGCTCTGGGTCACTGCTCAACAATGCCATAAAGGAGGAGTAGAAGATGAAGTG	3340	
Qy	1585	A-CCT--TCCG-----GCC-----CA--AG-----CGT	1602	
Db	3341	ACCTCTCCGCTATATACCATCGCCCTCTTGGAGATTCTCTCAAGTCACTCACCT	3400	
Qy	1603	G-----GC--GC-----TGC--GG-G-CA--CTTTGGTAGAC-----	1626	
Db	3401	GTGTGCGCAATGCCCTGTTTTCCTTGAGTCAAGCT--GGAGACAGCACAGAAGGGG	3458	
Qy	1627	----TG--TGCC-----ACCA-----C-GCGGTGT-----TG-----A	1651	
Db	3459	ACCATGCAGCCATGTATATACCAAAAGCACTGCTGGCTATGCTTTTGGCCTGGCAGTA	3518	
Qy	1652	A-----AC-----GTGAATA--AA-----AA-GAGCAA-----AA-AAA--	1677	
Db	3519	ACCAGGACAGAGGAAG-GAAGTACTCAAGTCACTTAATGAGGAGAGCTGTGAGAGAAAGAC	3577	
Qy	1678	AA	1679	
Db	3578	AA	3579	

RESULT 25

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US-09-125-635-1
; Sequence 1, Application US/09125635
; Patent No. 6562589
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1

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1058	Db	ATCCTCATGAGCCTGGCTTTGGAAGATATAATCCGAAGGTGATTACAGAGATTTTTAG	1117
1113	Qy	---AAAAGA---AG--A---AGAAA---AA--A---AAT--	1332
1118	Db	TCTAATGATGGCAGTCATGGTCCCGAAGACGTCACTATCAAGAGCTTATCTTAATGG	1177
1133	Qy	---CATG-A-AAACC---ATC---ATC---CA	147
1178	Db	CCATGCAGAAACCCAGTATATCGATTCTCGTTGGCTGATGGAACATATAGTACTGCACA	1237
148	Qy	GCACAAATGCA---C-AATCT---ATC---TCT--	172
1238	Db	GACAAAAA-GCAAACCTTCCGAAATCCTGTAAACAATGATCGACATGGCTTTGTCTCAA	1296
173	Qy	-----TG---G-----C-AATC---TT---CAGC	187
1297	Db	CCCACCTCTTCAGAGAGAACAGAAATGGATATAGACCAAAACCCAAATCCTGTTGGACAAG	1356
188	Qy	-----GGCTGGCTGC---TC-----TG---TGCTCTC--T	209
1357	Db	GGATTAGACACCTATGGCTGGATGCAACAGTTCGGTAGGGCGGCATGATATGTCGCCAA	1416
210	Qy	TCCAAGG-----AG-TGCCCGTCGCGAGCGAG--ATGCC-----ACCTT--CCCCCA	251
1417	Db	ACCAAGGCTTACAGATGCC--GAGCAGCAGGCGCTATGGCTTTGGCAGACCTTAGCACCA	1473
252	Qy	AAGCTATGGACAAG-TGA-CGGTCC--GGCA-GGGGG--AG-----AGCGCCA---	293
1474	Db	CAG-----GG-CA--GATGAGTGGAGCTAGGATATGGGGGTTCCAGTAACATAGCTTCATTG	1526
294	Qy	--CCCT--CAGG--TG-----CACTAT-----T---G-ACAAC-C---GGG-TCA---	323
1527	Db	ACCCCTGGCGCAGCATGCAATCACCATCTTCCTACCAAGAACAACTATGGGCTCAAC	1586
324	Qy	-----CCC---GGGTGGCTGG-CT-----AAACC-GCAG-----CACCA---	353
1587	Db	ATGAGTAGCCCCCACCATGGGAGTCTCGTCTTGGCCCCAAACCAGCAGAAATCATGATT	1646
354	Qy	--TCCTC-T-ATGCTGGGA-----AT-G---ACA-AGT-----GGT	380
1647	Db	TCTCTCGTAATCGTGGAGTCCAAAGATAGCCTCAATCAGTTTCTCCTGTGGCAGGT	1706
381	Qy	GCCTGGATCCTCGGTGGTC--CTTCTGACCAAC--C---CCAAACGCAG---TACA	428
1707	Db	G--TGCACCTCCCATGG-CATCTCTG-GCAATACTGGGAACCA---CAGCTTTTCCA	1758
429	Qy	GCA-----TCGAG-----ATCCA--GAAGT-----GGA-----	450
1759	Db	GCAGCTCTCTC-ATGGCCCTGGAAGCCATCAGTGAAGGTGTGGGACTTCCCTTTTATCT	1817
451	Qy	--TGTGT-ATGACGAGGCC--TT--ACACCTGCTCGGTGCA---GACAGA-----C	493
1818	Db	ACTGTGTCATCACCGGCCCAAATTGGATAACT-CTC---CCAATATGA-ATATTACCC	1872
494	Qy	AACCA-----C-----CCAA-AGACTCTAGG-----GTCCA--	519
1873	Db	AACCAAGTAAAGTAAGCAATCAGATTCCAGAGTCTCTGGGCTTTTATGCGACCAAA	1932
520	Qy	--CC-----TCATTGTG---CAAGT-----ATCTCC-----CAAA-ATT	547
1933	Db	ATCAGTGGAGATTCAATGTGTCAGTCAATAGCAGATCACTCAGTGCAAGAA	1992
548	Qy	GTA--GAGA--TTTCTT-----CAGA-TATC-----TCCATT--AATG--AAG--	582
1993	Db	GTAGGAGACGAGTGTGTAGGGGGCAGAAATCAAAGGGGTCTCTTTGGAAGCAAAGTC	2052
583	Qy	-GAACATATTA-GC-----CTCACCTG-----CAT--	606
2053	Db	ATAA-AAAAATCTGCGAGTTACTTACTGTCTTCTGTATGACCGGGGTCAATCTCTCTG	2111
607	Qy	AGCAACT-----GGTAGA--CCAG-----AG--CCTACGGTTA-----CT--T	638

Db 2112 ACCAACTCCCCCTAGATTCAAGTTGTAAAGAACTCTCTGTAGTGTACCAGGCCCTCT 2171
QY GGAGAC-----ACATCT-----CTC-----CCAA-A-CC-----GT-----TG 665
Db 2172 GGAGTCTCCTCTTACATCTGGAGGATATCCTCTATCAATCAATATCATGGGTCACTG 2231
QY 666 GCTTTGTGAGTGAAG-AC--GAAT-----AC-----TTG-----GA-----AATTC----- 698
Db 2232 ---TTACAAGAGAAGCAGCGGATTTTGACAAAGTTTGCTGAGAAATGGAATTCACCACT 2288
QY 699 -AGG--GC--ATCAC-----CC--GGG-----AGCAGTCA----- 721
Db 2289 GAGGTAGCCAGATTAATCTGCAAGAGCCACTGGGAAAGACACCAGCAGT-ATAACTTCTTG 2347
QY 722 -GGGCA-----CTA--C-----GAG-----TGC 736
Db 2348 TGGGACGGAAATGTTGTCAGCAGGAGCAGTAAGTCTTAAGAAAGAGAGATAATATGC 2407
QY 737 ---AG-TGCCT-C---CA---ATGA--C-GTG--GC--CGC----- 759
Db 2408 ACTTCTTAGATACCTGCTGGACAGGATGATCCTAGTGTGATGCACTCTCTAAAGAACTACA 2467
QY 760 GCCC---GTGTACGGAG---AGTAA--G-GTCACGTTGAACCTA--TCCACCAT--- 803
Db 2468 GCCCCAAGTGG--AAGGAGTGGATATAAATAGTCTA--GTGCACCGCTCCACCAATTC 2524
QY 804 -----AC--ATTTCAGA--AGCCAAG----- 820
Db 2525 TAGCTCAAGTCAGAGAAGACCTTAAATTAAGACAGACAGACAGTGAAGAGGATCTGG 2584
QY 821 ---GG-----TACA-----GGTG----- 830
Db 2585 AGACTTGGATAATCTAGATGCTATTTCTTGGTGTGATCTGACTAGTCTGACTTTTACAATAA 2644
QY 831 -TCC-----CC-----GT-----GGGA-----CAAAAGG-----GGA----- 851
Db 2645 TTCCATATCTCAAAATGATAGTATGCTATCTGTTGCTGATCTGACTAGTCTGACTTTTACAATAA 2704
QY 852 -CACTG-----CAG--TGTGAAG-----CCTC-----AGC 873
Db 2705 TTCTCTGGGTTGAAAAGTTTCACTCTGTGCAGTCTATTCTGCTCTCCATATACCGAGC 2764
QY 874 AGT-----CCC-----CTC-AG-----CAG-----AATTCAGTG- 897
Db 2765 AGTGTCTCGATAGCCCTGTTTCTGTTGCTCAAGTCTCCAGTAAATAATATCAGTGC 2824
QY 898 -----G-TAC--AAGGA-----TGACAA--AAGACTGATTGA-----A 925
Db 2825 TTTCCCCATGTTTACCAAGCAACCCATGTTGGTGGGAATCCAGAATGATGATAGTCA 2884
QY 926 GGAAGA-----AAG--GGGTG---AAA--G--TG-GA-----AAACAGAC-C 957
Db 2885 GGAA-AATTATGGCTCAAGTATGGTGGCCAAACCGAAATGTGACTGTGACTCAGACTC 2943
QY 958 TTTCTCTC-----T-CAAACTCA--TCTTCTTC--AATGTCTCTGAAC-- 995
Db 2944 CTTCCTCAGGAGACTGGGGCTTACCAAACTCAAAGGC--CGGAGAATG-----GAACT 2996
QY 996 ATG-----ACT--ATGSGRA-----C-TAC-----ACT 1016
Db 2997 ATGAATTCAACTCCATGGGAAGACAGAGAGAGATATAATATCTTTTACCCAGACT 3056
QY 1017 GC-----GTGGC-C--TCCACA-----AGC-T-----GG-GCCACA 1043
Db 3057 GCACTGGGTGGTCTATTCCCATTTGCTCTCTCGTCTAATAGCATACCAGTGGGAGA 3116
QY 1044 CCA--A-TGC-----CAGATC--ATGCT-----ATTGTCCAGCG-----CCGTCA-G 1083
Db 3117 CCAGTATTGCAACAGCAGCAGCAGATGCTTCAAAATGAGG--CCTGTGTAATCCC--CATG 3173
QY 1084 CCA--GGTGAGC-AA--C---GGCAGCTCGAGGAGGCGAG-----GCTGGCT-- 1122
Db 3174 GGAATGG--GGGCTAATCTCCTATGGC-----CAAGCA--GCAGCATCTTAACCAACTGGGTC 3226

QY 1123 CTGGC---TGCTGCTCTT---C-TGG-----TCT-TG-----CA-----CCT 1152
Db 3227 CTGGCCCGATG--GCATGTTGTCCATGGACAAAGTTTCTCATGCACTCAAAATAGGCT 3284
QY 1153 GCTTCTCA--AATT---TTGATG---TG-AGTGCCA-CTTCCCAACCCGGGAAAGGC-- 1199
Db 3285 -CTTCTTAGGAATTCCTCGATGATCTTGTGGGCCACTT--CCAACCTGG-AAGGCCA 3340
QY 1200 ---TGCCG-----CCA-C-CACAC-----CACCAACACA-----A 1225
Db 3341 GAGTGACGAAGAGACATTTATGGACCAGTCA-CACTCTTCTCAGCAACACAGATGCCA 3399
QY 1226 CAG--C-----AAT-----GSC-----AAC-----ACC--GACA-G 1246
Db 3400 CAGCCTGGAAGAAATTCACAGAGCTTTGGGCATCTTCTGAATTTGTCAATCAGGACAGG 3459
QY 1247 CA---A--CAATCA-GAT-----ATATA-----CA--AATGA----- 1271
Db 3460 CATTAGAGCCCAACAGAGATGCTTTTCCAAGGCCAAGA-AGCAGCAGTAATGATGATCAG 3518
QY 1272 -----A-ATTA---GA-AGA-----AACAG-----CC-----T 1291
Db 3519 AAGCAGGATTATATGGACAGACATACCCAGCACAGGGGCCCTCCAATGCAAGAGGCTTT 3578
QY 1292 CAT-----GGGACA-----GAG-----GGA-----G----- 1302
Db 3579 CATCTTCAGGACAAATCACCATCTTTAACTCTATGATGAATCAGATGAACCCAGCAAGC 3638
QY 1303 AATTG-----AGG-----GAG-----GGG-----ACAA----- 1322
Db 3639 AATTTCTCTCCAAAGAAATGCACCAGAGCAACATCATGAGACCCCGGCAACACC 3698
QY 1323 -----AGAA--A-CTT-----TGGGGGAAAAGAGTTT--AA----- 1351
Db 3699 CCCAAGCACTTAGAATGACGCTTCAGCAGAGGCTGCGGGCCAGCAGTTTTTGAATCAG 3758
QY 1352 A---AAAG--A---AATTGAAAATTG---CCT--TGCAAT-----ATT 1382
Db 3759 AGCCGACAGGCACCTTGAATTTGAAATGGAACCCCTACTGCTGTTGCTGCGGTGA-T 3817
QY 1383 TAGG--TCAATG-----GAGTTTCTT----- 1403
Db 3818 GAGCCTATGATGAGCCCGCCAGCAGGGTTTCTTAATGCTCAAATGCTCGCCCAACGACG 3877
QY 1404 -----TTCCCA-AAC-----GGG----- 1415
Db 3878 CAGAGAGCTGTAAGTCACTCTCCGACAAAGAGGTGGCTATGATGATGACGACGA 3937
QY 1416 ----- 1415
Db 3938 GCAGCAGCAACACAGCAGCAGCAGCAGCAGCAACAGCAACAGCAACAGCA 3997
QY 1416 --A--AG-AACA-CAGCACACC----- 1432
Db 3998 ACAGCAGCAACAGCAGCAACCCAGGCTTCAGCCCACTCTTAATGTGACTGTCTCC 4057
QY 1433 -----GGCTT-----GGACCCAC--TG--CAAGCT-----GCATC-GT----- 1460
Db 4058 CAGCATGATGGCTTTTGGCAGGACCCCAATGCCAAGCTCTCTCCGCAACAGTTTCC 4117
QY 1461 ---GCAACC---TCTTTGG--TG-----CCAG--TGTTGGCAAGGGCTC- 1494
Db 4118 ATATCAACCAAT-TATGGAATGGCAACAAACACAGATCCAGCCTTTGGTCGATG-TCT 4175
QY 1495 AG-CCTCTC--TGC-----C-CACAGA-----GTGCC-CCCACGTGGAA---CATTC 1533
Db 4176 AGTCTCCCAATGAATGATGTCGTCA-AGAATGGTCCCTCCCA-----GAATCCCATGA 4230
QY 1534 TGGG-----GCTGGC--CATCCCAAAATTCATCAGTCCATAGAGACGAA----- 1575
Db 4231 TGCACACCCGAGGCTGCATCC---A-TCTATCAGTCTCAGAAATGAAGGGCTGGCCA 4286

Db 3766 GCAGGATGAGTGGACCCGACGAGGAGCAGGTG-CTCCGACGAA-----GGCCAAAG- 3817
Qy 760 G-----CC-C-----GTG-GRAC-CCA-----GAGT-A-----AAG-GTCAC 786
Db 3818 GAAGAAGAAGACCACAAATAGAGGTGCAGAACTGGAAATATGAGTCACTCAAGCGTCA- 3876
Qy 787 CDTGAACCT--ATC-----CACCATACATTTTCAGA--AGC-----CRAAG-- 821
Db 3877 --AGAACTAGATCAGAAACAAACAACTGAGAAATGAGCTAAATGAGTTGGCAAGGCC 3934
Qy 822 ----GT-----ACAGGTGTCCCGTGG-CA-----CAAAAGGGACCA-CTGC--A--GTGT 862
Db 3935 CTCAGTGAGAAAGTCCCGCAGAGGTGACCGCCCC-----AGGTG-CACCTGCCTACTGTGT 3990
Qy 863 ----GA--AG-----CCTC-----AGC--A-GTCC-----CCT 881
Db 3991 CCTCATGGAGCAGTCACTCTGTGAGCGAGGAGCTTGTGTCGCAAGGAGGAAGTCTCT 4050
Qy 882 CAGC--AG-----AATT-----CCAG-----TGG--T--A--CAAGGATGACAA-- 912
Db 4051 CATCTTAAGGTCTCAACTGTGTGAGCCAGAAAGAGGCCATCCAAACCAAGGATGACAGAA 4110
Qy 913 ---AA-GACTGATT-----GAAG-----GAAAG--AAAGGGGT 939
Db 4111 TACAATGACAGATTCACAAATCTTTTGAAGATGTACAAATAATGAAAGATAAA--GGT 4168
Qy 940 GAAAGTGGG-AAAACAGACCTT--TCCTCTCA--AAAC-----TCATCT--TC---T 980
Db 4169 GAAATAGCACAGCATACATTTGT--T-TGAAGAAACAAATAGATCATCTGCTCTGGAT 4225
Qy 981 T-CAATGTCTTGAACATGACTATGG-GAATACACTTGC--GT-----GSCCTCCAA 1029
Db 4226 TACCATGAT-TGA--ATGAGATGAGAGCT--GTGGCTGTTTATGAAGGGTTTAAA 4279
Qy 1030 CRAAG--TGGGCCACACC--AATGCCA--GCA-TCA-----TGCTATT--T 1066
Db 4280 CAAAGCAATAGG--CTCTGGAATCCAGCTGCAGTCAAGAGAGGAGCCATGAGAT 4336
Qy 1067 G-GTCC-AGGCGCGCTCAGCGAGGTGAG--CAAAG-GC--ACGTGAGAGGAG----- 1110
Db 4337 GAGGCGAGGC-CC-TC--CGTGGGAGATCCA--GAGCTGAG--GAGGAGAACAAAC 4388
Qy 1111 G---CGAG--GCTGGGTCTGG-----CT--GCTGCTCTTC--TGGTC-----TTG- 1147
Db 4389 GACAGCAGCAGCTG--CTGGCCAGAACCTGCAGCTGCCCC--CAGAGSCCGCATGA 4443
Qy 1148 ---CA-CTTGC-----TTCTC-----AAATTTGATGTAGTG---C 1177
Db 4444 GGCCAGCCTGACAGCAGATCACCCTGCTGACCAAGAAACTTGGATTTGA-TGGAAC 4502
Qy 1178 CACT-----TCC-----C-----CACCCTGGGAAAG--GCTGC 1202
Db 4503 AACTTGAATAACAGGATAGAGCGTCCGTAAACTGAAATAACAC--TGAAGTATTTCG 4560
Qy 1203 C-----GGCACCACA-----CCA-----CCAACA-----CA--ACAG--C 1229
Db 4561 CAAAAAAATTTGGCGA--ACTAGAGTGGGCCAGATGGAGAACATATCCCCAGCAGATC 4618
Qy 1230 A--ATGGCAA--CA-CCGA-CAG-CAA-----CCA-----AT-----CA--GA 1258
Db 4619 ATGTATG--AACCATCCAGCAGTCAATTTCCAGGAAAGAAAGGATTTCCAGGGA 4676
Qy 1259 T-----ATATACAA-----ATG-----AAA-----TT-AGAA--GA-----AAC-- 1284
Db 4677 TGTGGA-ATACAGAAGGAGGTGAGCAAAACTTTGTAAGAACTGATTTCTGNACTG 4735
Qy 1285 ACAGCTCATGG-G-A-CAG-AAATTTGA-----GGGA-----GG----- 1315
Db 4736 A-AGCCACGTGTGAGCAGTCAATTTGATTCAGGATTTACCGCATATATCTGTGTAT 4794
Qy 1316 -----G--GA--AC--AA-----AGAA--TA-----CTTTG----- 1333
Db 4795 GTGTGTCACATGCTGACTACTGTAATGATGATCAGAAAGTAAAGTCTGTGTAACATC 4854

Qy 1334 -----GGGGHAAAGAGT-TTTAA-AAAAGA--A--A--TTGAAA----- 1365
Db 4855 AACAAATTAACAGCATCAAAAAAGTATTGAAGAAAAGAGGTGATGATTTTGAACCGTCTC 4914
Qy 1366 ATT--GC--CT-----TGCAATATTT--A-----G-----GTCAAATGGAG-- 1396
Db 4915 CTTCTGGCTCTTAACACATGCCGATTTTTCACCTGCTTGAACACAGTACGTGGAGAGA 4974
Qy 1397 ----TTT-T-----CTTTTC-CCAAACGGGAA-GAACACAG--CAC----- 1428
Db 4975 GGGCTTTATGAAGCACACACATCTCGCCA-----GAATGAACACTGCTCCACCAATTT 5029
Qy 1429 ACCCGGCT-----TG---GAC-----CCA-----CTGCAAGCTGCAT 1457
Db 5030 GACCTGGCTGAGTATCGGCAGGTGCTGAGTGAATCTGGCCATTCAGATCTACACAGCAGC-T 5088
Qy 1458 CGTGC-----AACCTCTTTGGTGCCAGTG--TG-----GGCAAG--GG----- 1491
Db 5089 CGTGGGGGTGTAGAGACATCTTT-CAGCCATGATTTGCTCAGGCATGCTGGAACATG 5147
Qy 1492 ---C--TCA--GCTCTCT-----GCCCAACAGAT-----GC-----CC----- 1518
Db 5148 AAACGATTCAGGGCGTGTCTGGGGTCAAGCCCAAGGGTTGAGAAAGCGAACCTCCAGTA 5207
Qy 1519 ---CC-ACGTGG--A--ACATTTCTGGAGCTGCCATCC-----CA-----AA-----TTCA 1556
Db 5208 TCGCCGAGAGGGCACCTACACACTGGA-CT--CAATCTCCGGCAGCTCAACTCTCTCC 5264
Qy 1557 A-----TCA--GTC--CATAG-A-GAC--GAACAGA-----A 1580
Db 5265 ACTCGGTATGTTGATGATGCGATGCGACCTGAACTGATCAAGCAGGTGGTCAAGCAGA 5324
Qy 1581 TG-----AG-----ACCTTC-----CGGCCCAAG--CGTG- 1603
Db 5325 TGTTCATCATATAGGGGCCATCACCTGAAACAACTTCTCTCTGCGG--AAGGACATGT 5381
Qy 1604 GC-GCTGGG-----GGCA--C--TTTGGTAGACTGT--GCCACC-----ACGGC-G 1641
Db 5382 GTCCTTG--GAGTAAGGAGATGAGATCAGATCAGATCAATGTCAACTGGAAGATGGCTG 5440
Qy 1642 TGTG-----T-TG-TGAAACGTG-----AAATAAA-----AA----- 1666
Db 5441 CGTGACAAGATCTGATGATGATGAGTGGGGTAAAGAAACCTTGAACCTCTCATTCAGGCT 5500
Qy 1667 G----A-----GCRA-----AAAAA-AA 1679
Db 5501 GCTCAACTTTTGAAGTGAAGAAAGAA 5526

RESULT 27

US-09-620-312D-345

; Sequence 345, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yunqing

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Drmanac, Radolje T.

; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and

; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 784IP2B
 ; CURRENT APPLICATION NUMBER: US/09/620,312D
 ; CURRENT FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 1105
 ; SOFTWARE: pt_FL_genes Version 1.0
 ; SEQ ID NO 345
 ; LENGTH: 5364
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (328)..(4818)
 US-09-620-312D-345

Query Match 41.3%; Score 694.2; DB 4; Length 5364;
 Best Local Similarity 38.6%; Pred. No. 0.0003;
 Matches 1408; Conservative 0; Mismatches 177; Indels 2066; Gaps 404;

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QY      2  TTGTCTCTTCA---GC---AA---AA---CAGTGGAT--TTAAATCTCTTGCACA 44
DB      1271 TTCTG-CCTCCAAAGGCTGGGAATGGGAAGAGAGAGTAGTGA--TCCTGAAAGA 1326

QY      45  AGCTTG-----AGA-GCA---ACAC-----AA-TCTATCAGGAA 73
DB      1327 AGCTTGCTGACTGAGCGAGATCGAGTCACACGGAGTTCACGTGATGAAGTCTATCA-GAA 1385

QY      74  -AGA-----A-----A---GAA-----AGAAA-----A-----AA 90
DB      1386 CGAGAGCCGCTACCCCGGGGCGACTGGAAGCCGCGAGGACACTACAGGATGCGAA 1445

QY      91  C--CGA-----ACC-----TGA-----CA-----AA-----AAAGA 109
DB      1446 CGGGATTAAGCAGCATCACCAGCGAGTTGACTTGCTCCAGTTGGGAATGGGAAGA 1505

QY      110 AGA-----A-AAA--GA-----AGA--AGAAA-----AA-A---AAT 132
DB      1506 TGATGATGGTCTTATGATACATAAATCGAGCGGTGGATGAGAAAGCTGGGAATATGGAT 1565

QY      133  CA-----TGA-----AACC--ATC-----CAGCCA---AAAATG--CACA 161
DB      1566 CACATTCCTCTGATCATATAAGCCCAATCTGGGTTCGAG-CAGAGAAAATGTACCACA 1624

QY      162  ---AT-----TC-----TA-----TCT-CTT--- 173
DB      1625 CTCATAGACGGGAGGCTGCTCGAARACGCAAGAAGATTTACACAGACTGCTTCAA 1684

QY      174  ---GGG-----AATCTCAG-----GGGCTG-----GCTGCTCT- 201
DB      1685 GCACCGCAAGGGCCATGAGGGAAT-TGCAAGACCAAGAGGGCTGGGAATATGCTTCTTA 1743

QY      202  -GTGTCT---CTTC-----CAA-GGAGTGC-----CGGT-G-CGCA---GC--- 232
DB      1744 ATTGCTGGAATTTCACTGGAACACACGTAGTTCAGATACCTTCGCGCGCAGACGCTGG 1803

QY      233  -GGAG---ATGCCACCTTC-----CCCA-----AAGCT---ATGGAC---AAGCTGAC 270
DB      1804 AGGAGAAAATGGCTCTCTTCAGAAACACATGGTGCAGCTGCCAT--CTTTAACTTGAA 1860

QY      271  GGT--CC---GGCAG-----GGGG-----AGAGC----- 289
DB      1861 GGTGCCCTTGGGGCAGACACTACCAGAGATGGGGATGAGAAAGAGCCTGGAGAAAACAGAA 1920

QY      290  ---GCCACC-C---TC--AG-----G-----G-----TGCACTATTGACA-- 314
DB      1921 CACAGTGCACCACTGTGTTGGAGCAAAACCCCCCATTTGCTCGCAATTTTGACAGA 1980

QY      315  -----AC-----CG-G---GTC-----ACC-----C----- 326
  
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DB      1981 GACTACATCTACCATCTGCGCTGCTATGTCTATCAAGCCGAAACCTCTTGGCTTTAGAT 2040
QY      327  --GGGTGGC-----CTG-----GCTAAACCGC- 346
DB      2041 AAGGATAGCTTTTCAGATCCATTTGCTCATATCTGTTTCTCTCCATCGGAGCAAAACCACT 2100
QY      347  -AG--CA--CCAT-----CC----- 356
DB      2101 GAGATCATCCATTCAACCCCTGAATCCCACTGGGACCAACAATATATTCGATGAAGTT 2160
QY      357  ---TCTATG-----CT-----G-----GGAA--- 369
DB      2161 GAAATCTATGGGAAACCCCAACAGATTTCTACAGAAATCCACCCAAAGTTATCATGGAACTT 2220
QY      370  --TGAC-----AAGTGG-----TGCCT--GGA-----TC-CTCGCTG 397
DB      2221 TTTGACAATGACCAAGTGGGCAAGATGAATTTTGTAACTGSCAGAGCTGATTTCTCTCTGTG 2280
QY      398  GT---CCT---TCTGA---G-CA--ACACCCAAAC-----G-----CAGTACAGCAT 432
DB      2281 GTGAAATGTAACCTCAGAAATGGACATCACACCCCAAACTTCTCTGGCACCCAGTAATGAAT 2340
QY      433  CGAGATCCAGAA-----CGTGGATG--TGTA-----TGA--C-GAGGG----- 465
DB      2341 GGAGA--CA--AAGCCTCGGGGATGTTCTTTGTAACTGSCAGAGCTGATTTCTGAGGGGCAAG 2397
QY      466  -----C--CCTT-ACA-----CCTGCTC--GGTG--CAGA-C-AGACA--ACCAC 499
DB      2398 GATGGCTCCAACTTCCATTTCTCCCTTCAAGGGGCGCAATCTATACATGCTCC-C 2456
QY      500  CCA-----A--AGACTCTAGGTCACCT-----CATTG-----T--GC--A 531
DB      2457 CCAGGGGATCAGGCGCTGT--GGTCCAGCTCACTGCCATTGAGATTTCTAGCTTGGGGCTTA 2514
QY      532  AG-----TATC-----TCCC----- 541
DB      2515 AGAAATATGAAAACTTCCAGATGGCTTATCATATCATTCCCCCAGCTCTTGTGTGGAGTGT 2574
QY      542  -----AA-----AAT-----TG-----T--AG-AGA----- 554
DB      2575 GGAGGAGAAAGGTGGGATCGGTGGTATCAAAAACCTTAAGAGACACCAACTTTCCA 2634
QY      555  -----TT-TCTTCA-GATA---TCT--CCA-----T-TA-ATG----- 578
DB      2635 AGTTCTGTTCTCTCATGAAAGTGTCTTGCCCAAGAGGAAATGTACATGCCCCCACTG 2694
QY      579  -----AAGG-----GA--ACA--ATATT-----AGCC--TC--A--CC--TG--C 604
DB      2695 GTGATCAAGTTCATCGCACACAGGCACTTTGGGGGGAAGCCTGTCGTAGCCAGTGCACC 2754
QY      605  AT--AGCAACTGG-----TA-----GAC----- 620
DB      2755 ATCGAGCGCTGGATCGTTTCGTGTGACCCCTTATGCGGGAAGAGGACATCGTCCCA 2814
QY      621  CAG-----AGCCT-----AC-----G-----GTTACT--TGG- 640
DB      2815 CAGCTCAAGGCTCCCTTCTGTCTGCCCCACCATGCCGGACATCGTTA--TCGAAATGGA 2873
QY      641  AGACA-----CAT--CT--CTCCA-----AAGCGGT----- 663
DB      2874 AGACCAACCACTACTGCTTCTAAGTCTTAAGCAGATGTCAACAGCACTCAGCAA 2933
QY      664  --TGGCTT-----TG-----T-----GAGTGAAGACGAAT-----ACT- 689
DB      2934 AATGGCTTCTCCAGCGACAGTGCATCTGACAGAAAAGGAG-GAAGA--AATCGTGGACTG 2990
QY      690  -TGG--AAAT-----TCAGG--CATCA-----CCCGGAGCAG--TC 720
DB      2991 GTGGAGTAAATTTTATGCTTCTCAGGGGAACATGAAAAATGC---GGA-CAGTATATTC 3046
QY      721  AG---GG-----G-----G--ACTACGA---GT-GCAG---T 739
DB      3047 AGAAAGGCTATTCNAAGCTCAAGATATATTAATTTGTGACTTA-GAAATGTAGCAGAAATTT 3105
  
```

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QY 740 -----GCC-----TC-CA-ATGAGT-----G-G-CCG-----CG----- 760
Db 3106 GAGGGCTCAGACACTTCTCAGAT-ACGTTCAAGTTGTACCGAGGCAAGTCGATGAAAA 3164
QY 761 -----CC--C-GTGGTACGAGAG-TAAAGGTACCGT-----GAACTA----- 795
Db 3165 TGAAGATCCTTCTGTGGT-TGGAGAGTTTAAAGGGCTCCTTTCGGATCTACCTCTGCGG 3223
QY 796 -----T-CCA-----CCATACA-TTTC-----A-AG-AG-----CCA- 818
Db 3224 ATGACCCCGAGGTGCCAGCCCTCCAGACAGTTTCGGGAATTAACCTGACAGCGTCCAC 3283
QY 819 AGG-----GTAC-----AGG-----TGT-----CCCGTGGGACAA 844
Db 3284 AGGAATGCACGGTTAGATTACATTGTTGGAGGCTTAGAGTCCAGCCCC--AGGACAA 3341
QY 845 -AAGGG-----G-----ACACT--GC-----AGT--GTGAAG-CC- 868
Db 3342 CAATGGCCTGTGTGACCTTACATAAAAATAACACTGGGCAAAAAGTCATTGAAGACG 3401
QY 869 ---TCA--GCAGTCCC-----CTCA-----GCAGAT-TCC-----AG-TG 897
Db 3402 AGATCACTACATCCCAACACTCTCAACCCAGTCTTTGGCAGATGTACGAACCTGAGCTG 3461
QY 898 GTA-----CAAG--GATGAC-----AAAA-----GAC--TGAT--TGA-----A----- 925
Db 3462 CTACTTACCTCAAGAAAAGACCTGAATAATTTCTGTCTATGATTATGACACCTTTACCCG 3521
QY 926 GGA--AAGAAAG-GGGTGAAA-----G-----TGGAAAACAGA-CCTTTTC----- 962
Db 3522 GGATGAA-AAAGTAGGAGAAACAAATTATTGATCTGGAACACCGATTCTTTTCCCGCTTG 3580
QY 963 --TCTCAAACT--CAT-----C-----TTCT-----TCAATGCT--C-TG 992
Db 3581 GGTCCC--ACTGGCGCATACAGAGGAGTACTGTGTTTCTGGAGTCAATACCTGGCGAG 3637
QY 993 AACATGACTPANGGAACCTACAC--TTGC-----GTGGCC--TCCAAACAGCTGGGC 1039
Db 3638 ATCA--AC--TGACCAACACACAGCTGCTTCAAAATGTCGCCAGATTCAA-AGGCT-TCC 3691
QY 1040 CAC-ACCAATGCC-----ACATCATGCTATTGTCCTCAGG-CG--C 1077
Db 3692 CACAAACCAT-CTTTTCCGAAGATGGAGTAGAATCA--TATATGG--AGGACGAGAC 3744
QY 1078 CGT-CAGC--CAGG--TG-AG-CAAC-----G-----GCAGCTCAGG----- 1108
Db 3745 --TACAGCTTGATGAAATTTGAAGCCAAACAAATCTCTGCACCAACCTCGGGGCCCTG 3802
QY 1109 -AGGGCAGGC-TGCGTCT-----GG-CT-----GCTG--CCTCTTCTG-----G 1142
Db 3803 AAGAGC-GGCTTGC-TCTTCACTCTCAGGACTCAGGGCTGCTGCTC--CTGAGCAGC 3856
QY 1143 T-----CTT-----GCACCT--GC-----TTC-----TCAA 1162
Db 3857 TGGAAACAGGACTTTGCACAGACCTTCCAGCCCAACATTTCCAGGGAACATCTCAGA 3916
QY 1163 T-T--TTGATGT-----GAGT-----GCCAC-----TTC-----CCCA 1188
Db 3917 TGTGGGTGATGTTTCCCAAGAGTTTGGGGCCACAGGCCCTCTTTCAACATCAAC 3976
QY 1189 CCGGAAAG-----G-----CTGCC-GC-----CACACC--ACCAACCA-CA- 1224
Db 3977 CCGGAAAGCCAAAGATATACCTCTCGTGTGATCATCTGGAACACCAAGGACGTTATCT 4036
QY 1225 ---AC-AGCAATGGCAACCG-ACAGCAACCAATCA--GATATATA---CHAA---T-G 1270
Db 4037 TGGACGAG-AAAGCATCAAGAGAGGA--AATGAGTGACATCTACGTCAAAGCGCTGG 4092
QY 1271 A-----AATTAGAG-----AAAC-----ACAGCCTCATG---G-CACAGAAATTTG 1308
Db 4093 ATTCTGGCAAT--GAAGAAACAAACAGAAACAG-----ATGTCGTTACAGATCTTTG 4146
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QY 1309 -----AGGGA-----GGCGA-----ACAA-----A--GAA 1326
Db 4147 GATGTGAGGGAATTTTAACTGGCGATTTGTTTCCGTTTGACTACTCTCCAGCCGAA 4206
QY 1327 -TACTTTG-----GGGGAAAAGAG-TTT-----TA--A--AAAAGAAAT--GA 1363
Db 4207 CAACCTCTGATCGTTGCGAATAAAGAGCATTTCTGGAGTATTGACAAACGGAATTTTCG- 4265
QY 1364 AAT-----TG--CCTTGAGATATTAGGTACAATG--GAGTTTCT----- 1402
Db 4266 -AATCCCAACCCAGGCTGATCAAT-CAGATAT--GGGCAATGACAAGTTTTCTCTGGAT 4320
QY 1403 -----TTTCCCA-AAC-----GGG--AAAGAACA--CAGCA--CACCC 1432
Db 4321 GACTACTTTGGGTTTCTTAGAATCTGACTTGGCTCACAGATCAATCTTGCAAAATCACCA 4380
QY 1433 G-----GC--TTGGAC-----CC--A-CTGCAAGCTGCAT-----CGT---G-CA 1463
Db 4381 GAGAAATGCAGATTGGACATGATTCGGGACCTCAAAGC--CATGAACCCCTTAAAGCCA 4438
QY 1464 A-----CCTCTTTG-----GTGCCAGTGTG--GGCAAG--GGCTCAGCTCTC 1502
Db 4439 AGACAGCCTCCCTCTTTGAGCAGAAAT-CCA--TGAAGG-ATGGTGGC-CA----- 4485
QY 1503 TGC-CCACAGAG-----T-GCCCCCAGCT-----GGAACATTTCTGAGCTGGCCATC 1547
Db 4486 TGCTAGCGCAGAAAGATGCGGCCCGCTTAATGGCTGGGA-A--GTGAGAT-GACATT 4541
QY 1548 CCAAT--TCAATC-----AGTCC--ATAG-----A-----GACGAAC 1576
Db 4542 GGAATCTCTCAA-CGAGAAGGAGGCGCGACGAGGCCAGCGGGAAGGGCGGAGCAAC 4600
QY 1577 -----AG-----AAT-G--AGA-----CCTTCC--GG--- 1593
Db 4601 CCAACATGAACCCCAAGCTGGACTTACCAATTCGACAGAAACCTCTCTCTGTTCA 4660
QY 1594 -----CCCAAGC-----GTGGCGTGC-----GGG---CA--- 1615
Db 4661 CCAACCCATGAAGACCATGAGTTTCATCGTGGCGCGCTTTAAGTGGGTATCATCG 4720
QY 1616 -CTT--TG-----G--TAGACTG-TGC-CACACGG-GGT-----TG--- 1645
Db 4721 GCTTCTCTTCTGCTTATCTCTGCTCTTCTGTCGCGTCTCTCTACTCTTTTSCGA 4780
QY 1646 -----TTCGAAACCTGAA-AT-----AA--AAA-GAGCAAAAAA---AAA 1679
Db 4781 ACTATTCTCAA--TGAAGATTGTAAGCCAAATGTGTACAAAGGCAAA 4828
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RESULT 28

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US-09-220-132-24
; Sequence 24, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANC
; FILE OF INVENTION: 074001
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 7672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-24
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Query Match 41.3%; Score 694.2; DB 4; Length 7672;

QY 926 ---GGAA---AGA---AAGGGTGAAAGT---GGAAA---ACAGACCT--- 958
Db 4039 CTGGGGAACGTGCAGATCAGCGCAAGG---CAAAGTTGGGTGATCCCCAC-GACCTGCA 4094
QY 959 ---TTCCTCT---CAA---AACTCATCTTCT---TCAA--- 984
Db 4095 GCGCTTCTCT-TAGCGATTTCCGGGACCTCAT-GTCTTGGATCAATGGAATACGGGGTTG 4152
QY 985 -TGT-CTC---TGAAC---AT---GA-CT---AT---G--- 1004
Db 4153 GTGTCTCTCAGATGAGCTAGCCAAAGATGTCAACCGAGCTGAGGCATCTGTGAGCGCAC 4212
QY 1005 -GGAACCTAC---AC---T---TGC---G-TGGC-C---TCCA--- 1028
Db 4213 CAGGAAC-ACCGGACAGAAATCGATCCAGGCTGGCCTTTCCAGGCATTTGAGCAGTT 4271
QY 1029 ---ACA---AGCTG---GGC-CAC---AC-CAATGCCAGC---ATCA---TGC 1061
Db 4272 TGGACAGCAGCTGTGTGGCTCAGGACACTATGCCAGCCCTGAGATCAAGCAGAACTTGA 4331
QY 1062 TAT---TTG---GTCAGGC---GCC---G-TCAGCG-AGG-TGA--- 1091
Db 4332 TATTTCTTACCAGGAGCGTGACAGCTTGAGAAAGCCTGGGTTCAGCGCAGGATGATGCT 4391
QY 1092 ---GC---AACGGCA---CGTCGAGGA---GGGCGAGCTGG-TCTGGC 1127
Db 4392 GGATCAGTGCCTTGAATGACGCTGCTTCCATCG-GGACTGTGAGCAGCTGAGAACTGGA 4450
QY 1128 T-GCTGCTCTTCTGG---TCTTG---TCTTG---CAC---CTGC 1154
Db 4451 TGGCTGCC---CGGGAGGCTTCTTGAATACCGAAGACAAAGGAGAGCTCACTGGACACG 4506
QY 1155 -T---TCAA---AT---TTTG---ATGTGAGTGCCACTTCCCCACCC 1190
Db 4507 GTAGAGCTCTGATCAAAAACATGAGACTTTGACAAAGCGATT--AACGT--CCA--- 4559
QY 1191 GG--GA-AAG---GCT---GCC-ACCA-C-CA---CCG--- 1216
Db 4560 GGAAGAGAAGATTGCTGCTCTGAGGCTTTTCCGACCACTCATCGTCCGGCCATTA 4619
QY 1217 ---CCAACACA-ACA---GCATGGCA---ACA---C---CGACAG 1246
Db 4620 TGCCAAAGGAGACATTTCTAGCGCGGCAATG--AGGTCTTGGACAGGTGGCGAGCTGTG 4677
QY 1247 CAA-CCAATCAGAT-AT-ATACAAA--TGAAA--TTAGAAGA--- 1285
Db 4678 AAGGCC---CAGATGATTGAGA-AAGGTCAAAGCTAGAGAAATCTCAAACTCTCAACA 4733
QY 1286 ---CAGCC---TCA---TG---GGA-CAG---AAATTTG---AGGGAG 1314
Db 4734 GTTCAGCGGGATGTGGATGAGATTGAGGCTTGGATCAGTGAAATAATTGCAACAGCGAG 4793
QY 1315 GG--GA---ACRAAGA---AT-A-CTTT---G-G---GGGAA--- 1340
Db 4794 TGATGAGTCGTACAAAGGATCCCAACATCAGCTTTCCAGAGCTGCTGAGCAAGCAACA 4853
QY 1341 -AAG---AG---TTTTAAA---AAAG---AA--- 1360
Db 4854 GAAGCACCAGGCTTTTGAAGCAGAGCTGCATGCCAACGCTGACCGGATCCGTGGGGTTAT 4913
QY 1361 TGA-----AA-----ATT-----GCCT-TGC-----A-GAT-----A 1380
Db 4914 CGACATGGGCACTCCCTCATTTGAACGTGGAGCCTGTGCGGCGAGTGAGGATGCTGTCA 4973
QY 1381 -----T---TTAGT-A-CAATGG-AGTTTCTT-T-----TC----- 1406
Db 4974 GGGCCCGCTGGCTGCTTAGCTGACGAGTGGCAG--TTCTTTGGTCAAAAGTCAGCGGAA 5031
QY 1407 -----CC---AAACGG---GAAG---AACA---CAGC-----ACAC----- 1430
Db 5032 AAGACCCAGAACTGAAGAGGCCAACAGCAGCAGAACTTCAACACAGGGATCAGGAC 5091

QY 1431 -----CGGCT---TGGA---CCCACTGC-----AAG 1451
Db 5092 TTTGACTTCTGCTGTCTGAGGTGAGGCC---CTGCTGGCATCCGAGATTATGGCAAG 5149
QY 1452 ---CT-GCATC-GTG---CAACCT-CT-----T-TGG-----TG 1475
Db 5150 ACCTGGCTTCTGTGAACAACCTGTGAAAGAGCATCAACTGCTGGAAGCAGATATATCTG 5209
QY 1476 CCAGTGTG---GC---AAGG-GCT---CAGCC-TG---TCTGCC---CACAG-AGT 1514
Db 5210 CCCATGAGGATCGCTGAGGACCTGAAACAGCCAGGAGCAGCCTGTATGAC-CAGCAGT 5268
QY 1515 GCC-----CCACGT---GGA-----ACA-----TTC----- 1533
Db 5269 GCCTTGCACACCTCCCAAGTAAAGGACNAGAGGACACCATCAACGGCGCTTCAGAG 5328
QY 1534 -----TGG-----AGCTG---G---CCAT--CC--CA--AA 1552
Db 5329 ATCAAGAGCATGGCGGCTCCCGCGAGCCAAAGCTGAATGAATCCCATCGCTGCACCA 5388
QY 1553 TT-----CA--AT--C---AGTCC---AT--A-GAGACGAA----- 1575
Db 5389 TTCTTCGGGACATGGATGACGAGGAGTCTCTGGATCAAGGAGAGAAAGCTGCTGTGGGC 5448
QY 1576 -CAGA--A-T-----GAGACCT-----T-----CC-----G--GCCAAGCG- 1601
Db 5449 TCAGAGGACTACGGCGCGGACCTTAACCTGGCTGCAGAACCTGAGGAAGAGCAGCGG 5508
QY 1602 -TGG-----C-GTGGG-----GGCATT-----TGG---T---AG 1624
Db 5509 CTGGAAGCAGAACTGGCTGCGCATGAGCGGCTATTGAGGCTGCTGGACACTGGCAAG 5568
QY 1625 A--CTGTGC-----CACCA-----CGGC-----GTGT 1644
Db 5569 AAGCTGTCCGATGACACACCATCGGAAAGAGAGATCCAGCAGCGCTGCGCAGTTT 5628
QY 1645 GT-----TG-----TGAA-----A-CG----- 1655
Db 5629 GTGAGCAGCTGGAAGAGCTGAAGCAGCTGCGCAGCTGCCGGGCTCAGCGCTGGAAGAG 5688
QY 1656 ---TGAATA---AA-----AAGACGCAAAA----- 1675
Db 5689 TCCTTGAATATCAGCAGTTTGTAGCCAAATTTGAGGAGGAGGAGGAGCCTGGATCAATGAG 5748
QY 1676 AAAA 1679
Db 5749 AAAA 5752

RESULT 29

PCT-US96-01735-5
; Sequence 5, Application PC/TUS9601735
; GENERAL INFORMATION:
; APPLICANT: Marks, Andrew R.
; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01735
; FILING DATE:
; CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/386,039
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kole, Lisa B
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A30042 - 165/30555
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2628
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8791 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
;
PCT-US96-01735-5

Query Match 41.3%; Score 694.1; DB 5; Length 8791;
Best Local Similarity 39.9%; Pred. No. 0.00081;
Matches 1384; Conservative 0; Mismatches 194; Indels 1895; Gaps 384;

QY 2 TTGTGTC-----CTTCAGCAAAA--CAGTGG----- 26
Db 3477 TGTGTGTCAGGGCCCTGCAGCTCTCTTCGGCACCTTCAGCCAGGCA--GGAGTGCT 3534

QY 27 -----TTTAAA-----T-----CTCCCTG-----CA--CAAGCT--TGAGAGCAAC-----A 59
Db 3535 CCAGGCCCTTCAAAACAGGTTCAACTGCTGTGTTACGAGCCAAGATGTG-GA-CAACTACAAA 3592

QY 60 CA-ATCTATCA-----GGA-AA-----G-AAAAGA----- 84
Db 3593 CAGATCAACACAGACTTGGATCACTGAGGTCCATGTGAAAAGTCAGAGCTTTGGGTG 3652

QY 85 -AAAAA-----A-----CCGA-----AC-----CT-GACAAA--AA-AGAAG 111
Db 3653 TACAAAGGCGAGGCCCGATGAGACTGATGGTGTGCATCTGGAGAAATGAACATAAG 3712

QY 112 AAAA---AGAG---AAGAA-AA-----AAATCATGAAA--ACCATCCAGC--CAA--- 152
Db 3713 AAACCGAGGAGGGAATAACAGGCCACAAAAGCATGAAAGCACCA--GCAGCTACAACTA 3771

QY 153 -A-AATG--CACA---ATTCT-ATCTCTTGG---GCAA--TC---TTCACG---GGGC 191
Db 3772 CAGAGTGGTCAAGAGATTTTGAT-TC--GCCTTAGCAAACTCTGTGTTCAAGAGAGTGC 3828

QY 192 ----TG-----GTCG-C-TCTGTGCTCTTCC--AA-----GGAGTGC--C 222
Db 3829 CTCAGTCAGAAAGAGCAGGAAGCAGCAACAGCGCTCTGCTCGGAACATGCGCGCAGCG 3888

QY 223 CGTGGCCAGC--GGAGATGC--CACCTTCC-----CAAAGCT-----ATG--- 259
Db 3889 CGTG-G-TGCTGAGCTGTGTCAGATTCCTCTATGAGAAGGCCGAAGATACCAAGATGCAA 3946

QY 260 --GACACAGCTGACGGTCCGG--CAGG-----GGGAGA-----GGGC---CACCC--- 296
Db 3947 GAGATAA--TGA--GGT-TGGCTCATGNATTTTGCAGANTTCTGCGCAGCAACGACGA 4002

QY 297 ----TCAGG---TGC-ACTATGTAC-----AACCGG---GTC-ACCC--GGG-TGGCCT--- 335
Db 4003 GAATCAAGCTTTGCTAC-ATAAAACACATAAACCTGTTTCTCAACCCAGGGAT--CCTGGA 4059

QY 336 GGCCTA--AACC--GCAGGCAC-----CA--TCC-TCTATGC--TGGG--AATG 371
Db 4060 GGC-AGTAACCATGCGACGACATCTCATGAACAAATTTTCAGCTTTGCAGTGAGATCAACG 4118

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Db 5172 CAGACCCAGAGGAATGTAAGTGGCGGTTTCATTTGCAAGTTAAATAAGCATACAA 5231
QY 950 AACAGACCTTTCT-CTCA--AAACTCA--TCTTCTTCAATGT-CT-----989
Db 5232 AACAG-----CTGCT-AGAAGAAATGAAGAGAGCTCTGCAATTAAGTCTCTACAGAC 5283
QY 990 -CTGA--ACATGA-----CTATGG-GAACTACACTTGGCT--GSC-CT 1025
Db 5284 CTGAGGGAATGATGACCAAGATAGAGGCTATGGAGAA--A-A--GGGTGAGGCGCT 5337
QY 1026 CCAA--CAAG--CTGGGCCAC--AC-----CAATGCCAG--CATC-----1057
Db 5338 C--AGCAAGTCTTGCTCAACCTTACTATGAAACGTCAGACCTTCGGGACGAAGAGAG 5395
QY 1058 ATGC--TA-----TTTGTCCA--GGCCGC--GTACGC--GAGGTGACCAAGCGACGT 1103
Db 5396 A-GCCTTACCAGCTTTGG--CAATGGC-CCACTGTCAGCAGGAG--GACC--CGGCAAGC 5447
QY 1104 C-----GAGGAGGG-----CAG-----GC-----TGCGTCTGG 1126
Db 5448 CCGGGGAGGAGGGGAGGTTCCGGATCCAGCTCTATGAGCAGGGGTGAGATGAGTCTGG 5507
QY 1127 CTGCTGCTCTTCTGTCTGTG-CACT-----GCTTCTCAA--ATTT-----1165
Db 5508 CCGAGG-----TTTCAG-----TGTCACTTGACAAGGAGGGGCTTC-CAATCTAGTTATCG 5558
QY 1166 -----TG-----AT-----CT-----GAGTG--CCA-----C--T-TCC--CCA-----1187
Db 5559 ACCTCATGTAAGCGTATCCAGTGACCGAGTGTTCATGAAGAGCAATTCCTCGGCCATTG 5618
QY 1188 CCC-----GGGAAGGCTGC--CGCCACCA-CCACCAC-----C-----1218
Db 5619 CCTTCTGG--AAGGAGGCAACACCACCATCAGCACTCTTTTCTGTGCTTGACAGA 5676
QY 1219 -----AA--CA-----C-----AA-----CAGCA 1230
Db 5677 AGATAAGAGTCAGAGAAATTTCTTAAGGTGTTTATGACCGGATGAAGGTGGCCACGA 5736
QY 1231 ATG-----GCAACACCGACAG--CAACC-----AATCA-----1256
Db 5737 A-GAAATCAAGCAACAGTGACAGTGAAC-ACCACTGACTTGGGAATAAAAAGAAAGAC 5794
QY 1257 GAT-A--TATACA--A-----AT-----GAAATTAG--AAGA-----AACACAG--1288
Db 5795 GATGAGTAGACAGGATGCCCATCAGCTCCGAGGAGGCTCCGCTGCCACCAAGGAAAGCTTAAGAGCCCAACACACAGATA 5854
QY 1289 -----CC--TCA-----TGG-----GACA-----GAAA-----1304
Db 5855 ACAGAGAGGTCGGGATCAGCTCTCGGAGGCTCCGCTGCCACCAAGGAAAGCTTCACCC 5914
QY 1305 --TTT--GAGGAGG-----GGA-----1318
Db 5915 ACTTTGAGGAGGAGGCTGATCCCGACGACCACTACCGACTTGGAGAGGCGCACCGGCC 5974
QY 1319 -----ACAA-----AGA-----1325
Db 5975 ACTGCCGACCAAGGCCAAGCAGACCTGGAGATGAGCGGCTCATCACCATCATGACGCC 6034
QY 1326 ATACT-----TT-----G-----GGGGHAAA-----GAG-----TT-----1347
Db 6035 ATCTTCGCTTCTTTCAGCTCTGCTGTGTAAGAACCAACACCGAGACCTGCAGAACTTCCTC 6094
QY 1348 --TT--AAAA--AAGA--AATTGMAAAT--G-CCTTGCA-----GA 1378
Db 6095 CGTTGCCAAATAACAGACCAACT-ACATTTGATATGTGAGACCTCGCATTTCTCGA 6153
QY 1379 ---TATTT---AGGTACAA--TGGAG--TT-----TTCT-----TCCCAACGG 1414
Db 6154 CTGTATTTGTGAAGCACAACCTGGAGGCTTGTCTTCTGGGCTGTATAT--AAATGA 6210
QY 1415 GAAAGAACACGC-----AC-----ACCC-----GG--C 1435

Db 6211 AAAGAACGTAGCGCTTATCAACCAACCCCTGGAAGTCTGACCGAATACTGTCAAGGACC 6270
QY 1436 TTG-----GACCC--ACTGCA-AGC-----TGCAATC-----GTGCA--ACCTCTT--1470
Db 6271 TTGCCATGAGAACCAAGAACTGCAATGACCAACCCATGAATCCAATG-GCATTGACATCATCA 6329
QY 1471 -----TGGTGC-CAGTG-----TGGGCAAG-----GG-----1491
Db 6330 CAGCCCTGATCTCAATGATATCAATCCCTTTGGGAAAGAAGAGGATGGACCTTGTGTGTTAG 6389
QY 1492 --CT-----CA--GCCT-----CT-CTGCCCCA-----CAG-----AGTG 1515
Db 6390 AACTGAAGAACAATGCTCGAAGTTGCTCTCGCCATCATGGAAGACGACGACGAGTG 6449
QY 1516 -----C-----C-----CCC-----AC--GTGGA-----1527
Db 6450 AAAACGACAGAGGATACTTTTATACATGAGGCCCAAGAACTGGTGGAAATGATCAAGA 6509
QY 1528 -----ACATTC-----TGGAG-----C-----TGG-----1542
Db 6510 AAGCCTCATGCAAGGTGAAGTGGAAATTTGAGGATGGAGAAACCGTGAGGATGGCGG 6569
QY 1543 -----CCA-----T-----CCCAA-----ATT-----CAATCAG--TC--CATA 1567
Db 6570 CGTCCCCCAGGAACGTGGGGCACACATCTACATATTAGCCCATCAGTTGGCTCGGCATA 6629
QY 1568 GAGAC--GAA--CAGA--A--TGAGACCT--TCCGGCCCAAG--CG--TG--G 1604
Db 6630 ---ACAAAGAACTTCAGAGCATGCTGAAACCTGGT--GG--CCAGTGGACGAGATGAAG 6683
QY 1605 CGCTG-----CGG--GCA-----C--TT-----1618
Db 6684 CCTGGAGTTTATGCCAAGCACACGCGCAGATAGAGATTGTCAATTAGACCAACAA 6743
QY 1619 TGG-----TAGACT-----GTGCCACACCGCGT--GTG--TT-----GTGA 1651
Db 6744 TGAACAGATAGTCTTTCCCGTGC--CCA--GCATATGTGAATTCCTAACCAAGAGTCA 6799
QY 1652 AACGT--CAA-----ATA-----AA--AAG--AGCAAAA--AA 1676
Db 6800 AACTACGAATTTACTATACTACAGAGAGACGAAACCAAGGACGCAAAATCAA 6852

RESULT 30
US-09-566-921-45
; Sequence 45, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 9610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 996794.11
US-09-566-921-45

Query Match 41.3%; Score 694.1; DB 4; Length 9610;
Best Local Similarity 39.9%; Pred. No. 0.00096;
Matches 1384; Conservative 0; Mismatches 194; Indels 1895; Gaps 384;
QY 2 TTGTGTC-----CTTCAGCAAAA--CAGTGG-----26
Db 3422 TGGTGTAGGGGGCCCTGCGACTCTTCCGGCACTTCAGCCAGAGGCA--GGAGGTGCT 3479

QY 27 -----TTTAAA-----T-----CTCCTTG-----CA--CAAGCT-TGAGAGCAAC-----A 59
Db 3480 CCAGGCGCTTCAACAGAGTTCAACTGCTGCTGTGTACAGCCAGATGTG-GA-CAACTACAAA 3537
QY 60 CA-ATCTATCA-----GGA-AA-----G-AAAGAAAGA-----84
Db 3538 CAGATCAACAAGAGCTTGGATCAACTGAGGTCCATCGTGGAAAGTCAAGGCTTTGGGTG 3597
QY 85 -AAAAA--A-----CCGA-----AC-----CT-GACAAA-----AA-AGAA 111
Db 3598 TACAAAGGCGAGGCGCCGATGAGACTATGATGGTGCATCTGGAGAAATGAAACATAAG 3657
QY 112 AAAA--AGAA--AA-----AAATCATGAAA--ACATCCAGC--CAA---152
Db 3658 AAAACGAGGAGGGAATAAACAAGCCACAAAGCATGAAGCACCA--GCAGCTACACTA 3716
QY 153 -A-AATG--CACA--ATTCT-ATCTCTTGG-----GMAA--TC-----TTACG-----GGGC 191
Db 3717 CAGAGTGGTCAAGAGATTTTGTAT-TC--GGCTTAGCAAACTCTGTGTTCAAGAGAGTGC 3773
QY 192 -----TG-----GCTGC-TCTGTGCTCTTCC--AA-----GGAGTGC--C 222
Db 3774 CTCAGTGAAAGAGCAGGAGCAGACAGCTCTGCTCCGGAACATGGGCGCGCAGC 3833
QY 223 CGTGGCAGC--GGAGATGC--CACTTTCC-----CCAAAGCT-----ATG---259
Db 3834 CGTG-G-TGCTGAGCTGCTGCAGATTCCTATGAGAAGCGCGAAGATACCAAGATCAA 3891
QY 260 --GACACGTGACGCTCGG--CAGG-----GGGGA-----GGCG--CACCC---296
Db 3892 GAGATAA--TGA-GGT-TGGCTCATGAATTTTTCAGAAATTTCCAGACTTCAGTGGATCAACG 3947
QY 297 ---TCAGG---TGC-ACTATTGAC-----AACCAG--GTC-ACCC--GGG-TGSCCT---335
Db 3948 GAATCAAGCTTTGTAC--ATPAAACACATAAACCTGTTTCTCAACCCAGGAT--CCTGGA 4004
QY 336 GGCTA--AACC--GCAGAC-----CA--TCC-TCTATGC--TGGG---AATG 371
Db 4005 GGC-AGTAACCATCAGCAGACATCTTCAATGAACAAATTTCCAGCTTCAGTGGATCAACG 4063
QY 372 ACA-AGTGGT--GC-----CTG-----GATCCTCG-GT--G---GTCC-----401
Db 4064 AGAGAGTTGTACAGACTTCTGTTCACTGCAATAGAGACTCAGCTCGGTGGAATGTCCAGTATA 4123
QY 402 -----TTCT--GA-----GCA-----ACA 413
Db 4124 TAAAGTTCTTACAGACAATTTGCAAGGCGAGAGGGAATTTATTAATAAATGCCAAGACA 4183
QY 414 -----CC-----CA-----AAGC-CAG--424
Db 4184 TGGTTATGCGCGAGCTGGTCAATTCGGGAGAGGATGTCTCTGTTCTTACAAAGCAGAG 4243
QY 425 -----TACAG--C--ATCGAGAT--C--CAGAACTGGAT--G-TGTATGACGAG 463
Db 4244 CCTCTTTCCAGACTCTGATCCAGATGATGGGTGAGAACG--GGATCGATGGATGAGAAC 4302
QY 464 GGCCT-----TA-CAC-----CT-----GCTC-----G-GTGCA--GACAG--AC 493
Db 4303 AGCCCTCTCATGTACACATCCACTTGGTGGAGCTCTGGCTGTGTGCAAGGAGGTAAAG 4362
QY 494 AA---CCACCACCAAGCTCTAG-----GGTCC-----ACCTCAT--526
Db 4363 AATGTCTACAGAGA--TCAAGTGCAACTCCCTGCTCCCGCTGGATGACATCGTTCCGG 4420
QY 527 --GTG--CA--AGTA-T-C-TCCC-----AAATTTGATGAGAT--TT-CT--TC 561
Db 4421 TGGTGACCCAGGAGCTGATCCCTGAGGTTAAATGATGATTAATCTCCTGAATC 4480
QY 562 A--GATATCTCCAT-----T-----AATGAAGG-GA-----A-CAAT-----589
Db 4481 ACTGCTATGTGGATACAGAGGTGGAATGAAGGAGATTTATACAGCAATCAGATGTGA 4540

QY 590 -ATT-----AG-----CCT-----CACCTGCA-----TAGCA--ACTGGT--AG--618
Db 4541 AATTGTTGAGAAATTTCTTTGTAGACATCTGCAAGGCGCTGTAAACAACACTAGTGACAGGA 4600
QY 619 -AC---CAGAGCCTTACGTTTACTTTGGAGACACATCTCTCCCAAGCG-----G--TTG--665
Db 4601 AACATGCAGA--CT-CGATT--TTGGAGAGATGTGTACCGAATCGTCATGATGATTGT 4655
QY 666 -----GCT-----TTGT-----GAGT--GA-----AGAC-----682
Db 4656 TACTACTTTTCTCAGCTCTCCCTTCTCAGACAGAGTACGACTTTGACAGACTGCCAGCC 4715
QY 683 -----GAATACT--TGGAA--ATTCCAGG-----CA-T-CACCG-----G--713
Db 4716 TGTCTTTGTGCA--ACTGCTCAAGGCGTGTTCAGGTTTACCACCTGCACTGGTTAATGC 4774
QY 714 --AGC-----AG--TCAGGGA--C--TA--CGAGTGCAGTGCCT-----CCATGA 750
Db 4775 CAAGCCAAAAGGCTCGTGGAGAGCTGTATTCCGGTGC--TGTCTGATGTAGCCAA-GA 4831
QY 751 --CGTGGCC--GC--GCCGTGGTAC--GGAGGTAAAGGTACCGTGAA--CTATC 797
Db 4832 GCCG-GGCCAATGCCAATTCCTCGTGG-ACCTGGACAGCCAA-GTCAA--AACCTCTTTC 4885
QY 798 -CA-----CCATA-CATT-T-CAGA-----AGCCAAG--GGTACAGTGTG--CCCG--836
Db 4886 TCAAGTCCCACAGCATTTGCGAAGAACAGCCATGAACGTG--CGCTCTCAGCCCGCAA 4943
QY 837 TG--GACAAAAGGGGACACTG-----CAG-----TG--861
Db 4944 TGCCGACGCA--GGGACTCTGTTCTGGCAGCTTCCAGAGACTACCGGAATATCATTTGAG 5001
QY 862 ----TGAG--C-CTC-----AG-----CAGTCCCT--CA-GCAGAA 889
Db 5002 AGATTGAGGACATGCTCTCCGCTGGAGGACCGTCTCAGGCGCTTGGTGCAGGCGAG 5061
QY 890 TT--CCAGTG--GTACAAAGATG-----ACAAA--AGACTGATT-----922
Db 5062 TTATCTGTCTGT-----GGAATGTTCTCCACAGACCCGAG-CTGCTTTTCCAGAGAA 5116
QY 923 -----GAGGAAA--GAAAGGG-----TG-----AAAG--TGGAA 949
Db 5117 CAGACGCCAGAGAAATGTGAAGTGGCGGTTTCAATTTGCAAGTTAATAAGCATACAA 5176
QY 950 AACAGACCTTTCTCT-CTCA--AAACTCA-----TCTTCTTCAATGT-CT-----989
Db 5177 AACAG-----CTGCT-AGAGAAATGAAGAGAGCTCTGCATTAAGTCTCTACAGAC 5228
QY 990 -CTGA--ACATGA-----CTATGG-GAACTACACTTTCGT--GGC-CT 1025
Db 5229 CCTGAGGAAATGATGACCAAGATAGAGGTATGGAGAA--A-A--GGGTGAGGCGCT 5282
QY 1026 CCAA--CRAAG--CTGGGCCAC--AC-----CAATGCCAG--CATC-----1057
Db 5283 C--AGCAAGTCTGTGTCAACCGTTACTATGAAACGTCAGACCTTCGGGACGAAGAGAG 5340
QY 1058 ATGC--TA-----TTTGTGTTCCA--GGCGCC--GTCAGC--GAGGTGACCAACGGCACCT 1103
Db 5341 A-GCCTTACAGCTTTGG--CAATGGC--CACTGTGACAGGAG--GACC--CGGACAG 5392
QY 1104 C-----GAGGAGG-----CAG-----GC-----TGCGTCTGG 1126
Db 5393 CCGGGGAGGAGGAGGAGGTTCCGGATCCAGCTCTATGACGAGGGGTGAGATGAGTCTGG 5452
QY 1127 CTGCTGCCTCTTCTGTCTTTG-CACCT-----GCTTCTCAA--ATTT-----1165
Db 5453 CCGAGG-----TTGAG-----TGTCACCTTGCAAGGAGGCGGCTTC-CAATCTAGTTATGC 5503
QY 1166 -----TG-----AT-----GAGTG--CCA-----C--T-TCC--CCA---1187
Db 5504 ACCTCATCATGAACGATCCAGTGCAGGAGTGTTCATGAAAGCATTTCTCTGGCAATG 5563
QY 1188 CCC---GGGAAAGGCTGC--CGCCACCA-CCACCAC-----C-----1218

Db	5564	CCCTTCGG--AAGGAGCAACACCACTCAGCACTCCTTTTCGTGCTTGACAGA	5621
Qy	1219	---AA--CA-----C-----AA-----CAGCA	1230
Db	5622	AGATAAGAAGTCACAGAAAATCTTTAAGGTGTTTTATGACCGGATGAAGGTGGCCACGA	5681
Qy	1231	ATG-----GCAACACCGACAG---CAACC-----AATCA-----	1256
Db	5682	A-GAAATCAAGACCAAGTCAGCAGTGAAC-ACCAGTCAGCTTGGGAAATAAAAAGAAC	5739
Qy	1257	GAT-A--TATACA--A-----AT-----GAAATTAG--AAGA--AACACAG--	1288
Db	5740	GATGAGGTAGACAGGGATGCCCATCAGGAAAAAGCTAAGAGGCCCAACAACAGATA	5799
Qy	1289	-----CC--TCA-----TGG-----GACA-----GAAA-----	1304
Db	5800	ACGAAGAGGTCGGGGATCAGTCTCTGGAGGCCTCCGCTGCCACAGGAAAGCCTTCACC	5859
Qy	1305	---TTT---GAGGGAGG-----GGA-----	1318
Db	5860	ACTTTCAGGAGGAGGCTGATCCCGACGACCACTACCAGCCTGGAGGGGCACCAGGCC	5919
Qy	1319	-----ACAA-----AGA-----	1325
Db	5920	ACTGCCGACAGCGCAAGGACGACCTGGAGATGAGCGGTCATCACCATCATGCAGCCC	5979
Qy	1326	ATACT---TT-----G-----GGGGGAAA-----TT-----	1347
Db	5980	ATCTCCGCTTCCTTCAGTCTCTGTGTGTAAGAACCAACCGAGACCTGCAGAACTTCCTC	6039
Qy	1348	--TT-----AAAA--AAGA--AATTGAAAAAT-----G-CCTTGCA-----GA	1378
Db	6040	CGTTGCCAAATAACAAGACCAACT-ACAATTTGGTATGTGAGACCCCTGCAGTTCTGGA	6098
Qy	1379	---TAATTT---AGGTACAA--TGGAG--TT-----TTCT-----TTCCCAACGG	1414
Db	6099	CTGTATTGTGGAGACCAACTGGAGCCCTTGSTCTTCTGGGCTGTATAT---AAATGA	6155
Qy	1415	GAAGAACACAGC-----AC---AGCC-----GG--C	1435
Db	6156	AAAGAACTAGCGCTTATCAACCAACCTTGGAAAGTCTGACCGAATCTGTCAAGAAC	6215
Qy	1436	TTG-----GACCC---ACTGCA--AGC-----TGCATC---GTGCA---ACCTCTT--	1470
Db	6216	TTGCCATGAGAAACAGAACTGCTATAGCACCCCATGAATCCAATG-GCATGATCATCA	6274
Qy	1471	-----TGGTGC-CAGTG-----TGGSCAAG-----GG-----	1491
Db	6275	CAGCCCTGATCCTCAATGATATCAATCCTTTTGGAAAGAGAGATGACCTTGTGTAG	6334
Qy	1492	--CT-----CA--GCCT-----CT-CTGCCCA-----CAG-----AGTG	1515
Db	6335	AACTGAAGAACAAATGCCTCGAAGTTGCTCTCTGGCCATCATGGAAGCAGCAACAGTG	6394
Qy	1516	-----C-----C-----CCC-----AC--GTGGA-----	1527
Db	6395	AAAACGACGAGAGATCTTTATTAACATGAGGCCCAAGAACTGGTGGAAAGTGAATCAAGA	6454
Qy	1528	-----ACATTC-----TGAG-----C-----TGG-----	1542
Db	6455	AAGCCTACATGCAAGGTGAAGTGAATTTTGAGGATGAGAAACCGGTGAGGATGGGGCGG	6514
Qy	1543	-----CCA-----T-----CCCAA-----ATT--CAATCAG-----TC--CATTA	1567
Db	6515	CGTCCCCCAGGAACGTGGGGCACAACATCTACATATTAGCCCATCAGTTGCGTCGGCATA	6574
Qy	1568	GAGAC---GAA---CAGA--A---TGAGACCT--TCCGGCCCCAAG---CG-----TG--G	1604
Db	6575	---ACAAAGAACTTCAGAGCATGCTGAACCTGCT--GG--CCAAAGTGAAGGAGATGAAG	6628
Qy	1605	CGCTG-----CGG-GCA-----C-----TT-----	1618

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:19:20 ; Search time 4830.37 Seconds
(without alignments)
10379.861 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679

Sequence: 1 gttgttccttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 1.0 , Gapext 0.1

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319	78.6	1808	11	AK045973 Mus muscu
2	1319	78.6	1808	11	AK046377 Mus muscu
3	923.4	55.0	1083	12	BM09227 AGENCOURT
4	894.9	53.3	1033	12	BM07426 AGENCOURT

5	892.4	53.2	3166	11	AK042854	AK042854 Mus muscu
6	866.4	51.6	874	29	AY406347	AY406347 Homo sapi
7	844.2	50.3	1085	9	AL533026	AL533026 AL533026
8	834.8	49.7	1039	10	BE798585	BE798585 601581610
9	769	45.8	865	12	BI666583	BI666583 603291469
10	761.3	45.3	856	13	BU155617	BU155617 AGENCOURT
11	757.6	45.1	773	29	AY406348	AY406348 Pan trogl
12	739.5	44.0	2798	11	AK028345	AK028345 Mus muscu
13	724	43.1	874	29	AY406349	AY406349 Mus muscu
14	708.8	42.2	2768	11	AK030681	AK030681 Mus muscu
15	707.7	42.2	14278	11	AY318958	AY318958 Rattus no
16	707.7	42.2	14278	11	AY321317	AY321317 Rattus no
17	707.2	42.1	770	10	AW117456	AW117456 xd92a06.x
18	702.2	41.8	4667	11	BC049868	BC049868 Mus muscu
19	701.1	41.8	5570	11	BC044081	BC044081 Xenopus l
20	701	41.8	11415	29	AY418622	AY418622 Mus muscu
21	699.9	41.7	4754	29	AY408639	AY408639 Homo sapi
22	698.9	41.6	4035	11	AK044634	AK044634 Mus muscu
23	698.9	41.6	5118	11	AK036018	AK036018 Mus muscu
24	698.5	41.6	4728	11	AK087828	AK087828 Mus muscu
25	698.2	41.6	10481	11	AK090138	AK090138 Mus muscu
26	697	41.5	3971	11	AK054393	AK054393 Mus muscu
27	696.7	41.5	4540	11	AK087352	AK087352 Mus muscu
28	696.4	41.5	9022	29	AY402248	AY402248 Mus muscu
29	696.2	41.5	4379	11	AK086942	AK086942 Mus muscu
30	695.5	41.4	4529	11	AK014607	AK014607 Mus muscu
31	695.3	41.4	4059	11	AK083598	AK083598 Mus muscu
32	694.9	41.4	4000	11	AK031491	AK031491 Mus muscu
33	694.7	41.4	3955	11	AK054356	AK054356 Mus muscu
34	694.4	41.4	3808	11	AK087443	AK087443 Mus muscu
35	694.3	41.4	3970	11	AK049454	AK049454 Mus muscu
36	694	41.3	7626	29	AY406123	AY406123 Pan trogl
37	693.9	41.3	7886	11	BC034956	BC034956 Homo sapi
38	693.8	41.3	8315	11	AK090135	AK090135 Mus muscu
39	693.4	41.3	784	12	BI549918	BI549918 603194765
40	693.2	41.3	4626	11	AK052174	AK052174 Mus muscu
41	692.9	41.3	4463	11	AK083374	AK083374 Mus muscu
42	692.8	41.3	5002	11	AK029828	AK029828 Mus muscu
43	692.5	41.2	8329	11	AK090130	AK090130 Mus muscu
44	692.4	41.2	4827	11	AK043675	AK043675 Mus muscu
45	692.3	41.2	4168	11	BC060216	BC060216 Mus muscu
46	692.3	41.2	5855	29	AY418964	AY418964 Mus muscu
47	692.2	41.2	5072	11	AK082062	AK082062 Mus muscu
48	692	41.2	4213	11	AK085022	AK085022 Mus muscu
49	692	41.2	4384	11	BC036366	BC036366 Homo sapi
50	692	41.2	4729	11	BC035209	BC035209 Mus muscu
51	691.9	41.2	3885	29	AY403281	AY403281 Homo sapi
52	691.9	41.2	3912	11	BC049876	BC049876 Mus muscu
53	691.9	41.2	4257	11	AK029726	AK029726 Mus muscu
54	691.9	41.2	4441	11	AK081990	AK081990 Mus muscu
55	691.8	41.2	4126	11	AK015017	AK015017 Mus muscu
56	691.8	41.2	4346	11	AK046357	AK046357 Mus muscu
57	691.7	41.2	7211	29	AY419435	AY419435 Mus muscu
58	691.5	41.2	8528	11	AK090134	AK090134 Mus muscu
59	691.2	41.2	3744	11	AK030109	AK030109 Mus muscu
60	691	41.2	3595	11	AK032617	AK032617 Mus muscu
61	690.8	41.1	4187	11	AK029952	AK029952 Mus muscu
62	690.5	41.1	4253	11	AK034140	AK034140 Mus muscu
63	690.5	41.1	4484	11	AK082497	AK082497 Mus muscu
64	690.3	41.1	4831	11	BC018614	BC018614 Mus muscu
65	690.3	41.1	4857	11	AK049216	AK049216 Mus muscu
66	690.2	41.1	4751	11	AK038568	AK038568 Mus muscu
67	690.2	41.1	7060	11	BC043838	BC043838 Xenopus l
68	690.1	41.1	4294	11	AK083129	AK083129 Mus muscu
69	690.1	41.1	4329	11	AK054507	AK054507 Mus muscu
70	690	41.1	3379	11	AK088860	AK088860 Mus muscu
71	690	41.1	5400	29	AY407796	AY407796 Homo sapi
72	689.8	41.1	7529	29	AY406124	AY406124 Mus muscu
73	689.7	41.1	3441	11	BC023933	BC023933 Mus muscu
74	689.6	41.1	5550	11	BC054077	BC054077 Mus muscu
75	689.5	41.1	4694	11	BC027787	BC027787 Mus muscu
76	689.2	41.0	3685	11	AK034114	AK034114 Mus muscu
77	689.1	41.0	3839	11	AK054229	AK054229 Mus muscu

78	689.1	41.0	5758	11	AK038638	Mus muscu	
79	689	41.0	7596	11	AY383707	Rattus no	
80	688.9	41.0	6882	11	AK029252	Mus muscu	
81	688.7	41.0	3829	11	AK014481	Mus muscu	
82	688.6	41.0	4187	11	AK087617	Mus muscu	
c	83	688.5	41.0	4195	11	BC021044	Homo sapi
84	688.5	41.0	4561	11	AK054014	Mus muscu	
85	688.5	41.0	7008	29	AY414399	Homo sapi	
86	688.3	41.0	5400	29	AY407798	Mus muscu	
c	87	688.2	41.0	4051	11	AK086467	Mus muscu
88	688.1	41.0	3429	11	AK052117	Mus muscu	
89	688.1	41.0	3939	11	AY325194	Rattus no	
90	688.1	41.0	5487	29	AY404243	Mus muscu	
91	688	41.0	4489	11	AK028459	Mus muscu	
92	688	41.0	4805	11	AK040543	Mus muscu	
c	93	688	41.0	8259	11	BC038478	Mus muscu
94	687.9	41.0	3602	11	AK080960	Mus muscu	
c	95	687.9	41.0	4510	11	AK039975	Mus muscu
96	687.9	41.0	5433	29	AY406469	Mus muscu	
97	687.7	41.0	4193	11	AK033851	Mus muscu	
98	687.7	41.0	4193	11	BC033851	Mus muscu	
99	687.6	41.0	3590	11	AK036419	Mus muscu	
100	687.5	40.9	6333	29	AY414807	Homo sapi	

ALIGNMENTS

RESULT 1

AK045973

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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Db	119	AATCTATCAGAGGAAAGAAAGAGAGAGACAGAGGAAAGAAAAAACCATCTGACA	178
QY	103	AAAAAGAAAGAAAGAAAGAAAGAAATCATGAAAAACCATCAGACCAGAAATATGCAAA	162
Db	179	AAAAAGAAAGAAAGAG-----AAAAAAT-ATGAAAACCAATCCAGGCAAAAATGCAACA	232
QY	163	TTCTATCTCTTTGGGCAATCTTCAAGGGCTGGCTGCTCTGTCTCTTTCGAAGAGTGC	222
Db	233	TTCTATCTCGTGGGCAATCTTCAAGGGCTGGCGGCTCTGTGCTCTTTCGAAGAGTGC	292
QY	223	CGTGGCAGCGGAGATGCCACTTCCCAAGAGCTATGGACAACGTGACGCTCCGCGAGG	282
Db	293	GGTGGCTAGCGAGATGCCACTTTCACAAGCTATGGACAACGTGACGCTCAGCGCAGG	352
QY	283	GGAGAGCGCCACCTTCAGTGCACATATTGACAAACGGGTCAACCGGGTGGCTGGCTAAA	342
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QY	463	GGGCCCCATACAGCTGCTCGGTGCGAGACAGACAAACCAACCAAGAGCTCTAGGGTCCAGCT	522
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QY	1637	CG--GCGTGTGT-----TGTGAACGCTG-----AAATAAA--AAGAGCAAAAAA	1677
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Db	1768	AA 1769	
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DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230377K1.7 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK046377		
VERSION	AK046377.1	GI:26338018	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS			
TITLE	Carninci, P. and Hayashizaki, Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS			
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	20499374		
REFERENCE	11042159		
AUTHORS			
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nacakaoka, S., Sasaki, N., Carninci, P.		

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1808)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohmoto, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

FEATURES
SOURCE

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Db 1537 CTCCTTCCAGGTTGGGCAAGGCTCAGCCTCTCTGCGCCAC-ATAAGTGCCCCACCA--T 1594
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Db 1768 AA 1769

RESULT 3
LOCUS BM809227
DEFINITION AGENCOURT_6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
5', mRNA sequence.
ACCESSION BM809227
VERSION BM809227.1 GI:19126050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1083)
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AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: L10M1971 row: h column: 14
High quality sequence stop: 656.

FEATURES
source

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GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 55.0%; Score 923.4; DB 12; Length 1083;
Best Local Similarity 90.6%; Pred. No. 2.6e-11;
Matches 977; Conservative 0; Mismatches 33; Indels 68; Gaps 30;

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818	Qy	---AAGG---GTACAGGTGC--CCC-----GTGGG-----A-----CAAAAG	847
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848	Qy	GG-----G-----ACA--CTGAGTGTGAGCC-----TC	870
1216	Db	GGTTCTCATCTCTGCTTCTCATPATCACAGGCTG--GTGTTCAGCCCTTTTCAAAATC	1273
871	Qy	AGCA--GTCCCTCT---CAGCAGA---ATT---CCAG--TG-----GT-----	899
1274	Db	AGAATGCT--CCTGAGCAGCAGACACATTTAACAAGTAGATGAATTTCTAGTTACTGA	1331
900	Qy	ACAA-----GG--A-----TGAC--A--AAAG-----ACT	918
1332	Db	ACAACAGCTTTGGGCTACATTGTCTGTTTCTGACGGAGAAAGGCTCAAAATATTACT	1391
919	Qy	G-A-----TTG--AA--GG-AAA-----GAAAGGGGTGA-----	942
1392	Db	GCACCCCTGGGCTTTTCTTGGAAATAGGTTAAATGTGAGGAGTGGGGTGAAGATAC	1451
943	Qy	-----A-GT--GGAAC--AGACCTT-----TCCTCTC-----A--A--A--A--	970
1452	Db	ATTATATGTAGGTAAACTAAAGCCCTTAGGAGAAGCCCTCACCTGTGGAGGACTATTTA	1511
971	Qy	C-----TCATC-T--TCTTCAATGC-----TC-----TG-----	992
1512	Db	CTGTGTTGTCATGCTATGTAATGTCCTTTGAATCTTTTCAATACAGTGATAT	1571

QY	993	-----AACAT---GAC-----TATGGGAAGCT--ACACTTGC-GTGGCCTC---CAAC-1030
Db	1572	TTTTAAACAATTAGTCATGTGTTTATAGTAATAAATACTGCTTTGTTCTCTCGAAGAACT1631
QY	1031	AAGCTGGCCACACCACCAATGCCAGCA--TCATGCT--ATTT-----GG-----TCCAG1073
Db	1632	AAA-----CATACC-ATG-ANGTAANAATCTTGTTGGATTTTGTGGGTTCTTCCC--1680
QY	1074	GCG--C-CGTG-----AG-CGA-----GG-----T-GAGCA--AC1096
Db	1681	TGCTGCTCGTCTCCTCTTCTTTCTTAGTCTAATCCCTGGCTTTCTCATCCAGCATGAT1740
QY	1097	GGCACGTCG--AGG-AGGGC-----AGGCTGCTCTGGCTGCTGCTT--CTT-CTG--G1142
Db	1741	GGCAGGT-GTCCAGGCAAGCAATGAAG--TTCGTCTTGCACAGCCTGCTCTCTCGAAG1797
QY	1143	T---CTTG-----CACCTG-----CT-----1155
Db	1798	TACACTTTGAGTAGGATGAATAAACCTGAGGTGACTGGAGAGACAAAAAGATAGGGGA1857
QY	1156	TCT-----CAAAT-----TTGATGTGAGTGCCACT-TCCCCACCCG----GGAAG1197
Db	1858	T-TGAGAAGACAATTTGGAAGAGTGA-GCAGAGGCCACTGT--GAGCAGAGAAGAGAAA-1911
QY	1198	GC---TGCCGCCACACCACCACCAACA--CAAC-----AGCAAT--GSCACACCC1241
Db	1912	GCAGAATGCCATCATGA--ACCA--AACAGAGCTACGAGGAGTAG-AATGGGGCA-----1961
QY	1242	GACAGCAACA---ATCAGA-TAT-----AT-----ACAAATGA--A-A--TPAGA-1278
Db	1962	---AGCAGCCATGAGATGAGACTATGTAGAAATGAGGGGACACTTGCAGCATATGTTAGAG2018
QY	1279	-A---GAA---ACACAGC---C---TCA---TGG--GA-----C1299
Db	2019	GGAGGTGAAGGTA-GCAGCTGACTGCCAATGATCAGGCTGTGGTAGAGTATGGTCACTC2077
QY	1300	AG-----AAATTTG-----AGG-----GAGG-----1315
Db	2078	AGGGTTTATCACTTTTGTGCTGCTGTTTTTCTCTCCCCCAAGGAAAGTATGATGTTT2137
QY	1316	-----GGA---ACAA--GATACTTT-----GG-----GGGAAA--AGAG1345
Db	2138	CTTTTATGTAGTCTATAATGACTACTTTTTTTTTTGCAAACAGGTTAGTGCANAATAGAG2197
QY	1346	TTTTAAAAAGAAATTGAA-----A--ATTGCTTT-----GCAGATATTAGG1386
Db	2198	TTTTAAANTAG-AATTGCATAGCCAGTACTTGTAGTGTCTTATAAATAGCAGA--TTAGG2253
QY	1387	TA--CAATG-GA-----GTTT-----T-C-TTTTC-C---CAAAG-----1413
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QY	1414	-----GGAAGA---ACACA-----G-CACA--CCCG-----GCTTG-1438
Db	2314	TGTAGTAGAAGATAGACAAATAAAGTTAAGGTACAGTCTGTGGGTAGCTTGG2373
QY	1439	GACCCACTGC-----AAGCTGCATCTGTGCNACTCT-TT--G-GTGGC-----AG-1479
Db	2374	TGA---A-TGCTCCGGGAAGC--CATC-TGCCATCTCTATTAGGCAGTACCTCAAGT2426
QY	1480	--TG--TGGG-----CAAG--GGCT-----CAGCC1498
Db	2427	CCTTGTCTGGCAGATGCTCTGCANTGACCAAGAAATGGCTAGGAGATTGGAGCAAGCT2486
QY	1499	TCTCTGC-----CCAC-A-GA-GTG-----C-----C1517
Db	2487	TTGCTGCAGGAAGCAGCACCCTATGGAACGTGAACAGCAGCAAAATAGAAAACAGAGC2546
QY	1518	CCCAAGT-G-----GAACA--TTCTGGAG-C-TG-----G---CCATC--C-----1548
Db	2547	ACCTCTTAGAAAATAAAGAACACAGTTTTT--AGTCATCTTTTTTGTATACATCTCTTTGG2604

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCW779 row: d column: 04
 High quality sequence stop: 849.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3935955"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 49.7%; Score 834.8; DB 10; Length 1039;
 Best Local Similarity 69.6%; Pred. No. 4.3e-09;
 Matches 964; Conservative 0; Mismatches 37; Indels 385; Gaps 71;

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QY 227 CGCAGCGGAGATGCCACCTTCCCAAGATATGGACACGTACGGTCCGGCAGGGGAG 286
DB 53 -----C-AGAT-----CTT-----CAGG----- 64
QY 287 AGCGCACCTCAGGTGCACATTTGACACACCGGGTCACCGGGTGGCTGGCTAAACCGC 346
DB 65 -----CAGGTGCATATTGACACACCGGGTCGCCGGGTGGCTGGCTAAACCGC 113
QY 347 AGCACATCTCTATGCTGGGAATGACAAGTGGTGGCTGGATCTCGGTGTCCTCTCTG 406
DB 114 AGCACATCTCTATGCTGGGAATGACAAGTGGTGGCTGGATCTCGGTGTCCTCTCTG 173
QY 407 AGCAACACCCAAACGAGTACAGCATCGAGATCCAGAACGTGGATGTGTATCAGCAGGGC 466
DB 174 AGCAACACCCAAACGAGTACAGCATCGAGATCCAGAACGTGGATGTGTATCAGCAGGGC 233
QY 467 CTTTACACTGCTCGGTGCAGACAGACACACCCAAAGACCTCTAGGGTCCACCTCATTT 526
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QY 527 GTGCAAGTATCTCCAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 586
DB 294 GTGCAAGTATCTCCAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 353
QY 587 AATATTAGCTCACTCTGATAGCACTGGTAGACAGAGCTTACGTTACTTTGGAGACAC 646
DB 354 AATATTAGCTCACTCTGATAGCACTGGTAGACAGAGCTTACGTTACTTTGGAGACAC 413
QY 647 ATCTCTCCAAAGCGGTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATC 706
DB 414 ATCTCTCCAAAGCGGTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATC 473
QY 707 ACCCGGGAGCACTCAGGGGACTACGAGTGCAGTGCCTCCAAATGAGTGGCCCGCCCGTG 766
DB 474 ACCCGGGAGCACTCAGGGGACTACGAGTGCAGTGCCTCCAAATGAGTGGCCCGCCCGTG 533

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QY 767 GTACGAGAGTAAAGGTCAACCGTGAACCTATCCACATATATTCAGAGCCCAAGGGTACA 826
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DB 594 GGTGTCCCGTGGGACAAAAGGGGACACTGCGAGTGTGAAGCCTCAGCAGTCCCTCAGCA 653
QY 887 GAATTCACAGTGGTCAACAGGATGACAAAAGACTGATTGAAGGAA-AGAAAGGGGTGAA-AG 944
DB 654 GAATTCACAGTGGTCAACAGGATGACAAAAGACTGATTGAAGGAAACAGACAGGGGTGAACAG 713
QY 945 -TGGAAAACAGACC--TTTCTCT-CTCAAACTCAT--CTTC-TTCAATGT-CTCTGAA-C 995
DB 714 TTGGA AAAACAGACCTTTTCTCTCTCAAAAGTCATTTCTTCAATGTCTCTTGANCC 773
QY 996 AT-GACTAT-GGGAACTACACTTGGTGGCTTCCAAAGCTCCAAAGCTGGGCCACACCAATGCCAG 1053
DB 774 ATGACTATGGGAACTACACTTGGG-GGGTCTCCAAAGCTGGG-CACACCAATGCCAG 831
QY 1054 CATCATGTATTGTGTCAGGCGCGTCCAGCGAGT-GAGCAACGGCAGCTCGAGGAGG 1112
DB 832 -ATCATGCTATT-----GACGTAA---A--TAGAG-A--GCA-GTAGAAGAG-- 868
QY 1113 CAGGCTGGCTGGGCTGCTCTCTCTGTGCTTTCGACCTGCTTCTCAAAATTTGATGTG 1172
DB 869 -----T-TGGT-----ACCAG-----TG-G 881
QY 1173 AGTGCCACTTCCCAACCGGGAAGGCTGCCGCCACACCAACCAACACACAGCAAT 1232
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DB 900 AG-----GACAG--TCCAGTC-----T-----ACAGCC-C 921
QY 1293 ATGGGACAGAAATTTGAGGGAGGGGAAACAAAGATATTTTG--GGGG--GAAAAGATTT 1348
DB 922 -----CAG--TGTGAGCGAG-----CCAAAGAAGA-----GCAGGGGCGC--CGAG--- 958
QY 1349 TAAAAAGAAATGAAATTTGCCCTTGACAGATATTTAGGTACAAATGGAGTTTCTTTTCCC 1408
DB 959 -----TGA-----GCA-----AGCTA-----GA----- 971
QY 1409 AAACGGGAAGAACACAGCACACCGGCTTGGACCCACCTGCAAGCTGCATCTGCAACCTC 1468
DB 972 ---GGG-----CGGGTTG-----GTG---CCTC 988
QY 1469 TTTGTGTCAGTGTGGGCAA-----GGGC-TCAGCCTCTCTGCCACACAGAGTG--CCCCC 1520
DB 989 --TGTGTCGG-GT---CAATTGTTGGGCGT-----TCCCGG-----GAG-GCCCCCCC 1030
QY 1521 ACGTGG 1526
DB 1031 ACGTGG 1036

RESULT 9
BI666583
LOCUS
DEFINITION
603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
mRNA sequence.
ACCESSION
BI666583
VERSION
BI666583.1 GI:15580816
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 865)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

```

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11787 row: j column: 18
High quality sequence stop: 742.
Location/Qualifiers
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/tissue_type="hypothalamus"
/lab_host="DH108"
/clone_lib="NIH_MGC_96"
/note="Organ: Brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtc9ag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected to ROT 5. This is a
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 45.8%; Score 769; DB 12; Length 865;
Best Local Similarity 96.9%; Pred. No. 1.1e-07;
Matches 791; Conservative 0; Mismatches 11; Indels 14; Gaps 14;
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DB 50 GTTGTCTCTTCCAGCAAAACAGTGGATTAAATCTCTTCCACAAAGCTTGAGAGCAAC 109
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 110 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 169
QY 121 AAGAAAAAATCATGAACCAATCCAGCCAAATGCAAAATGCAAAATCTCTCTTGGGCAAT 180
DB 170 AAGAAAAAATCATGAACCAATCCAGCCAAATGCAAAATGCAAAATCTCTCTTGGGCAAT 229
QY 181 CTTTACGGGGCTGGCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGC 240
DB 230 CTTTACGGGGCTGGCTGCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGC 289
QY 241 CACCTTCCCAAGACTATGACAAAGTGAAGTGGTCCGGCAGGGGGAGAGCCCAACCTTCAG 300
DB 290 CACCTTCCCAAGACTATGACAAAGTGAAGTGGTCCGGCAGGGGGAGAGCCCAACCTTCAG 349
QY 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTTAAACCGGAGCAACCTCTCTA 360
DB 350 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTTAAACCGGAGCAACCTCTCTA 409
QY 361 TGCTGGGAATGACAAAGTGGTGGCTTGGATCTCGCGTGGTCTTCTGAGCAACCCCAAC 420
DB 410 TGCTGGGAATGACAAAGTGGTGGCTTGGATCTCGCGTGGTCTTCTGAGCAACCCCAAC 469
QY 421 GCAGTACAGATCAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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QY 481 GGTGCACACAGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
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QY 541 CAAAATTGTAGAGATTCTTCAGATATCTCCATTATTAAGAGGAAC-AAATATTAGCTCA 599
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QY 600 CTGTCATAGCAACTGTGTAGACAGAGCCCTACGTTACTTTGGAGACACATCTCTCCCAAAG 659
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QY 660 CGGTTGGCTTTGTGAGTGAAGACGAA-TACTTT-GGAATTCAGGG-CATCACCCGGGAG- 715
DB 710 CGGTTGGCTTTGTGAGTGAAGACGAACTACTTTGGGAACTTCAGGGCCATCTCCCGGAGC 769
QY 716 CAGTC-AGGGGACT-ACGAG-TG-CAGTGCCTCCAT-CACGTGGCCGCG-CCCTGGTA 769
DB 770 CAGTCAAGGGGACTAACGAGTTGCCAGTGCCTCCATGAGACGTTGGCGGCCCGGTGTA 829
QY 770 CGGAG-AGTA-AAGGTCACCGTGA-ACTATCCACCA 802
DB 830 CGGAGAGTACACAGTCCACGGGATATTTCCACCA 865

RESULT 10
BUI55617

LOCUS BUI55617 856 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
5', mRNA sequence.

ACCESSION BUI55617
VERSION BUI55617.1 GI:22669149
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 856)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE

AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs-remail.nih.gov
COMMENT Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13527 row: m column: 16
High quality sequence stop: 593.

FEATURES

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1. 856
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 45.3%; Score 761.3; DB 13; Length 856;
Best Local Similarity 89.9%; Pred. No. 1.7e-07;
Matches 805; Conservative 0; Mismatches 22; Indels 68; Gaps 25;
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DB 5 CTGTC-----GAGATG--GGGG-----TCTGTGGGTACCTGTTCTGCCCTG 45
QY 153 -AAATGCACAAATCTATCTTTGG-----GCAATCT-TCACGGGGGTGGCTGCTGTGTC 206

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Db 46 GAAGTGC-----CTGCTGGTCTG--TCTCTCA-----GGCTG--CTGT--TC 82
QY 207 TCTT-----CCA--AGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAGCTATGGA 261
Db 83 -CTTGTACCCACAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAGCTATGGA 141
QY 262 CAACTGTACCGTCCCGCAGCGAGAGCGCCACCTCAGTGCATATGACAAACCGGGT 321
Db 142 CAACTGTACCGTCCCGCAGCGAGAGCGCCACCTCAGTGCATATGACAAACCGGGT 201
QY 322 CACCCGGTGGCTGGCTAAACCGCAGACCACTCTCTATGCTGGCAATGACAAAGTGGT 381
Db 202 CACCCGGTGGCTGGCTAAACCGCAGACCACTCTCTATGCTGGCAATGACAAAGTGGT 261
QY 382 CTGTGATCTCCGCTGGCTCTCTGAGCAACACCCAAACGCAAGTACAGATCGATCA 441
Db 262 CCGTATCTCCGCTGGCTCTCTGAGCAACACCCAAACGCAAGTACAGATCGATCA 321
QY 442 GAACTGGATGTATGAGAGGGGCCCTTACACCTGCTCGGTGCGACAGACCAACCC 501
Db 322 GAACTGGATGTATGAGAGGGGCCCTTACACCTGCTCGGTGCGACAGACCAACCC 381
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Db 622 CTCGAATGACGTGGCGCGCGCTGTGTCAGGAGATGAAGTCAACCTATCCACC 681
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QY 860 TGTGAAGCTCAGCAGTCCCTCAGCAG-ATTTCCAGTGGTACAAGGATG-ACAAAAGAC 917
Db 742 TGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGGATGAACCAAGAC 801
QY 918 TGA-TTGA-GGAAAGAGGGGT-GAAGTGG--AAAACAGACCTTT-CTCTC 966
Db 802 TGAATTTGAAGGAAAAAGGGGTGAAAGGGGAAAAAGAAACGAACTTTCCCTCTC 856

RESULT 11
LOCUS AY406348
DEFINITION Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY406348
VERSION AY406348.1 GI:39762322
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 773)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
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TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
Gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 773)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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location/Qualifiers
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/organism="Pan troglodytes"
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gene
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Query Match 45.1%; Score 757.6; DB 29; Length 773;
Best Local Similarity 98.4%; Pred. No. 1.5e-07;
Matches 761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;
QY 301 GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCAGCATCTCTA 360
Db 1 GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCAGCATCTCTA 60
QY 361 TGCTGGGAATGACAAAGTGGTGGCTGGATCTCTGGGTGGTCTCTGAGCAACACCCAAAC 420
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QY 421 GCAGTACAGCATCGAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACCTGCTC 480
Db 121 GCAGTACAGCATCGAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACCTGCTC 180
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Db 181 GGTGAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 240
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QY 658 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATATCTTGAAGAAATTCAGGGCATCACCGGGA 714
Db 361 CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATATCTTGAAGAAATTCAGGGCATCACCGGGA 420
QY 715 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAAATGAGTGGCGCCCGCTGTCAGGAG 774
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Db 481 AGTAAAGGTTCACCGTGAACCTATCCACCATATATTTTCAGAAACCAAGGGTACAGGTGTCCC 540
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Qy 464 GGCCTTACACCTGCTGGTGCAGACAGACAAACCCAAAGACCTCTAGGGTCCACCTC 523
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Qy 582 GCACAAATATTAAGCC--TCACCTGCATAGCACTGTGAGACAGACCTTACGGTACTTGT 639
Db 513 GAAAGCAGTGTACCTGTGA--TGCTTGCATTTGGCAGACCAAGAACCGGTGACATG 570
Qy 640 GAGACACATCTC--TC-----CC----- 655
Db 571 GAGGCACCTGTGAGTCAAGGTAAGTATTTTACCATGCAAACTTTTAAGAGTGTACTTTA 630
Qy 656 AAAG--CGG--TTGGCTT--TG-T-----GAG-TGA-----AGACGAAT-AC-TTG--- 691
Db 631 AAAGCCGCTTGG-TTCTCATGCTAAAGGAGATCAGTATCCAGA-AAATAACATTTGTAT 688
Qy 692 --GAA--AT-----TCAGG-----GCAT----- 705
Db 689 GTGATGATCAATAGCCATCTCAGGACCAATCTGTTTATGTAATCTGTGCTGAAGTGC 748
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Qy 1107 -G-GAGGG----- 1118
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TITLE
JOURNAL
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Takeda, Y., Tanaka, T., Tomaru, A., Toyota, I., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="FANTOM DB:5430428119"
/db_xref="MGI:233151"
/db_xref="taxon:10090"

FEATURES
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polyA_signal
polyA_site
ORIGIN

Query Match 42.2%; Score 708.8; DB 11; Length 2768;
Best Local Similarity 45.0%; Pred. No. 0.00023;
Matches 1255; Conservative 256; Indels 1276; Gaps 265;

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DB 49 TTGACAGTCGGCTCTCTCATCTAATTAAGCA-T---TTTATAT---TTGCAC--TCTTCT 98
QY 50 ---GAGAGCAA---CACATCT---A-TC---AGGA---A--AG--- 75
DB 99 TCGGA-A--AATTGTTCTCCACTTCTCCCGACTCTCTGATTTGATGAGGCT 155
QY 76 -----AA-----AGAAAGAAAAAACCAGACTGACAAA-----AAAG---AAGAAA 115
DB 156 TTGTTAAATCCAGAGGAAAA---GA-----GACTAAGCGAGGAAAGAGCAAGCAA 206
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DB 207 AGTGAAGGAGAGTGGCGCTGGACCCCGCAGCAGCGCTTGGCAGTGGCTCGGAGCCCG 266
QY 138 -----AAA---CCATC-----CAGC---CAAA---AATGAC-----AATTCT 166
DB 267 CGCGTAGAGCCCTCTCCGTGGCCAGCAGCGCGCACACCGAGTCCACCGCGA---CC 323
QY 167 ATCTCTTG---GGCAA-----TC-----TTCA-----CGG-----G--GCT 192
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DB 441 -----TTTAACCGAGGC--ACGGACAAATCACCTGAGACAGGGGACACGGCCATCTC 494
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QY 347 AGCACCATCTCTATGCTGGGAATGACAAGTGGTGGTCTGGATCTCGGTGGTCTTCTG 406
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QY 407 AGC-----AA--CACCCAAACGC-----AGTACAGCAT--CGAGATCCAGAGACGTGGATGTG 454
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Qy 843 AAAGGG--GACA--CTGC-----AGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTC 893
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Qy 995 CATGACTATGGAACTACACTTGGTGGCTCCAAAGCTGGGCCACACCAATGCGCAGC 1054
Db 1191 C---ACTATGGCAACTATACCTGTGTGGCTGCCAACAAAGCTCGGTGTCACTATGCCAGC 1247
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Db 1248 CTAGTCT-TTT---CAGAC-CGGGTC-----GGTGAGAGNATCAACGG-ATCCGT- 1294
Qy 1105 GAGGAGGCGAGGTG--CGT---C--TGCTGCT---GCTCTTCTGCTTGTGACCT 1152
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Qy 1153 GCTTCT---CAAAATTTGAT-G-----TGAGTGC-----CAC----- 1180
Db 1341 -CTTCTCAGCAATGTTTAAATAGAAATAAAATTTAAATAATTAACAAAAACACAAAAA 1399
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Qy 1408 -----CAA-----ACG-GGAAGAAC-----C-AGC--- 1426
Db 2055 GTGCGGTGCGTGTCTCAAGTCTCTCGCTCTCACGTAGATGTACATGTGTCGAGCGTG 2114
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Qy 1450 AGCTGCA-----TCGTGCAACCTCT--TT--GGTGC-----C-AGT---GT 1482
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AY318958
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VERSION
AY318958.1 GI:32492561
KEYWORDS
HTC.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM

AY318958 14278 bp mRNA linear HTC 15-JUL-2003
Rattus norvegicus Aal064 mRNA, complete cds.

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Db 2229 AGGATGACAAACATGAACAGGACATGGTGAATGGAATCATGCCCATTTGGACAAAGTTGA 2288
QY 692 ---GAGC-----AGTCAGS---GGA-CTAGAGTGC-----AGTGCCTCC---AATG 749
Db 2349 AAGAGCTTGGCTTTTTCAGGCTCCAGACCTCCAGTCTCTGGAAAGTTACTGTCTGAATG 2408
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Db 2409 ---GTG---CGCAAACTTTTCGGGAGTGCCTCAGATGATTTGACAGCCATCAGAG---AAG 2462
QY 782 G-TCACCG---TGAAC-----TATCCACCATACAT-TTC-----AGAA-GCC----- 817
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QY 922 TGAAG-----GAA-----GAA-AGG---GGTGA----- 942
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QY 1013 ACTTG---C-GTGGC---CTCCAA---CAAGCTGGGCCACA----- 1043
Db 2930 ---TGTAACACAGGGGCTTACTCCAAATGCCAGCT---CCACAGAGTCTGCTTACTTAC 2983
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QY 1140 ---T-----GG-----TCT---TG---C---ACC-----TG-----CTT 1156
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Qy 1209 -----TAGAAG---A-----AACA-----C-AGCCT---CATGG-----GA---CA 1300
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Qy 1226 CAGCAAT--GG--CAACACCGACAG-----CAACCAATCAGATATATACAAAGAA--A 1273
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AV321317
LOCUS 14278 bp mRNA linear HTC 16-JUL-2003
DEFINITION Rattus norvegicus Acl-060 mRNA, complete cds.
ACCESSION AY321317
VERSION AY321317.1 GI:32527694
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2478)
Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F.,
Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M.,
Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Liver regeneration after PH
2 (bases 1 to 14278)
Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F.,
Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M.,
Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Direct Submission
Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China

Location/Qualifiers

1. 14278
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41. 14272
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ORIGIN

Query Match	42.2%	Score	707.7;	DB	11;	Length	14278;
Best Local Similarity	38.5%	Pred. No.	0.079;				
Matches	1430;	Conservative	0;	Mismatches	175;	Indels	2113;
				Gaps	406;		
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QY	73	-----AAG	-----A	-----AAAAACCGAA	-----CCTG	-----	99
Db	751	GCCCAAGAGGAGCATGTGTGAAGCCATCTGTGAATGAACACGATCTTTTCTCGCCTTT	810				
QY	100	-----ACAA	-----AA	-----AAAGAA	-----AAAGAA	-----GAAGA	124
Db	811	CTCCTACAAGAA	TAAGTATGGAATCATGACCCATGTTACACAGAACTAGTCTTGAAGA	870			
QY	125	-----AA	-----AAAA	-----ATCA	-----	-----T	135
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QY	264	-----ACGTGACGG	-----TCC	-----G	-----GCAG	-----GG	-----
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QY 1079 G---TCAGCCAG-G-----TGAGC-----AA-CGG-CACGTC-----1104
Db 3043 GTATTCGCCAGTCAACCTATGAGTCTCTAAAGAGAGCAAGTCTTTTGGTTGACACT 3102

QY 1105 GAGG-----AGGC-----AGG-----CTGC-GTCTG--GTGCTGC-CTCTTC-----1139
Db 3103 GAAGTTCTCTAGTGCAGCAAGAGGAGTCCAGCAGTCTGAAGCTACTTGAATGTTCAATA 3162
QY 1140 ---T-----GG-----TCT-TG-----C-ACC-----TG-----CTT 1156
Db 3163 TAATCGGCAAGCAGGACCTTATCTAGTGAAGTCTTAATACCAGGGTTTGATGTCAACTT 3222
QY 1157 -----CTCAAAATTT--TGATG-----TGAGTGC-----CACATT-C-----CCCA- 1187
Db 3223 TGGAAACAATCTCTCAGATTAAATGATGAATCTTCTTAAGGACAAACACATTCAAACTCAT 3282
QY 1188 CCGG-----GAA-----AGG-CTGCC-----GCCAC-----1208
Db 3283 CCTGACATTCAGAACAAAGAAATCACTGAGGTTCTGTGCTGGGCCAGCTGAGTTATGA 3342
QY 1209 -----CA-----CC-ACCAC-----CAA-GACAA--1225
Db 3343 CAAAAGGAGATGGCAAGGTCAAAGGTGTTGTTTCCATACCACTTTTGCAGCAGAAAGC 3402
QY 3226 CAGCAAT--GG--CAACACCCGACAG-----CAACCAATCAGATATATACAAATGAA--A 1273
Db 3403 CAGGAGTGAAGTTC-ATACCCCACTGCTCCGCCCAACCAACTGCTCT-TCCAAATGACATCA 3460
QY 1274 T-----TAGAAG--A-----AACA-----C-AGCCT--CATGG-----GA--CA 1300
Db 3461 TCTGCTA-CAGCTTACGGCTCAACAAATTTCCAGAGAGTTGATGCGGTTATGATAATGA 3519
QY 1301 GA-----AATTGTA-----GGG-----A-GGGA-AC--AAG-----AA 1326
Db 3520 GAAATCGAATTTGATTTGGAACACGGGACCAATGTGATACCAAAAGGTGGGCTCCAA 3579
QY 1327 TACTT--TGGGGGAAAAGA-----GTT-T--TAAAA-----AAGA-----AA 1359
Db 3580 T--TTCCCTGTG-----GATCTTCCCGTTATCTTAGATGTTGATGATGATGCCA 3630
QY 1360 T-----TG-----A-AAATTTGCT-TG-CAGATA-----TTTAGGTACA-ATGG-----1394
Db 3631 TGGTCTCTGATCACAGAGTCCCTCAGACAGATATGACTTTCCG-ACACATGGGTTCCA 3689
QY 1395 -----A-GTT-----T-TCT-----TT-----TCCCAA--CGGA-----1416
Db 3690 AACTAATTTGATCCTCATGCGCTCTCAGAGTTGAACCTCCCAAAAGTGGGATGTC 3749
QY 1417 -AGA-----A-CACAGCAC-ACC-----CGGCT-----TGG-----ACC 1442
Db 3750 CAGACTTCCATATCCCAG-ACAACCTCTTC--CTAATACTGATGGCGGATCAATACA 3806
QY 1443 CACT--GCAAG--C-----TG-CAT-----C-----GT-GCAACCTCTT--1470
Db 3807 CACTAACAAGAACAGAAATAGAGATTGACATTTCTTTGCGCTTTTGGGTGGCAA-GTCTTCA 3865
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Db 3866 AAGACCTCAAGGTGCCAGAAAGTGTGAGACACCCAGCCCTCAACTTCAAGTCTGTGGG 3925
QY 1501 -----TCTGCC-----CA-----CAGAGTGC-----CCCAAG-----1523
Db 3926 TTCCATCTGCGCTCAAGAGGTCCAGATTCCCACTTTTACATTTCCCAAGACACATCAG 3985
QY 1524 -TGGAA-----CATCTGGAGCTGGCA-----TC--C-CAAAAT--C 1555
Db 3986 CTGCAAGTGCCTCTTTGGGCACTTCTGGACCTTTTCCACAAATGTCTACAGCACTTTGTAC 4045
QY 1556 AA-----TCAGTC-----CA--TAGAGACGAACA-----GA--A--TGAGACTTCCGG 1593
Db 4046 AACTGTGCTAGTCTCTACACTGTGTGGC-AACACAGCAGAGGATCATCTTCAAG-CTTCAAG 4103
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Db 4104 CTCA---GTACCGCATGAAGGCTGACTCTGTGTGTGACCTGTGTTTCTCTACAGTGTGCAAG 4160

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 4667)
 Strausberg, R.
 Direct Submission
 Submitted (31-MAR-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Srantripop, S., Thomas, P.J., Touchman, J.W.,
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 Young, A., Zhang, L.-H. and Green, E.D.
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 Series: IRAK Plate: 99 Row: h Column: 5
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 This clone has the following problem: frame shifted.
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ORIGIN

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QY 21 -----AG--TGGAT-----TTAAATCTC-----CTTG-C-ACAA--GC 47
 Db 898 GTCTGCCGTGAGACTGAGCTGGATGCGAGAGAGTCAATTCCTCAGCTAGACAAATGGC 957

QY 48 TTGAGAGCA--ACACAA--T-----CTATCA--G-G-----AAAGAAA--CAA----- 81
 Db 958 T-----GCAGTACACAGAGAGTGAAC-ATCACTGAGTCCCATCAAGAAAGGAATAT 1011

QY 82 -AG-----A-----A--AA-----ACCGAA----- 95
 Db 1012 GAGGTTCAGCTTTTCCATGTGAATGCAACTGTTACAGAGAGGGACAGGATGGAGTTC 1071

QY 96 ---C---CTG--ACAA--AAAA--G--NAGAA-----AAAGAA-----GAAG--- 123

Db 1072 AGTCGATCTGGNACAACTAAATTTGAAGAATCAAAACAGCTCATATTTCTGAAGCA 1131
 QY 124 -----A-----AAAA--AAT--CA-----TGAAA-----ACC-----ATCCAG 148
 Db 1132 GATTACACACTTCAGACATGGAATTCATTTCTTTGTAAGATCCGCTAGTGATATCAAG 1191
 QY 149 -----CCAAA-----AATGACAA-----TT--CTAT----- 168
 Db 1192 GGAGACCTATCCCAATGAGAAAGTCTTCATCAAGACCAAGAACTTTAGCTATACCAGT 1251
 QY 169 ---CT---CT---TG---GGCA-A--TCT---T--CAC--G-----G 188
 Db 1252 GCTACTACCACTGATCAGATGGCTGCGAGAGTCTCCATAGATACCAATGATCTCG 1311
 QY 189 GGCT-----GG-----C-TGCT-CTGTGTCTCT 209
 Db 1312 GGTCTTTTCCCTCATATCAAAAGTCAACCAAGAGGAAGATTTCATGTTCTTATTTCTAT 1371
 QY 210 TCCAAGGAG-----TGCCCGTGC--GCA--GGG--AGATGC--CACCTTCCC-- 249
 Db 1372 TGCATGGAGAAAGACATGCAAGTCAAGATGTGGCTATGCTGTTTAC--TCCCTCA 1429
 QY 250 -CAA-AGCTA-----TGGACA-----AC-----G--TG----- 268
 Db 1430 GCAAGAGCTACATCTTACCTTGACACAGAGACCAAGAGATCTTGCCTTGCAACCAAGATTC 1489
 QY 269 --AC-GGTCCGGCA-----GGGG-----AGAGCGC----- 291
 Db 1490 ACACAGTTTCAGGCACATTTTATTCTGAAGGGGGAGCTTGGGAGTCTGAAAGAGCTCATTT 1549
 QY 292 -C-AC--CC--TCA-GGTGCA-----CTAT--T--GAC-----AAC-----CGGCTCAC 324
 Db 1550 TCTACTACTGTGTCATGCGCAGGGAAGC-ATCATCCAGATGGAACCATAC--TCA- 1604
 QY 325 CCGGGTG--GCCTG--GCT-----AAA--CC-----G--C----- 346
 Db 1605 CCAGGTGGAGCCAGGAGAGCTCCAGTAAAGGAATAATTTGCTTGGAGATCCCTGTGGA 1664
 QY 347 ----AGCA-----CCA-----TCTCTTA-----TG-CTGGGAAT-GACA 374
 Db 1665 GTTTAGCATGTTCCCATGCTAAATGCTCATCTACAGCATCTTGCTG--ATGGAGA 1721
 QY 375 AGTG-GTGC-----CTG-----GA-----TCCTGCG-----GTGG----- 398
 Db 1722 AGTGATTCAGATCTCTTAACCTTGAATTTGAAGTGTCTTCGCAACAAAGTGGACCT 1781
 QY 399 ----TC-----CTTCTGAGCAA-----CACC-----CAAAAC-----GCA-GT-ACAGC 430
 Db 1782 GCGCTTCAGCATTCT--CAAAAGTCTTCCGCTCTCAAAACCCGCTGCGAGGTTCACAGC 1838
 QY 431 ATC---GAGATCC-----AGAAC-GTGG-----TGTG-TA-----TGA----- 459
 Db 1839 TTTCTCTCAG--TCCCTCTGTGGCTGAGAGCTGTGGACCAAGAGTGTGCTACTCTCTGAAC 1897
 QY 460 -CGAG--G-G-----CCCTT-----AC-ACCTGCTCGG--TGCACACAGACAA-- 495
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 Db 2018 TGGCTGAGAGCAACAAACTTAGTA--CCACATGAACTGAGAAGGATGTCTATAGAT 2074
 QY 547 -TGTAGAG--A-----TTT-----C-TTCA-----GAT-ATC-----TCCATTAA-- 576
 Db 2075 ATGTGGAGGACATGGGGTTTAAAGCATTCACAACTTGTATGATCAAACTTCTTATATTT 2134
 QY 577 ----TGA--AGGAA-----CAATATTAG--CCTC-----A-CCTGCAT-- 606
 Db 2135 GTTTTGACTATGGCATGGTTCCAATATACGACCTCTGTTGGAAATTTGATCTTGCATTTA 2194


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Db 4310 CACGTGAGCAGAAACAGAGTGTCTTAATATATTTGGATCAGGTGACC 4369
QY 1592 -----GGCC-----CAAG----- 1599
Db 4370 AATCAGACACTGGCCTTCTCCTTCATCAATCAACAGAGATATCCAGTAGGAACCTGCAG 4429
QY 1600 -----G-----C-----G-----TGSC-----GCTG----- 1609
Db 4430 CTGGCCATTGTGAAGTCTATGACTACTATGAGACAGATGAATGGCTTTTCTGAATAC 4489
QY 1610 -----CGG--GCAC-----TTTG-----GTAGAC----- 1626
Db 4490 AGCAGCCCTGAGCAGCAGACACAAATAATGTTTGAACCTCTATTTGTAGACAAGGCAT 4549
QY 1627 TG-TG-----CCA-----C-----GGCG-----TGTC-TTG-----TGAA----- 1652
Db 4550 TGCTGGATCCCGACCCAGGACCTTCAAGATGGTGATTTGTGTTGTTCTCTGAATA 4609
QY 1653 -----ACGTGAA-----ATAA-----GAGCAAAAAAAA 1679
Db 4610 CAACTAC-TGAACAAGCTTGATAAATAATGCTAGTCTCTGAGAAAAAAA 4662

RESULT 19
BC044081
LOCUS
DEFINITION
Xenopus laevis, 5570 bp mRNA linear HTC 19-FEB-2003
IMAGE:4682702, mRNA.
ACCESSION
BC044081
VERSION
BC044081.1 GI:28422174
KEYWORDS
HTC.
SOURCE
Xenopus laevis (African clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1. (bases 1 to 5570)
Klein, S. and Strausberg, R.
Submitted (13-JAN-2003) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4801, Rockville, MD
20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
Email: cgapbe@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 94 Row: d Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Smilarity but not identity to protein
This clone has the following problem: frame shifted.
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FEATURES
source

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ORIGIN

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Query Match      41.8%; Score 701.1; DB 11; Length 5570;
Best Local Similarity 39.2%; Pred. No. 0.0043;
Matches 1393; Conservative 0; Mismatches 174; Indels 1985; Gaps 389;

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Db 1501 GTTGAGCCCAATAATTTAGCTATTATCCCTGGA--ATGGGAATC-CCTGAGCACTGAA 1556
QY 44 AA--GCT--TGAGAGC--AACA-----CAA--TCT-----A 66
Db 1557 AATGCTATG-GAGCAGGAACAATGGTAAAGAGAGTCAAGTTCTTGAGATGACCA 1615
QY 67 T--CAGG-----AAAGA-----AAGA----- 83
Db 1616 TACCAGGGCTTGACTGGGGGATGGAAGAAGTAATGCAAAAAGACCAGAGAAGATGCTCTC 1675
QY 84 ---AAAA-----AAACC----- 92
Db 1676 AGAAAAAGTTCCCTATGTCTAAACCCATTCGGGCTCAGTTCACAGAGGCATGGATGCAAA 1735
QY 93 -----GAA-----CCTGAC--AA--AAAAGAA----- 110
Db 1736 ACAAAGTACCGTAATGCCACCGTCAGAGAGGTTCTGACCGTAAAGAGAAATGT 1795
QY 111 --GA--AAAGAAGAAGAA--A-----AAAAT--CATGA-----AA--AC 141
Db 1796 CTGATGAAAGAGAGAGAACCCAGGCAGAGATTGACAGAGATGCGAGCTTTTACAATATAC 1855
QY 142 C-ATCC-----AGC--C-----AAA-BAT-GCACA-ATTCTATCT----- 170
Db 1856 CAATCTCAGCTGCTGGAGCAACTAAAGATAGAAAGATAGACAGAGCAAGCTGAGAC 1915
QY 171 -CTTGGGCAATCTTCA-----CG--GGGCTGG--CTGCTC-TGTG-TCTC- 208
Db 1916 ACCTGGGCAA-CTTCAGGGTCTCCATCTCGTTGGG-TGACCTTTCACATGGCCCTCA 1973
QY 209 ---TTCCA-----AGAGTGCCCGT--GC-----GCA--GGGAGAT-----G-CC 241
Db 1974 ACATTCAGGCTCCAGGA-----CC-TAGGCCACAGCAAGCCAAAGATTCCAGCAGCCCC 2028
QY 242 ACCTTCCCAAGC--T-ATGACAAC--GT-----GAC----- 270
Db 2029 ACC--CCCCACAGCAGATGATGTGCAACATGTCTCTGCAGACAGTTTCTTCCACAAG 2086
QY 271 -----GGTCC-----GG-----CGAGGGGAGAG--C 289
Db 2087 ATCTCAAGCAGCCCGAGTCCACAAAATTTTATGTTTCTGGTCCACAGGGGGTGAGTTC 2146
QY 290 GC-----CACCTCAGGTGCA-----CT-----ATG-----A 312
Db 2147 TCAAGAAATGATCCT--GGTGCAAGTAGACTACCAAGTTCTCATGACCAATTTGGTGA 2204
QY 313 CAACCGGTCACCCGGGTGGC-CTGG-----CTAAA-----CCGACG-----CACC- 352
Db 2205 CAA--GGTCCCCAGTAACTCTGGGCCCAAAATCAGTTAGGGCTCAGGGGCCATCT 2261
QY 353 -ATCCT-----CTATGCTGGGAATG-----A--CAAG-----TGGTGCC 383
Db 2262 GGTCTAGACCTATTCAAGGAATGTCTCTCACCATAGCATGCAAGGGGCACCTGGT-CC 2320
QY 384 T--GGATCCTC-----GGGT-----GGTC-----CTTCTGA 407
Db 2321 TCAAGGA-CCTCTTATGGGAGTTACTCCAAGGGAGGTCCGATGCCACATGGACTTTC-GA 2378
QY 408 GCAA--CA--CCC-AAAC-----GCAGTA-----CAGCATC-----GAGA-- 437
Db 2379 GAAAGCTCAGGCCCTTAATCAAGGTATGGCAATAGTGCATCCAGCA-CAAGACATGAGAG 2437
QY 438 -----TC-----CA-----GAACGTGG-----ATGTG-----TATG--AC--GAGG 464
Db 2438 CCCCTCTGGAGCAATAGTTGGACATGGACAAGATATGGGAGCCCTTATGGAATCTGAGAG 2497

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QY	501	CAAGA--CCTC--TA--GGGTCCACCT--CAITGTG--CA	531
Db	2555	CAATGATATGCGGGGCCCTCAGGATATGAGAGGGGC--CCTGACA-TGCGAGGCCCTCA	2611
QY	532	AG-TATC--TCCAA--A-AT--TG--TA-GAGATTCTTCA-GATAT	567
Db	2612	AGATATCAGGTACCAATGGATATGCGTGGTCTCAAGATATGAGAGGTCTCATGATAT	2671
QY	568	-C--TCCATTA--ATGA--AG--GGAA--CA--ATATTAG--	594
Db	2672	ACGTGGTCC-TCAAGACATGAGGATCCCTCTGGTATGGGTGGTCTCAAGATATTAGGG	2730
QY	595	--CCTC--TGC--ACC--TGC--	604
Db	2731	GACCTCCAGATTTCGTGGGCTCAGGATATTAGGGACCCCATGATATGCTGGACCCC	2790
QY	605	--ATA--G-CAACTGTAGACACAG-CC--TA-CGG--TTA	635
Db	2791	AAGATATGAGGGGTTCATCTG--ATATCAGAGCCCAAGATATGCGGGGGCCCCAAGA	2848
QY	636	CTTG-GA-GACAC--ATCTC--TCCCA--AAGCGTTGG--CT--TTGTG	673
Db	2849	CATGAGAGGACCCCATGATATCAGGGGCCCCACAGATATGG-TGGCCCTCAGGATATG	2906
QY	674	AGTGAAGAC--GA-ATACTTGG--AA--AT--	696
Db	2907	AGG--GACCCCCAGATATGCATGGCCCTCAGGATACAGAGGACCCCCAGACATCGTG	2964
QY	697	--TCAGGGCATC--ACC--CGGAGCATCTCAGG--GGA-726	
Db	2965	GCCTCAGG--ATCTTAGGGGACCCACAGACATCGGTG-GCCTTCAGGATATTAAGAGGAC	3021
QY	727	CTAGAG--TGCAGTG--CC--TCCA--ATGACGTGGCCGC-759	
Db	3022	CTATG-GACATGC-GTGGCCCAAAACATGAGGGGTCCAGCTGACATG-CGTGGGCCCC	3078
QY	760	-----GCC--CGTGGT--AC-GGA--GAGTAAAGTTC-----784	
Db	3079	AAGATATGAGGGGTATGCCTGACATGCGAGGTCCACAGGATATGAG--AGGTCTCTCTG	3135
QY	785	AC--CGTG--AA-CTAT--CCACC--ATA--CAT--TTCAGAG--815	
Db	3136	ACATGCGTGTCCACCAAGATATCGGGGACCCCTGATATGCGTGTGCCAAGATATGC	3195
QY	816	-----CC--AAG--GGT--ACAGG--TG-----TCC-----CCGTGG--839	
Db	3196	GGGACCTCTGTATATGCGTGTGCCAAGATATGCGGGACCTCTGATATGCGTGTCT	3255
QY	840	GACAAAA--GGGA-CAC--TGC--AG--TGTGAAG--CCT-869	
Db	3256	CACAAGATATGCGGGACCACTTGATATGCTGTTCACAAGATATGCGAGGTCCACCTG	3315
QY	870	-CA-GC--AGTCCCTCAGCAG-AAT--TCC--A--GTGG--TACAAG-904	
Db	3316	ACATGCGTGT--CTCA--AGAAATGCGAGGACATCTCTGATATGCGTGGCCCT-CAAGA	3370
QY	905	GATGACAA-A--AGA--CTGA-TTG--AAGGA-AAGA932	
Db	3371	TATG-CAAGGACCTCCAGATATGCGTGTGCCACCTGACTTGGTCTCTAGGATATG-3428	
QY	933	AAGGGT-----GAAA--GTGGA-AAACAGA-----CCTT-----959	
Db	3429	AGGGGTATCCAGAAATCGGTGGACACCCAGATATGCGCGCCCTTCAGGACATAAGAGG	3487
QY	960	---TCC-----TCTCA--A--AACTCAT-----CTT978	
Db	3488	CGGTCCGGACTTGGAGGTG-CACCGACATGCGTGGACCTCATGATTAAAGGGGACCTC	3546

QY	979	CTTCAATGCTC-TGAACATGAC--TAT--G-GG--AACTACACT-----TGCCTGG---1023
DB	3547	CTGAATG---CGTGGACATCAGCATATAGAGGCTCAAC---CTGAATGCGTGGTCAAT 3599
QY	1023	-----CCT-----CCAAACAGCT---G-GGCC-----1040
DB	3600	CAGGATATGAGGGTTCCTCGATATATGCGCCATCAAGATATGAGAGCCCGCAGGAGATG 3659
QY	1041	---ACACCAA-----TGCCAGCAT--CATGCTATTTG-GTCCAGGCGCGCTCAG--C 1084
DB	3660	AGAAGACCAAAGATATGAGAGCATCCCATG--ATATGCGT---GGC-CC-TCAGAAATAT 3712
QY	1085	GAGG---TG--AG--CA-----AC-----G-GCA-----C-G-TC-GAGGAG--G 1111
DB	3713	GAGGGGCATGCCAGACCATGGACCACAAGAAATAAGAGCATCCCTGATCTGAGAAGCCC 3772
QY	1112	GCAGG--CTGGG--TCT-----GG--CTGCTG-----CCTC-----1136
DB	3773	TCAGGATTTGGAATCTACAGGATAGTAGGGACCTGCTGACATTTGGTGGCCCCCAGGA 3832
QY	1137	---TT-----CTGCTCTT-----GCACCT-----1152
DB	3833	TTTAAAGGCCCTCAGCGCTGCACTTTCACAAGGAAATCCCAAGAGCCTCATAGCCAGCA 3892
QY	1153	-----CCTTCTCA-----A-ATT--T--TGATG-----1170
DB	3893	GAACACGGCAGCAGCATCTCACCCAGCACAACAAAGGACCACTTACTGGAGATGGACC 3952
QY	1171	-----T-----GAGTG-----CCACTTCCCC--A-CCC-----GG 1192
DB	3953	CAGGCTTTTAAACAGAGTGGAAAGGTGAGGCCCATCTCCCTTGATCCCTGGGCTAGG 4012
QY	1193	-----GA-----AAGG-C-TGCCGCCACCA-----CCA-----CC--ACCA-----ACA-- 1222
DB	4013	ATCACAGATTCAACAGGACGTG--GCCATCAGGTCCAAAGCCCTTAAACAAGTGCATC 4070
QY	1223	-----CAA--CAGCAAT--GG-----CAAC--ACC--GAC--AGCA--CCAA 1253
DB	4071	CGTGGTCTCTCAACCATCATGTTAGGCGCACCAACCAGACCGGAAGACGTGACAAAGCC-- 4128
QY	1254	TCAG--AT--AT--AT--ACAA-A-----TGAAATT--AGA--AGA--1281
DB	4129	CTGACCATGGCCCATTCATGCGGACAGAGATGGGGTG--ATTCCCGAGACAACAGAG 4185
QY	1282	-AAC--ACAG-----CCTCA--TG-----GGACAGAA-----1303
DB	4186	GACCTTCTGACAGACGGGGCCCTCACCTGATTCTCAGAGAGGCCAGAGATTTTCCTC 4245
QY	1304	-----ATTTGA-----G-GGAG-----1315
DB	4246	CAGATGATCGGTATGTCTCACGGGGCGTGAATTTGATGGAAGAGTGGAGGTTCTTCCT 4305
QY	1316	---GGA--ACAA---AGAAATCTTTGGGGGA-----AA---1341
DB	4306	CTCAGGTGACAGTGGAG--ACGT--GGGGGACCTGCTTCACAGTTCTCTTCTTAACCA 4360
QY	1342	-AGAG-TTTT--A-A-AAAAA---ATTGAAA-----ATTGCCTT--1373
DB	4361	CAGAGATTTTCCAGACAGAGAAACAGGGATTTCAATCGTGGGAGGTAGAGGCATTC 4420
QY	1374	---GCAGATATTTA--G-GTA-CA---ATGGA-GTTTTCTTTTTC-----CAAACGG 1414
DB	4421	AGAGGAGAGATATAACCGGAAATCAGAGATGGAAG-----TTACGAGACAAA--GG 4472
QY	1415	GAAGAA---CACAG-----CACA-----CCC-----1432
DB	4473	GATGAGCTTTTTCACAGGCGTGTCTCAAAAGCGGTGAAGGCGTGGGTCCCGAGGAGT 4532
QY	1433	---GGCTTG--GACCCA-----CTG-----CAA---G-CTGCATCG-TGCA 1463
DB	4533	GAAGGGTTTGCTAAACCCAGAGGAATTTGGTCTCTGATGACATTTTGTACTCCAAAGATG-A 4591
QY	1464	ACCTCTTTGGTCCAGTG-TG--GGCA-AG-----GGCTCAGCCTCTCTGCCACAG--- 1511


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QY      1512 -----AG-----TGC-----CCCCAGTGGAC-ATT--CTGG--AG-CTGGCCAT 1546
Db      4646 AGGAAGAAAGAGAGCTCTCTACCCCA-----GAACAATTCATGGATCAGACCGGGCA- 4700
QY      1547 CCCAATTCATCAATCAGTCC-----AT--AGAGA-----CGAACAGA 1579
Db      4701 -CCTAA--CCATCAGTCCCGAGAAATCAAGAGAAGCTGGACCTGATCATTCTTACAG- 4756
QY      1580 AT-----GAGACCTTCC-----GG-----CCCA---AGC-GTG-GCG----- 1606
Db      4757 -TCCTGCGCGTGACATTCCTACTCTCTGATGGTCAITTCCTCCAGCCAGCAGGAGCGATCTT 4815
QY      1607 -----CTGC-GGGCACTTTGGTAGAC-TG-----TGCCACCAC-----GG-CGTG--- 1643
Db      4816 CTTCACTGAGGGCA--TG--GACATGGCTTCCTTACCCCCAGCAAAAGGCCCTGGC 4869
QY      1644 ----TG-----TTGTGAAGCTGA-----A-AT--AAAAAG-AG-----CA-AA 1673
Db      4870 ACGATGGCCCTGGT-ACACCTGACCACAGGGACATGGACACAGCAGGGGGGGCCACCAGAA 4928
QY      1674 -AA-----AAAA 1679
Db      4929 GAACCTGTAAAA 4940

RESULT 20
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LOCUS      11415 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus MLL gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY418622
VERSION AY418622.1 GI:39774582
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11415)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 11415)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..11415
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>11415
/gene="MLL"
/locus_tag="HCM6618"
gene
Query Match 41.8%; Score 701; DB 29; Length 11415;
Best Local Similarity 37.8%; Pred. No. 0.054;
Matches 1425; Conservative 0; Mismatches 161; Indels 2184; Gaps 409;

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QY      1 GTTGTGTCCTT-----CAGCAAAAACAGTGG--ATTTA-----AA-----TC 34
Db      3812 GTAGTGTGCTTTCTCTGTGCCAG-----CAGTGGGCATGTAGAGATTGCCAAGTGTGTG 3866
QY      35 T-----CCTTTGACAA--GCTT--GAGA--GC-----A--AC-----A 59
Db      3867 TGAACCTTCCACAGTTTTGCTTAGAGAGAAATAGCGCCCCCTGGAGGACCACTGGA 3926
QY      60 CAA-----TC-----TAT--CA-----GGAA--AGAA--AG----- 79
Db      3927 AAACCTGGTGTGTCGCCGCTGCAAGTTTTGCACTGTGTGTGAAGACACAGCATCAGGCTAC 3986
QY      80 AAAGAA-----AAAA--CCGAA-----CCT--GA-C 101
Db      3987 AAGCAGTTGTGGAGTGAACAAGTGCAGAAACAGCTATCACCCCGAGTGCCTGGGACC 4046
QY      102 AAA-----AAAGAAAAAGAA--GAAGA-----AAAAAAT----- 132
Db      4047 AAACCTACCCCAACCAACCCACGAGAGAAAGAAAGTGTGGATCTGCACCAAGTGTGTCCG 4106
QY      133 CATGAAA-----ACCA-TCAGCCAAA-----AATGCACAAT--TCT----- 166
Db      4107 C-TGCAAGAGCTGTGGCTCCACCACTCCAGGCAAAAGGTGGGCGCACAGTGTCTCAG 4165
QY      167 ATCTCT-----TGGGC--AA-TCITT--C--ACGGG-----GCTGGCTGTCT 201
Db      4166 ATTCTCACTGTGCCATGACTGTGCCAAACTCTTTGCTAAAGGGAACCTCTGCTCCTCT 4225
QY      202 GT-----GT-CT-----CTTC-----CAAG-----G-AGTGC----- 221
Db      4226 GTGCAAGTGTCTACGATGACATGACTACGAGACCAAGATGATGATGATGATGATGATG 4285
QY      222 -CCG-----TGCG-----CAG--C-----G--GAGATG----- 239
Db      4286 ACCGCTGGGTCCACTCCAAGTGGCAGAGTCTCTCAGGTACAGAAGATGATGATGATGATG 4345
QY      240 -----CCACCTT-CCCCAAAGCTATCG-----AC-----AAC-G--TGA-CGG--T 273
Db      4346 TTCTGTCCAACTTGCCAGAAG-TGTGGCTTACAGTGTGTGAACCTCACTGAGCGGCAC 4404
QY      274 CCGGCAG-GGGGAGA--GC-----GC--CA-----CCCT--CAGGT----- 302
Db      4405 CCGCAGAGTGGAGACTGGCCCTCGAGAAGAGCTGCGAGCGTCCCTCAAGCAGGTCTC 4464
QY      303 ---GCAT-----ATT-----GACACCGGTACCCGGGTGGGCTG-GCTAAACCG-CAG 348
Db      4465 ACGGCCCTGTGAATTCTCGGACTACC-AGTCAC-----TTG-CTGGCT--ACCGTCAG 4515
QY      349 -----CACCATCCTC-----TA-----TG-----CTG-GGAATG--AC----- 377
Db      4516 GCTGCCA--AGCTTCAGACTTAAACCTGAGACTGAGGAAAGCATACCTTCCGAGACT 4573
QY      378 -----GCTGCTGGATCCTCGGTGCTCTTCTGAG--CAACACCCA-----AAC-GC 422
Db      4574 CCCCAGAGGGGCC-AGACCCTC-C-TGTTCTTACTGAGGTGAGGTGAGGAGTGAACAGC 4630
QY      423 AG-----TAGCATCA-----GATCAGAACTGGATGTGTATGACGAGGCG--CCTTAC- 472
Db      4631 AGCCGTTAGA-CCTCGAAGGGTCAAGAA-GAGATG-----GACCAGGGCAGC--TACG 4681
QY      473 -ACCTGCT-----CG-----GTGCAGA-----CAGACACCA-----CCCA 502
Db      4682 TATCTG-TGTTGAGTTGAGGATGATTTGTGAAGATCAITTCAGGACGCCATTAATCA 4740
QY      503 AA--GA-----CCTCTAG-GGT-----CC-ACCTCATTTGTGCAAGTATCTC----- 539
Db      4741 GATGGAGGGCAGCC---AGAGATAAAAAAGCAACACATGCT--CAATCTTCTTCAT 4796
QY      540 -C--CAAAATTTAGAGA---TTTC-----TTGAG-----ATA-TCTCCATT----- 574
Db      4797 TCGGCAAA--TGGAGCGAGTTTTTCCGTGGTTTCAGTGTCAAAAAGTCTAGATTTTGGGAG 4854
QY      575 ---AATGAAG---GGAACA-----ATATTA-----GCC-TCACCT 602

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Db 4855 CCAAATAAGATCAAAACAACAGTGGGATTTACCAACGCGAGTGGCTTCCGCCCTTCACTT 1111 4914
Qy 603 G-CATA-----GCA-----ACTGGTAGACAG-----AGCCTAC 630
Db 4915 GACCAATATTATGCTCAGTGGCAGGAGGAGG-AGAGCAGCCACACTGAGCAGCCTCC 1111 4973
Qy 631 GGTACT--TGAGA--CA--CATCTC--TCCCAAG--CGG-----T 663
Db 4974 --T-CTAATGAAGAAATCAATCCAGCTCCAAACCCAAAGGACCCGAGAGCCAGACT 1111 5029
Qy 664 TG-----GCT-----TTG-----T--GAGT--GAAG 680
Db 5030 CGCCACGCGCTCCACCGGCTACACCGGATCTTTGAGTACTGATCGGAGTCGAGAAG 1111 5089
Qy 681 ACGAATACTTGA--AAATCA--GGGATC--AC--CCG--G-GAGCA-----717
Db 5090 AC-AGTCC--AGACTGAATCCACCCGAGCATCGATCAACCCGACAGTGTGCACTGT 1111 5146
Qy 718 GTCAG-GGGACTACAGTG-CAGTGCCTCCAATGACG-TGSCCG--CGCCGCTGGTAC--770
Db 5147 GTCTGATGTACGGGA-TGACAGTG-CT--AATGATCTGGCCGTTGC--T-GTACAT 1111 5198
Qy 771 -GG-----A-CAGTAAGGTAC-CGTGAATATCCACCATACATT--TCAGAAGCCA 818
Db 5199 TGGCCAAAATGAGT--GGACATGTGAATCTGTC--T--TTGTGTCAGCAG--A 5246
Qy 819 AGGT--ACAGTG--TCCCG--TGGGACAA--AGGG--850
Db 5247 AGTGTGGA-AGATGATGACGGATCACTGAAGAATGTG-CATATGGCTGTGATTAGGGC 1111 5304
Qy 851 -A-CA-CTGAG--TGTGAA-----GCCTCA- 871
Db 5305 AAGCAGCTG-AGATGTGAATCTGCCAGAGCAGGAGCCAGTGGTGTGCTGCCTCAC 1111 5363
Qy 872 -----GCAGTCC-----CC--TCA-----GC--AGAA-----TTCC-- 893
Db 5364 ATCTTGCA--CCAGCAACTACCATTTATGTGTTCGGGCGCAAGAACTGTGTCTTCTG 1111 5421
Qy 894 -----AGTGTA--CA--A--GGA--TGA-CAAA-----913
Db 5422 GATGATAAAAAAGT-GTATGTGTCAGCGGATCGGATTTGATCAAGGCGAGGTGTTC 1111 5480
Qy 914 --AGACT-GA-TTGAG--GAA-----AGA-----AAGG-----GGT-----939
Db 5481 TGAGAATGGATTTGAAGTTTTAGAGAGTGTGTGTAGATTTTGAAGGAATCAGCTTGG 1111 5540
Qy 940 --GAAAGT-----G--GAAA-----CA--GAC 956
Db 5541 CAGGAAGTTCCTTAATGGCTTGAACCAAGAAATATCCATGATAGGCTCAATGAC 1111 5600
Qy 957 --C--TTT-----CCTCTC-----A-AAACTCATCTTC-- 979
Db 5601 AATCGACTGTTTGGGAATCCTGAATGACCTCTCTGACTGTGAAGATAAATC-T-TTCT 5658
Qy 980 -TT-----CAATG-TCTC--TGAACATG-----AC-TATG--GGAA--C-----1009
Db 5659 ATTGGATACAGTGTCTCGGGTGTAC-TGGAGCACCAAGATGCCCGGAAGCGTGTGT 1111 5717
Qy 1010 -TACACTTGC-----GTG--G-CCTC-----CAACAGC- 1034
Db 5718 GTACATCAAGATCATGGATGCGCGCTCTCTGTGTAGAGCCGGATATCAAC-AGCA 1111 5776
Qy 1035 ---TGGC-C--AC-----ACCAATGCC--AG--CATCATGC--TAT-----1064
Db 5777 CGGTTGAGCAGATGACATAGACCATTTGCCATAGCCCATCAT-CATTTATAGTCA 5835
Qy 1065 T--TG-----GTC-----CAG--GC-----G-----CGGTACG--GA--GG--1088
Db 5836 TCGTGAAGCAGTCAAGACAGTGCATTTCTCAGTCTCCGTC-GCCAGATCGGCC 5894
Qy 1089 -----TGAGCA-AC--GG-----CAG-----TCG-AGG-----AGG-----1111

Db 5895 TCATTCA-CAGACCTCAGGCTCCTGTTATTTATCATGTGTCATCGAAGGTCCTAGGATTC 5953
Qy 1112 G-----CAGGCT--GC-----GT-----CTGGCTGC-----TGCC-----1134
Db 5954 GAACACCCA-GCTACTCGCTACACAGAGTCCCTTGGCTGGCCCAATTGGCTTTGCA 6012
Qy 1135 -----1135-----TCTTCT 1140
Db 6013 GGAAGTCTACCCCAACCACTCAGAAATCGTCACAGTGGTGACCCGTTACTGTCTTCT 6072
Qy 1141 GGTCTT-----GCA--C-CT--GCTTCTCA--AATT-----TTG-----1167
Db 6073 GGTCTTGGAGCAATGGCTCTAGCGTCAAGTACTTCTTCTTGTGACCCCTGCGGTCC 6132
Qy 1168 -----ATGTG--AGTG-----AGG-----CCA-----C 1180
Db 6133 AAGCTCGCATATGCTCCAGTGAGACGGGGGCGCTTACTCCAGGAGTAGTGTTC 6192
Qy 1181 T---TCCCCACC--GGGA-----A-----AGGC--TGCC-----1203
Db 6193 TCAGTCCCGAGCTTGGAGCTGCGACATCTGAGGCGAGTGCCAAAGCATCGATCGA 6252
Qy 1204 -----GC-----CA-----C-CA-----CCACCAC--CAA--CA 1222
Db 6253 GGAGGCTGTGAGTTCAGTGTCAAGTGTCTGCGGCAAGCGCTCCCTTCAAGCTCA 6312
Qy 1223 CA-----ACAG-----CA-----ATGG-----1234
Db 6313 CAGAGCAGTGTGGAGGCTCCAAACCAAGTCTGATCTGATGGGTCGTCACCTCGGAGTG 6372
Qy 1235 -----CA-AC-----ACC-----G-----AC 1244
Db 6373 AAGCGGTGATGTGCTTCAAGTCTGATCTGATCCCAAGGCTCCTTAGTAAAGGAGAGAAAC 6432
Qy 1245 AG-----CAA-----CCAA-----TCAGAT--AT-----ATA-CAAA-----TGAAT- 1274
Db 6433 AGAATCTCAAGTTCAGAGGACAGATGATCTGCATAGCAGCTTACCTGGAATC 6492
Qy 1275 --TAGAA--GA-AACACA-----GC--CTATGG-G-----AC--AG--AAAT 1305
Db 5493 CCTA-AACTGACACCAAGTTCATAACGCAACTCTCGAGAACTAAACATTAGCAAT 6551
Qy 1306 TTGAGGGAG--G--GGA-----ACA-----AAGATA-----1328
Db 5552 T--GCGATTTGCTGAACCTCTACAGTGCCCTTTTCTTAAAGGATACAGTGTCTTA 6608
Qy 1329 -----CT-----TTGGGGG--AAA-----AGAG-----TT--1347
Db 6609 CCCACAGCTCCACTTGGGGGCAAGAGTGCACAGACCAAGCATGGATCTTCCCA 6668
Qy 1348 T--TAAA-----AAA-GAA-AT--TG-----AAAA--TTG-----CCT--T 1373
Db 6669 GTCAAGAGCCCTCTCCAAATGAAGATGTTGAATCAAAACCTTGAAGCTCCCTGGTAT 6728
Qy 1374 G-----CAG--AT--ATT-----TAGG-----TA-----C- 1389
Db 6729 GGGCCACAGGCATCCATCTACATGAACATAGGCTGTAGTCTTAGAGACAGAGACA 6788
Qy --390--AATGG-----AGTTTTCT-----TT-----TTC-----1407
Db 6789 GAAAGGAAAAAGTCTTCTAAAGAGACTTGCAGAAAGAGCATCCAGTAATCTTACTT 6848
Qy 1408 -----CAACG-----GGAAG--AAC--ACAGC-----1426
Db 6849 GGAACCTGGCAGGTGACACCGGTGAGAGAGAAACCTAAAGCCAGAGTTTGTGTATGA 6908
Qy 1427 -----ACACCGG--CTTGG--AC--CCAATGCA--GCTGCATC-----G- 1459
Db 6909 GGTGTGACTCTGGGTTCTTGGGACAGACCA-TGTAATAATGTTTTCATCTGAGAAGA 6967
Qy 1460 -TG-----CAA-----CCTCTTT--G-GTGCC--AG-----T-----GTG--G 1484
Db 6968 TTGGAGATAAAGTCTTCTTTCAGGAGTCCCTTAAAGGTCATCCACACAGTGAAG 7027

QY 501 -----CA--AAG--ACC--T-CT-----AGCG----- 515
Db 1765 CCAAAATGGTCAAGCAAGATACACCAATTAAGTGTGTGTGCCAGCGCTTACAGCCAAAG 1824
QY 516 -----TCCA-----CCT--C--ATTGTGGAAGT-----ATCT-----C--- 539
Db 1825 ACAAAACAGGATCCAGTCAAGCTTTACGTGTGATGTGCAAGTCAGCAAACTAAGAAGCGTA 1884
QY 540 CCAA-----AAT--TGT--A-GAGA--TT--TCTTCAG----- 563
Db 1885 CCAAGACCAATTTTGGAACTTGAATCTGTTTGGAGGAGAGTTCCATTTGAGTGCC 1944
QY 564 ATATCTC-----CATTA-----TG-AAGGG-----AA--CAA 588
Db 1945 ACAACTCTCTGACCGCATTAAGGTGGGTGTATGGGATGAGATGATGACATCAAGTCAA 2004
QY 589 TATT--AGCCTACCTGCATAGCAA-----CTGGT-----AGACCA-----GA 624
Db 2005 GAGTAAAGCAAGCGCT--AAAGCGAGAGTCTGATTTCTTGGCCAAACCATCAATGA 2062
QY 625 G-----CCTA-----CG-----GT--T--ACTTGG----- 645
Db 2063 GGTTCGGACCTTAAGTGGCGAGATGAGCGTCTGGTACAACTTGGAGAGGAGACAGCAA 2122
QY 646 --CA-----TCTC-----TCC-----CAAAGCGGT--TGGCTTT-----GTGAGTGA-- 678
Db 2123 ATCAGCGGTCTCAGGGGCTATCCGACTACAAATCAGTGTGGAGTCAAGGGGGAG--GAGA 2181
QY 679 --AG-----ACG--A--ATACTTG-----GAA----- 694
Db 2182 AAGTAGCCCCATACCAAGTGCATGATACATGTCTCCATGAGAATCTTTTCCATTACCTCA 2241
QY 695 -----ATTCAGGCA-----T--CA--CCGGGAGCAGTC--AGGGAC----- 727
Db 2242 CACACATTTCAGGCGAGTGGAGGAGTCCGATCCCTGAGC--TCGAGGAGACGATCCCTG 2299
QY 728 -----TAC--GAGTG--CAG-----TGCC----- 742
Db 2300 GAAGGTGTACTTTGA--TGAGACAGCCCAAGAAATTTGGATGAATTTGCCATGCGTTATG 2358
QY 743 -----TCCA-----ATGACG-----TG--G-----CC-----GC 759
Db 2359 GCATTGAGTCCATATATATCAGGCCAAGCAGCACTTTGATGTTTATCATCAAGTACATGT 2418
QY 760 GCGCTGGT-----A-C-G-GA-GAG-----TA-----AAGTCAACCG--TGAACATAT- 796
Db 2419 GTCC--TGGTGTGCCAGCAGTATGAGCACTTACTGGCCCAACATCAAGCCT--ACTATG 2475
QY 797 -CCAC-CA-----TAC-----A-----TTT-CAG----- 812
Db 2476 CCCACAACTGCCTCTACAAATGTCTGTGATCTGATCGCTTTGCGAGCTCCAACTTTG 2535
QY 813 -----AAG-----CCA-----AGG--G----- 822
Db 2536 GGAAGAGAGATTTGTAAACTGCTGGACCACTGATACAACTCACTGAGATCGACCTCT 2595
QY 823 -----TACAG-----TGTCCCG--TGGGA--C-AAAGG-----GGAC-----A-CTG 856
Db 2596 CTACATACAGGAATAATTTCCCTGTGGGAGTCTCTGAACGGCTTCAGGACTTTAAATCCA 2655
QY 857 CAGTG-----TGA--AGC-----C-TCAGCA-----GT-----C--CC 879
Db 2656 CAGTGGATTTGTGACCGCATTAATTTCTTCTCAGAAATGAAGTACAAAGACTGCAAGGCC 2715
QY 880 CTC-----AG-CAGAAATTCAG--TGGTACAAGGA-----TGACAAAGACTGATTGAA--- 925
Db 2716 CTCCAAGAGCCAG-----CCAGGTGTA--AAGATTTGTGTG---AAGGCTGTTTGAATC 2767
QY 926 -----GGA-----AAGAA-----AG-----G-----GGTGA 942
Db 2768 CACATATGAATATATCTTCAACAACACTGCCAGGACTTATACAGCCGCCAGTACCAGTGA 2827

QY 943 -----AGTGAA-AA-----CAG-----ACCT-----TTCCT----- 963
Db 2828 GCAGGAGCTTACCTCCAGAGGAAACAAGGGCCCGACGATTCGGAACTGTGATTTCTTGGCCAA 2887
QY 964 -CTCA--AAACTCATC-----A--TGACTATGGAACTA--CA-CTTGC-----GTGG 1022
Db 2888 GCTCATCACACTCATCGTGTCAATCATAGAGGAGATAGAAATTCCTACACACTGT-TT-CTTCA-A--TGTCTC 990
QY 991 TGAAC-----A--TGACTATGGAACTA--CA-CTTGC-----GTGG 1022
Db 2947 TGAACCACTTTTCTCAGGAGTTGAATGTGGAA--AAGTCAGC--GCAGAGTGTGTGG 3002
QY 1023 CCT-----CCAA-----CA-----AGC-TG-----GGCAGC- 1042
Db 3003 CATTTGTTTGGCCAGACATGAATATGCAATGGAGGAGCATGAGAAAGACCACTGTGT 3062
QY 1043 -----ACCA-ATG--CCAGCA--TCA-----T-GCT----- 1062
Db 3063 AAAAGTGTGACTTACATGAACCTGCACCTCAAGTGAAGTGGCTCCCAATGATAGGTG 3122
QY 1063 -----ATTG--GTCC-----AGCGCC--GT--CAGCGAGG--TGAGCA--AC 1096
Db 3123 CGGATCTGCTGCTCTCTCCAGGGCGAGGTGCTGAGTACCAGCGTGTGTTGAGCAGTTC 3182
QY 1097 G-GC-AC--GTC-----GAG--GAGG--G-----CAGG-----CTGCGT-----CTG 1125
Db 3183 GTGCTACAATGGCTGATGAGATGAGGATGATCCCTGGAATTCCTGCGTGGGCGCTG 3242
QY 1126 G-----CTGC-----TGC-CTCTTT-----CTGGTCT 1145
Db 3243 GAACGAGATGAAGAGATGGATTCCAGCAGACATCAGAGCATGCACCTCTTTCTGCTCT 3302
QY 1146 -----TGCACCTG-CTTCTCA-----AAT-----TTTGA-----TGTGAG 1174
Db 3303 GTGGTGA--TGTCTTCAACAACCTCAATCAGAGCTTTGAGATCATCCGAAGCTG-GAA 3359
QY 1175 TGC-----CA--CTTCCC-----ACC--CGGAAA 1196
Db 3360 TGCCAGACCCCGATCTTGTGCCCACTACATGAGAGGTTTGTGTAAGACCATCGGAAG 3419
QY 1197 G-GTGTCCGC-----CA-CCA-C-----CA-----CCA-CCAA-----CACA- 1225
Db 3420 GTGCTGATGCACTATGAGACATCTTGTCAAAGGACTTCCCGACCTATTCACAAAGAG 3479
QY 1226 -----CAGCA-----ATGGCAACCG-ACAGCAACCA-----T-CAGATATATACAA 1267
Db 3480 AAACGTGCTGATCTGATCTGATG--AACACGTGCAACAACTGAGGGTCCAGCTGGAGA-AA 3536
QY 1268 ATGAAAT-----AG--AAGAAAC--AC-----AGCCTCATGGACAGAAAT 1305
Db 3537 ATG-----TTTGAGGCCATGGGAGGAGGAGGCTTGGACCTTGAAGTGCA--GACAG---T 3587
QY 1306 TTGAGGAG--GG-GAACAAAGATATAC--TT--TGG-----GG-----GG 1338
Db 3588 CTGAAGGAGCTGCAAGGTGAA--ACTGAATACGCTTCTGATGAGCTCAGCATGTTGTTGG 3646
QY 1339 AAAAGAGTTTAAAAAGAA--ATTGA-----AAATGCTTTCAGATAT 1381
Db 3647 -AAACAGTTT--CCAGTACGGATTTGATGATGTTGTCGACAAATGCCC-----GACAT 3697
QY 1382 --T-----TAGGT-----AC-----AATGAGTTTCTTTTCCCAACG----- 1413
Db 3698 CCTGGCCAGGTTCCGGGCGACAGGAATGCA---TCT-----CCAGAGCCAGGCGCTCA 3749
QY 1414 -----GGAGAAACAGCAGCAAC-CCGG--CT--TGGAC--CCACTGCAAGCTGCAT 1457
Db 3750 GCGCTCAGGATGAGATAGCTACTCCGGCCTCTCATGGACTTC--CTGATG--GCAA 3805
QY 1458 CGTCAACCTCTTTTGGTGCA-----GTGTGGGCAAG--GGCTC--AGC-----CT----- 1499
Db 3806 CCT-CACCTCTTT--TGCCACTGTGTGTGAG--AAGACGGTTCTGAAGCGTGTACTGAAG 3860
QY 1500 ---CTCTGCC-----CAC-----AGAG-----TGCCCCCAC---GT 1524

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Db      3861 GAGCTCTGGCGGCTGGTGTGATGAACACAACTGGAGAGGATGATTTGTTCTGCCCACTCACT 3920
QY      1525 G-----GA-----AC-----AT-----T-CT-----GGAGCTG-GCATC---CCAAA 1552
Db      3921 GACCAGAGGGGACCCAGCTGATCTTCACTGCTGCTGCCAAGGAGCTGAGCCATCTTTCCAAA 3980
QY      1553 TTCA---ATCAGTCCA---TA-GAGACG-AAAC---GAA-----TG-A 1583
Db      3981 CTCAGGATCA---CATGTCAGAGGAGAAACACGATCTCACTCCAAAGAGTGTGCA 4037
QY      1584 GACCTT-----CC-GG---CC-CAAGC-----GTGGC-----GCTG 1609
Db      4038 GTCCTTGACCTCGCCCTGGACACCATCAAGCAATCTCCATCGAGGAGCAATGGGCTG 4097
QY      1610 -----C-GG-----GCA-----CTTTG-----G 1621
Db      4098 AAGAAAACCTTCCTGGAGAGAGAGCCAGATCTGCGATCTTACGCTATGCTGTCTCTG 4157
QY      1622 T-----AGAC---TGTCG---C-ACCAC-----GG 1639
Db      4158 TACACACAGACTACTGACACTCTCATCAGACCTTTGTCGCTCGCAGACCCCAAGGG 4217
QY      1640 -C-GTGTG---T-TGT---GAA-----ACGTGAA-----ATAAAA 1666
Db      4218 TCTGCTGTGGAGCATCTCTGTGGAGAGCTCTCTATTACGTGGACTGTTTACACACCT 4277
QY      1667 -----GAGCA-AA-----AAA---AAA 1679
Db      4278 GGTACTGGGAGACACAGGTACACAGTGAAA 4307

RESULT 22
AK044634
LOCUS
DEFINITION
Mus musculus adult retina cDNA, 4035 bp mRNA linear HTC 20-SEP-2003
clone:A930028N13 product:ankyrin 2, neuronal long splice form
homolog [Homo sapiens], full insert sequence.
ACCESSION
AK044634
VERSION
AK044634.1 GI:26336658
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
95279253
10349636
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2
Carninci, P., Shibata, Y., Hayatsu, N., Sugawara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
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3
Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Riken integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
REFERENCE
4
Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Riken integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
REFERENCE
4

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AUTHORS

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The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

6 (bases 1 to 4035)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuya, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

Location/Qualifiers

1. -4035

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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/db_xref="MGI:2409961"

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/clone="A930028N13"

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/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

379. ->4035

/note="unnamed protein product; ankyrin 2, neuronal long splice form homolog [Homo sapiens] (PIR S37431, evidence: FASIV, 93.5%ID, 41.9%length, match=4846)

putative"

/codon_start=1

/protein_id="BAC32012.1"

/db_xref="GI:26336659"

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QY 875 -----GTCCCTTCAGCAGAAATTCAGTGTATC-AGG-----ATGACA 911
Db 2389 ACAGACATGTTACCT-TGC-----TTC-ACAAAGGAGCCAAATTCACATGTCA 2439
QY 912 A-AGACTG-----A--TTG-----AAGGAAAGA-AAGGGGTGAAAGT 945
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Db 2496 TCGGACATTCACCAACACAGGGGCGGATCGGATGCTACACAAAGCTTGGTTACAC 2555
QY 974 ATCTT-----CT-TC-----AATG-----TC-TCTCAA--- 994
Db 2556 ACCTTTGATCGTGGCTGTCACTATGGAATGTGAATGGTCACTTTCTTCTGAACA 2615
QY 995 -----C--ATGACTATGGAA-----CTACA--CTTGGTGGCTCCAA--- 1029
Db 2616 GGGAGCAATGTCAATGCGAAACCAAGAAATGGCTACACACCTT--TG--CAACAGCT 2670
QY 1030 --CAAGCTGGGCGCAC--C--AATG-----CAGCA-----TCAT 1059
Db 2671 GCCCAGAGGGCCACACACATCAATTAATGTCTCTCCAGCAGGGGCCAAGCTAAT 2730
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QY 1079 GT-----CAGC--G-AGGT-----GAG--CA-----ACG-----GCAGC 1102
Db 2791 GTGGTTGACCTCTGAAGGTTGTGACTGAAGAGGTCAACCACCACACTATCAGC 2850
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QY 1253 ATC-----AGATAT-----ATA--CAA-----ATGAAA-----TTA----- 1276
Db 3145 ATCCCGACCCAGGTTCTGCGCTAGCCAGGAGGCA--GAAAGGAATTTCTTATCGTCT 3203
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Db 3204 GAGCTGGGCACTGAGAACTTAGCAACAGTGGCTCTTTCTTCCAGTCTTATTCATTCAGG 3263
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Db 3264 TTTCCTAGTCAG--TTTATGTTGATGCCCTGGTGGTGGCCATGGAGATGACAGACA 3320
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QY 1347 -----TT-TAAAA-----AAGAA-----AT--TGAAA-----ATT 1368

Db 3377 CTTGCGGCTTGTGAAACGCCCATCGACTCGGCAACAATGCCGCCCATGTTGGAAGGAGAG 3436
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Db 3497 ACCTGCC--AAGCGTCTCCGCCCACTTAATGAGGAGAA--AGTTGGTCAGCGCATCT 3554
QY 1432 -CGCTTGAGACCCACTG---CAA-----GC--TGCACTGTGCA-----AC- 1465
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QY 1466 -----CTCTT-----TGG-----TGC-CAGTG-----TGCG--CA 1487
Db 3614 TCGCGCTCTTTCGAGGAAAGGAGGAGGAGTGTGGTCTCGCGAGTGAATAATGGGACA 3673
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Db 3674 --GCTGGAAGAGCAATTTCTGCGACTACACTGAGATG-----AATTGAACGAATCT 3725
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QY 1654 C-----GTGAA--ATAAA-AAGA-----GCAAAAAA 1676
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RESULT 23
LOCUS AK036018
DEFINITION Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630027I02 product:ankyrin 2, neuronal long
splice form homolog (Homo sapiens), full insert sequence.
ACCESSION AK036018
VERSION AK036018.1 GI:26084967
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 2049374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,

AK036018 5118 bp mRNA linear HTC 19-SEP-2003
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630027I02 product:ankyrin 2, neuronal long
splice form homolog (Homo sapiens), full insert sequence.
AK036018
AK036018.1 GI:26084967
HTC; CAP trapper.
Mus musculus
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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QY 624 AGCCTAC--G--GTTACT-----TGGAGACACATCTCT-----CC--- 654
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QY 655 -----CA--AAGCGGT-----TG--GCT--TTGTG----- 673
Db 1613 CTGGCAGGTGGAAGTGGTCCGATGTCTTCTGAGGAATGGTCTCTTGTGTGATGCCAGAG 1672
QY 674 --AGTGA-----AGAC-----GCA-----TCACCCGGAGAGCTCA-----GGGGAC-TACG 731
Db 1673 CCAGGAGGAGACAGACCTTTACACATTTGCTTCAGGCTGGGGAAGAC--GGAAATTTGT 1730
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Db 1849 GGAGCAGCCCATCTCTTAGCAGCAACAGAGGGCTTCACTCCCTGTCATGTAGCAGCAAG 1908
QY 794 TAT-----CC-----AC-----CATACAT-----TTC----- 810
Db 1909 TATGGAAGCTTGGATGTGGCAAACTTCTCTGTGA-AGTGTGACGCGCAGATTCAGC 1967
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QY 895 GTGTAC-AAGG-----ATGACAA--AAGACTG-----A--T 921
Db 2138 -TGG-ACAAAGAGCCAAATATCCACATGTCAACCAAGAGTGGACTCATCTTACACCT 2195
QY 922 TG-----AAGGAAGA-AAGGGGTGAAGT--GGA-----GTCCCTCAGCAGAAATTTCCA 894
Db 2196 TGCAGCCCAAG--AAGATAA--GGTGAACGTGGGACATTTCTACCAAAACAGGGGCGG 2251
QY 958 -T-----TTCT-CTAAA-----ACTCATCTT-----CT-TC----- 982
Db 2252 ATCGGATGCTTACACAAAGCTTGGTTACACACCTTTGTGCTGGCTGTCACTATGGAA 2311
QY 983 -----AATG-----TC-TCTGAA-----C--ATGACTATGGAA----- 1008
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Db 2372 ATGGCTACACACCTT--TG--CACCAGCTGCCAGAGGGCCACACACATCATTTAA 2426

QY 1048 TG-----CCAGCA-----TCATGCTAAT-----TGCT-----CCA 1072
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Db 2607 AATGACGG-AGGTCTTGTATGATTTTCTGATGAAGAGGGGTGATGACACTGTGACAGGTGATG 2665
QY 1117 -----CT--GC-----G-TCT--GG--C-----TG-----CTGCC----- 1134
Db 2666 GGGGAGAAATACCTCAGGCCAGAGATCTCAAGAGCTGGAGATGACTCACTGCCCAGCA 2725
QY 1135 -TC--TT-CTGG-T--CTTGAC--CTGCTTC-----TC-----A-AAATTTGAT 1169
Db 2726 GTCAAGTCTCTGGATGGCATGAACCTAC--CTTCGGTACAGTCTGGAGGGAGAA--GAT 2779
QY 1170 GTGA-----GTGC--CACTTCC-----CCA-----C--CC 1190
Db 2780 CCGACAGCTCCGGTCTCTTCACTTCCAGAGGTCTCACTCTGAGGCATGCTATACC 2839
QY 1191 ---GGGAAAG-GC-----TGCCGCCA-----CCA-CCACCA----- 1216
Db 2840 TGAGGACAGTCCCATGATTTGACGACAGGTGTGTGATCCCGACCCACAGGTGTCTGGC 2899
QY 1217 ---CCAA---CACAAAGCAAT-----GGCA-----AC 1238
Db 2900 TAGCCAGAGGAGCAAA-AGGAATTTCTTATCTGTGAGCTGGGSCACTGAGAACTTAGAC 2958
QY 1239 ACCG-----ACAG-----CA--A--CC-AATCA-----GAT 1259
Db 2959 AACGTGCTCTTCTTCCAGTCTCTTCACTCACTAGGTCTTCTAGTCTGATTTTATGTTGAT 3018
QY 1260 -----AT-----AT-----ACA-AAUGAAATTAGAA----- 1279
Db 3019 GCCGTGTGTGCTGCGCATGCGAGGATGCAGACACATGGACTCAGAAATCATATCCACCT 3078
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Db 3079 CGAAATGACACAGCCCCCAACTCGCGTCACTCGCGCTTGTGAAACGCCATCGACTGGC 3138
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Db 3139 AACAAATGCCGCCCATGTTGAGAGGAGAGGCTTGGCCAGCGCTGATTTGAAGTCCGACC 3198
QY 1310 ---GGGAG-----GG-GA-----AC----- 1320
Db 3199 TTCCGGAGCTCACTTTCTTTGGGCGCGTGTGAGATCCCTCACTTCCGCCCTCTTCG 3258
QY 1321 ---AAGAATA--CT--TTGG-----GGGA-----AAAGAG-- 1345
Db 3259 AGAAAGGAGAGGAGCTGTGTCTCGGCGAGTGAATAATGGGACAGCTGGAAGAGCA 3318
QY 1346 TTT-----TAAAA--AAGA--AATTGA--AAATTTGCTT-----GCA--GAT--ATT- 1382
Db 3319 TTTCTCGACTACCTGAGGATGAATTGAACGAAT--CCTTAATGGCATGATGAAGT 3376
QY 1383 -TAG--GTACA--A--TGA-----G--TTT-----TCTT-----TTC 1406
Db 3377 CTGACAGTCCAGAGACCTGGAAGAAACGAATCTGGCGATCATCATCTCTGACTTC 3436
QY 1407 CMAA-----CGG-----GAA--GAAC---ACAGCACCCCGCTTGGACCC- 1443
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 Db 3495 AGGGTGGAGTACTG--AGCAGCAGTGGGTGCACAGTGCAGGCGTCTTCCAGAGGG 3552
 QY 1474 TGC-----CA-----GTGTGGC--AAGGCTCAGCCT--C-----1500
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 Db 3965 GTGCCATATATGCCAAA 3982

RESULT 24
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 LOCUS
 DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330026B02 product:hypothetical von Willebrand factor type A domain containing protein, full insert sequence.

ACCESSION AK087828
 VERSION AK087828.1 GI:26104533
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
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 10349636
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REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
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 6 (bases 1 to 4728)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.

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QY	227	---CGCAGCGGAGATGCCACCTT---CCCCAAGCTATG---GA---CA---ACGTGA-269	QY	741	--CCT---CCAATG-ACGT---GG-CGCGCCCGTGG---TAC	770
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HTC; CAP trapper.
Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Carninci, P. and Hayashizaki, Y.
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Functional annotation of a full-length mouse cDNA collection
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submision

JOURNAL
REFERENCE
AUTHORS

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Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>
Location/Qualifiers

FEATURES

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SVTLIMKVDLVKVEDMNLFTLSALVCASERLDTLTVLGSARTSTVGIQGLVIALVKS
TEKMOCKVADPDIPTPLVGLSMLSTVHSSIRSLVQCGAGLTLLMSPPDMYLLQHV
RATQOCRLLRATVPELIESHSLNTPSTWEPEDHLPSSIRKLLTLTLEVSATKL
TAFVADKFTILAAESVLSNRHSGSLQAYCELAAGFDGNSIFNKEVYVQLLEEE
MILHNPFPALQTLNRNVLLSLGVSVEFFQYDFSTLDEAVQVQWKLGLHRTGTH
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LVALDASFHGVEIQRELDPGSPPEAGMDLVTCWCMKLVNVTFLVRIDYP
RYLFEIRDRMLGRGLAQEQSGQSPSRRLQIHLGLPGNVAVERNMPKPFHDFHS
EIFQYTVMGFCMDPANTLIQCVDLLTKPSADPEPPLPMDKSRLLPHGDMHDIQ
ANLQGLATDPINTTENNHEWSHLSHFHWKQFVFRGDLVDNVTASKYDCCFHL
PDLCLMDLQWLCNPHDHSVTLRAPEFLPEFLPQLHDSVAFRENSLNLKMD
LTHSGTISQPRILVYSTLRMQNFWATSTIRPICRGLFNKLKPKSGKLGQHYK
QLSTYALFPQVHYWASFAOQIQIECSQHVTRGTORGLFNKLKPKSGKLGQHYK
VTOMVSLDSQVTVHMASPTENADHCLDPLITKTHLLSLSLYQHSNRTTEELS
ARDGDAFHOLYLVDLRISWTNTNDIARGLDGYKAAVLRKGLKID
POMSAKPKGIPSAQVPPHVSFSPGDKSGSGGAYMLKLIETEDRPFVTFEE
ESGMSDQLCGIAACOTDDIYNRNCLIELVNCQVLRGAETGCVIVSAAKQLQCCQ
HPAWYGTDLKQTSWTLCDMGQYFATTESTEDQDGRQLMVEVNTAERERSLDSV
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QIKPEVHEQKEDLLKQKQGVDTFTLHHELEISTNPAQYAMILDIYNNLLHVE
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TMNLLNLYKVVLPQSCQSGRLALRFSKVRPVGISVSKHFEVNVNVLPTQ
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KQVAGQUTRSRSGVRRSPKLEPHVDIDDKMKEAAMNSFIYIKIPOVLICVSKGE
KNSVDGMDLNLVPLCEVHNNTWMLDFANVRKDSKALVAQVKEKRLKPKATGSE
VRGLKFTCDLNMQQQEEKARLLIGLSVGDKNPGKKSIFGRRK"

ORIGIN

Query Match 41.6%; Score 698.2; DB 11; Length 10481;
Best Local Similarity 36.6%; Pred. No. 0.047;
Matches 1447; Conservative 0; Mismatches 166; Indels 2342; Gaps 415;
QY 1 GT-T--GTG-----TCCT--TCAGCA--A-----AACAGTGGAT----- 27
Db 5604 GTCTCAGTGGAGTTTCTCTTATCAGTATGACTTCTCTGCAACTCTGGAGGCTGTGGGA 5663
QY 28 -TT--AAAT-----CTC--CTTG-----CACAGC-- 47
Db 5664 GTTCAGAAATGGCTAAAGGGCTGCATCGAGGGAGCTATGCTTGGGCTTCTC-CAAGCCC 5722
QY 48 -----T-----TG-----AGAG-----CAACAC----- 60
Db 5723 TGCCCTCTTCCACCTGATTACTTCTCTAAAGGTTTCAGCACTTTTCTTGGGTTTCTCTGGA 5782
QY 61 --A-ATCTATCAG--GAAA-----GA-AA--GAA--A-GAA-----AAA-AA-- 90
Db 5783 TGACATCTTTGAGGTGAAACTTTCATGATACTAGCACTGATGAAGGATGAAAGTAAGGA 5842
QY 91 -----CCGAA-----C-----CT-GA-----CAAA-----AAAG-----A-- 109
Db 5843 GAGTGCAAAAGGCTGCAGTTGCTAGATGCCAAGTGGCTGCGCCCTGCGAAGAGCAGATGG 5902
QY 110 AGA-----AAAA--GAAGA-----A-----GAA-----AAAAAATC 133
Db 5903 AGAGCTATTGCCAGCTCGGAAATATTGAGGAGCTCTAGCCCTCTTTGGAGCGCAAAA--C 5960
QY 134 A-TGAAAC--CATCAGC-----AAAA-----CAAA-----A-----TGCA 159
Db 5961 ATTGAATCTACATCAGCGCTCTCGTCGTCTCTATGGCAACACACCCATCGCCCTGCA 6020
QY 160 -----CAATT-----CT--A--TCT-----CT--TGG-----GCA-----ATC--TTCAC 186
Db 6021 CTGCTCACTTGGAGCTTGGCAGGGCTAGAGCTGGTGGCTCTAGCAGATGATCATCTTTCT 6080
QY 187 GGG-----G-----CTGG-----CTGG-----CTGG-----CTGCT 199
Db 6081 GGGCCCGAGCATGTGATAGACAGGGTTCGAGAACTGTGCTGCTGAGAGCCCTTCTTCTGCT 6140

QY 200 -----CTGTGTCTCT-----TC-----CAAG-G-AGTGCC----- 222
Db 6141 GAAGGAATGGATCT-TGTCACTCAGTGTGTCTGTATGCTCAAGTGCATGTCAAAACTTT 6199
QY 223 -C-GTGGGAGCGGAG-ATGCC-----ACCT-----TCC-----CCAA 252
Db 6200 TCTGTGTCGGATCAGAGACTAT-CCACGGTACCTGTTTGAGATCCGGGACTGGCGGTAA 6258
QY 253 -----AGCTA--TGGACA--A-----CCT-GAGC--G-TC 274
Db 6259 TGGGTGACTTGGGGCACTGAGC-AGAGTGGCCAGCCATGCTCCCGTCGACGTGAGTC 6317
QY 275 CGGCA-----GGGG-----GAGAG-----C-GCCACC-CTCAGG 301
Db 6318 CTGCACTTGGGGTTCCTCGGGGTAACTGGCAGTGAAGAAAGAACATGCCCCCACTCAAG 6377
QY 302 -----TG-----GACT--A-TT--G-ACA-A-----CC-----GG 319
Db 6378 TTTTACCATGACTTCCACTCGGAATCTTCCAGTACACAGTGTGGGGCCCATGTTGG 6437
QY 320 G-TC-----ACCC-----GTGG-CC--TGCTAA-----AC 343
Db 6438 GATCCAGCCTGGACACTGATGTTGTGTCAGTGTGAGCCTCTTGACTAAGCCTTCAGCTGAC 6497
QY 344 CGCAG-CACC-----AT-----CC-----TCT-----ATGCTGGGAATGAC 373
Db 6498 CCAGGCCACTTGTGCTGCTGGGATAGAGCGCTCTCTGTTCATG--GGGACTGGC 6555
QY 374 AAGTGG--TG-----CCTGATC-CTCGC-----GTGGT--CCT--T----- 403
Db 6556 ATATGATATTGAACAGCAAACTGCAATGAGTGGCCACTGAGGACCCCTATPAATACAA 6615
QY 404 CTGAGCAACCCCAAC--GCAGTACAG-CA-----TC-----GA-----GATC-- 439
Db 6616 CTGAG-AACATGC--ACTGGAGTGGAGCCACCTTCTTTTCATGGAACCTGTGTCAGT 6672
QY 440 -----CAGA--ACGTGGATGT-----GTATGACGAGGGC- 466
Db 6673 TTGTGTTCAGGGGACCTGGATGTCAAGTGAAGAACAGCTTCTAAGTATGACGACTGCT 6732
QY 467 -----CCTTACACTG-----CTCGTGCA-GACA--GAC-A-A-----CCAC- 499
Db 6733 GCTTCTT-CACCTGCTGACCTC--TGATGACACTGACCTACAGTGGCTGTGCCAG 6789
QY 500 -----C-CAAAG--ACCTCT-AGGG-----TCC-ACCT----- 522
Db 6790 GGAATCCTCATGATCATCAGTGTC-ACTTGAGGGGCCAGAGTTCCTGCTGAGGTA 6848
QY 523 -CATTTGCAAG-T--AT-CTC-----CCAAAT--G--TAGAGATTTCTTCAG 563
Db 6849 CCGTTGGGCGAGTCCATGACTCTACCGGGCC-----TTCCGGTCT-GAGA--ACCTCA- 6900
QY 564 ATATCTCCATTAA-----TGA-----AG-GGAACAATAT--TAGCC-----TC 598
Db 6901 ATCTCTCCATCAAGATGGAATTTGACTCGGCATGAGTGGGCAATATCCAGCCCCGAAATTC 6960
QY 599 -----ACC-----TGCATA-----GCAAC-TGG--TAG-----A 619
Db 6961 TGGGTATAGTAGTACCTCGCTGCTGATGCAGAAATTTCTGGGCNACTTGGACTAGCATCA 7020
QY 620 CCAGAGCCT-----ACGGTT-----ACTT 638
Db 7021 CAAG-GCCTATCTGTAGAGAAACTGTTTAAATACTTGAAGCCAGCAAGAAAAACTT 7079
QY 639 GG-AG--AC--ACATCTCTCC-----CA-----AAGC-----GGT----- 663
Db 7080 GGCCAGCACTACAACAGCTTCTCTATACCTGACTGTTTCCCGACCTACAGGTAATTAC 7139
QY 664 TGG-----CTTTG-----TGAGTGAAGACGA-----AT----- 686
Db 7140 TGGGCTTCTTTGCCAGCAACGGGCATCCAGATTGAGTGCAGTC-AGGGCCATGTCTT 7198
QY 687 -ACT--TGGAA-----AT--TC-AG--GGCA-----TC 706

Db 7199 CACTCGGGAACTCAGCGGCTTATACCTCAAGCTGGCACAGTGAATGCGGCGCTTATTTT 7258
QY 707 -----ACCC-----GG-GAG--C--AGTCAGGGGACTACGAGTCA--G- 738
Db 7259 TGAGTGGAGTGAACCCAGATGCTGAGTGAATTAAGTCAAGTCACT-----GTTCTCTGA 7314
QY 739 TGGCTT-----CCTAATG-----ACG-TGGCC--GC--G--CCCGTGGT-AC--GGA-- 773
Db 7315 TGGCTTCAACCCCACTGAAGAGAACGCTGACCACTGCTTGTATCTGATCCTGATCACAAGACCC 7374
QY 774 -----GAG-----TA--AAGGTCA-----CG-----TGAA-- 792
Db 7375 ACCTATGAGCCTGTCTTCCCTTACTTACCAACGGCACAGCAATCGCACCCTGAGAGG 7434
QY 793 -----CT-----ATC-----CACCA----- 802
Db 7435 AGCTTCTCTCGAGATGGTGAATCCTGCTTTTCATACACACCAGCTGATTTGGTAGATT 7494
QY 803 TAC--ATTTT-----AGAAGCCA-----AGGG-----TAC 825
Db 7495 TAGCGATTTCTCTGGACAA--CCACCAATAGGACATTTGCCCTTATATGATGCTTAC 7553
QY 826 A-----GGTGT-CCC--CG-----TG-GGAC--AAAAG--GGACACT 855
Db 7554 AAAAAGCAGCTGTACTCAACGTAATCTCTACTGAGGGCCCTGAAAGGTTTGAAGATT 7613
QY 856 G-----CAG-TGT--G-----AAGCC-----TC-----AG--C-AGTCC-- 878
Db 7614 GATCTCAGATGTAGCCAAAGCCAAAGGGGTATCCACCTAGTGGCCCAAGTCCCA 7673
QY 879 CCTCA-G-CAGAAATC-----CAGTGG-----TA-----CA--AGGA--TG-- 908
Db 7674 CTTATGTGACACTCCAGCTTCCAGTGTCTGAGGACCGCCTGATAAGGGATCATCAGAGGTGT 7733
QY 909 -ACA-----A-AAGACTGATTGAAG-----GABAGA-----AAG----- 935
Db 7734 TACATGTTGCAGAG-CTGATTTGAAGACAGACAGATTTGTAGTATTCACAGAGAGA 7792
QY 936 -----GG-----GTGA-AA-----GTGG-A-----AAACAGACCTTTCCTCT-C 966
Db 7793 ATCCGGTATGAGTGACCAATTTGTGGCATTTGCTGCTGCCGACAGAGA--TCACATATAC 7850
QY 967 A-----AAACT-CATCTTCTT-----CA-ATG--TCT-----CTGA-A 994
Db 7851 AACCGAAACTGC--CTTATGAGCTGGTTAACTGCCAGATGGTTCTTCTGAGGACAGAGA 7908
QY 995 CA-----TGAC-----TATGGG-----AA-CTACACTTGC-----GTGGCCTCCAACA 1031
Db 7909 CAGAAAGGCTGTGTCACTTGTATCGGCTGCCAAAGCT-CAGTTGCTGCACTG-----CCAACA 7963
QY 1032 -----AGC-----TGG-GCCACAC-----CAA-----TGCC-----AGC 1054
Db 7964 CCATCCAGCTTGGTATGTTGTCACACACTGAACAAAGAACTTCTCGGACTTCCCTGTTAG- 8022
QY 1055 AT--CATSC--TATTTGCTC-----CAGGC-----GCCGTGACG 1084
Db 8023 ATGGCATGCACTATTTTGGCCACCCTGAAGCAGCCCTACTGAACAGAGATGGCCGACAGC 8082
QY 1085 -----GAGGTGA-----GCAAC--GGCACGTCG-----AGG 1108
Db 8083 TCTGTTAGAGGTGAAGATATTGAGGAGCACCGGGAACTGATCTGCGACTCTGTTCCAG 8142
QY 1109 A-----GGGCAGGC--T-----GC--GT-----CTGG----- 1126
Db 8143 AGCTGATGGAAGTGGCGAGCAGTGGGAGGCATGGTTACCACAACACAGACTGGAACC 8202
QY 1127 ---CTGCTG---CC-----TC-----TTC---TGGT--CTTGCA 1149
Db 8203 AGCCAGCGGAAGCCAGCAAGCCAGCAAGTCCAGAGGATCAATTCAGTTGTAATTTG-- 8260
QY 1150 CC---TGCTTCTCAAAAT-----TTGAT--GTGAG-T-GCCACTTC-- 1184

Db 8261 CCGATG-TACT-ATATTAGTACAGCCATGATGATCTCTGAGCTAGCAACT--CAGA 8316
 QY 1185 -----CCAC-----CGGGAAA----- 1196
 Db 8317 TTAAGCCACTGAGTTTCATGAGAACCGAGAAAGAGGATCTCTTAAGAAGCAGGAAG 8376
 QY 1197 -GGCTG--C-----CGC-CA-CACCCAC-----C-ACCAACACA--AC 1226
 Db 8377 GGGCTGTGGATATCTTTTACTCTCATCCACCGAATGGAAATTTCTACCAACCAGCTC 8436
 QY 1227 AG-----CATGGCAAC-ACC-G-----AC--AGCAACCAATC--- 1255
 Db 8437 AGTATGCTATGATCTGAGCATTTGTCAACACCTCTCTCCACGTAGAACCCAGCGGA 8496
 QY 1256 ---AG-ATA-T--ATACAA-----TGA-----A-----AT--TAG-AA--G 1280
 Db 8497 AGGACATAGTGAAGAAGAACAGCGGTGAGGTTCCAGCTGGAGATCTCTAGCATCTCTG 8556
 QY 1281 A--AACA-----CAGC--CT-CA--TG--GGA-----CAGAAATTTG----- 1308
 Db 8557 AGGACAGCGCAGCAGCATACTACACCTGCAGGAGGCTGTGGCGCAG-CATGTGGCCCGAG 8615
 QY 1309 -----AGGAGG-----GGA-ACA-AAG 1324
 Db 8616 ATAAGGCACCTAGGAAGCAGATGTACTCTATGTAAGTCTTTACAGGATGACAGCAAG 8675
 QY 1325 AAT-----ACTTTGGGG--GA--AAAGAGTT---TTA-A-----AA--AAGAAA----- 1359
 Db 8676 AATGAGAAC-TTGTGGACCTGAACCAAAATCTTCAGTTACAGCTGAACCAAGAAAGGC 8734
 QY 1360 -----TTGAA-----AATG-----CCT--TGCAATATTT--AGG----- 1386
 Db 8735 CAACCTGAGCTGGAAGCGGAAGTGAACATCTCAT-CAGATGTTTAAAGGATTTCC 8793
 QY 1387 -----TACAATG----- 1393
 Db 8794 AACTGCAGCAGCAATTAATGAGCTTCGAAACCAAGGAAGATGTGAGTGTGTCTC 8853
 QY 1394 -----GAGTTT-CTTTTCCCA--AACG-----G--GAAGAA--CACAGC 1426
 Db 8854 GTCCACCGAGTTTACTTTGCTCAGCAGCTGTGGCGCTGACAGAGAGATGACAGC 8913
 QY 1427 ---ACACCCGGCT---TGG--AC-----CC--ACTGCAAG-----CTG- 1454
 Db 8914 TGGGCATC--GCTGAGCTGGAGCTACAGAGGTTCTTTTACAGCAAGGTGAATAATCTGA 8971
 QY 1455 -----CATC-----G-----TG--CAACCT----- 1467
 Db 8972 TGACACAGCAGAACATCTCTGGAGTTGGGCTGTTCACTATGACAACTTCTCCCTAA 9031
 QY 1468 --CT-----TT-----GG-----TGCCAGTGTGGG--CAAGGGCT 1493
 Db 9032 TGCTATTATTAAGTGTGTTCTTAAGGCCCCAGAGTTCTCGCCAGTCTGGAGACA--GCT 9088
 QY 1494 CAGCTCTCTGCC---CA-CAGAGTGGCC--CCAC-----GT---GG 1526
 Db 9089 -AGCC-CTCCGCTTTCAGAAAGT--CCGGCCACCTGTGTGTGTATCTCTGTAAAG 9144
 QY 1527 AACATCTGTGAG-----CTGG-----CCATCCCAA--TTCAATCAG---TC 1563
 Db 9145 AACACT-TTGAGTAATGTGGTGGCTCTCACCATCC--AGTGTCCCAACCGGTCTTC 9200
 QY 1564 CATAGA-GA-----CGAAC--AGA--ATGA-GACCTTCGG--- 1592
 Db 9201 CATAGAATGATGGGCTTTTCTTTCTGTGTCGAATGTAGAAGATGATGAGTT--GGTG 9258
 QY 1593 -----GCCCAAGCTGGCG-CTGCGG-----CACTT----- 1618
 Db 9259 ATGAAGAGGATAAGTCCAAC-TGGTGACTACTGGAATCAACCTTGAAGCCTCGGCAG 9317
 QY 1619 -TGGTAG--AC---TG-TGC--CACCAC-----GGCGTG-----T- 1644
 Db 9318 CTGATAGCAACAGATGATGACGTACCTACCTCGGGCTCCGGGAAGGGCGTGGCACAGGGCTTG 9377

QY 1645 -----GTT-----GT--GAA-----ACGTGA-----A--AT 1661
 Db 9378 ACCAGGAGTTTGGAGTCAGAGATCATTTGCCAAATTTACCTGAGCACCAGCTGATGAT 9437
 QY 1662 A-----A-AAAGAGC-----AA-AA-----AAAA 1679
 Db 9438 ATTGACAGATGAAAGAGCGAGCTGCCATGAACAACCTCTTCATATATATAAAAA 9492

RESULT 26
 AK054393/c
 LOCUS
 DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330022B15 product:OXIDOSQUALENE CYCLASE homolog [Rattus norvegicus], full insert sequence.
 AK054393
 VERSION AK054393.1 GI:26096352
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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 2 High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
 3 9279253
 4 10349636

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 2 20499374
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Db 2334 GCAACGATCCAGCCACAGTCAGTGTGCTGAGAGGAGAAACCCCTTGCGCATATGGCGA 2275
QY 633 T--TACTT--GGA-----GACACATCTCT--CC-----CAA--AGC----- 660
Db 2274 TAGTACTTCTGTAGTACGAGCAGTGTCTGGAACCTGGATGACGAGGAGCATATGTG 2215
QY 661 -----G-----GTTGG--CT-----TTGTG-AGTGA-----AGAC-GA-ATACT 689
Db 2214 GAAAAACAGAAACATGTTGTGTGCTGGGACCTGTGCTGTGATCTGGGAGACAGACTTACT 2155
QY 690 TGGG--A-AATTCAG-----GAG--ATCAG-----GGC--ATCAC----- 708
Db 2154 TCGAGCCAGTCAGTCAGCCACCATGACACCCATGAGCCCCACATGCGCTTATCACTACTAG 2095
QY 709 -----CC-----GGGAG-----CAG--TCAGGG----- 725
Db 2094 GAAATTAGATCGTCCACAGAGGGGTGAACAACCTACTCTTGGGCCACAGCTTCATGGGTTT 2035
QY 726 ACTAC--GAG-----TG--CAGT-----GC-----CTCCA----- 746
Db 2034 ACTACTCTGAGCTGCATGACTCAGTTCAAACAAACAGCAAAACAAACAGGTCTGCATGTA 1975
QY 747 -----ATG-AGCT-----GGCGGGCC-----C-GTG--GTAC--GGAG-- 774
Db 1974 TGTGATGCACTGTCAGTGGCTTCTAAAGGCC--CGCCGTCCTCAGTGATGCTCTAGAGC 1916
QY 775 AG--TA--AAGGTCAACCTG--AACT-A-TC-----CAC-----CATACAT--TT 809
Db 1915 AGGCTCTGTAGGAG--ACAGTGTGATCTACTCTTAACCCCTAGAACAAACATGGG 1859
QY 810 CAGAGCC--AAGG-----TACAGGTGTCCCGTG-----GGACA-- 843
Db 1858 CAGAGCGCGAGGAGGATCCGAGGAGCTACA-----TCCCTGTGGATCAGAGGACAGG 1803
QY 844 --AAAG--GGACACT-----G-CAGTGTGA--A-GCCT-CAGCAGT 876
Db 1802 CGCAGAGAACATGAGGACATCAGAGGAGGACGCCAGTGGATCTAGGCCCTGCAGCA-T 1744
QY 877 CC-----CCTCAGCAGAAATTCAGTGTGTA--CAAGG--A--TGACAAAG--AC----- 917
Db 1743 CCAGTGGCTCTGCAG-----CAG--GTATGCAAGGCCAGTCTGA--AAAGCGGCACATGA 1691
QY 918 TGA-----TTGA-----AGG--AAAGAAAGGGGTGAAGTGGAAAA 951
Db 1690 TGATGGGGGCTTGAAGTGGATTTGGAAGGAGGAGGAATTAAGACAGTGTG-----CTGG-- 1639
QY 952 CAGAGC--TTTCTCT-CTCAAACTCAT--CTTCT-----TCA--ATGTCT-- 989
Db 1638 CAGGCCAGGTGGTGTCT--ACATGGCTCTTGGGAGGGCACCTCAAGATGGCTTAGG 1583
QY 990 --CTGAACATGACTATGG--GAA--CTAC-----ACT-TGC-----G--T 1020
Db 1582 ATATGAACA--GGCTATGGCACTCAAGGCTACACCTCTGACTGTGCTCATTAGGCTGGCTT 1524
QY 1021 GG--CCTCCA--ACA-----AGC--TGGGCCACACAA--TGCCA----- 1052
Db 1523 GGGCTTCCACACAGCGCTTCCAGCATGAGGAACAGAAATTCGACGTAGTGAAGTGGCC 1464
QY 1053 --GCA-----T--CATGCTA--TTTGTG--CCAGG--CGCC-----GTC-A--GCG 1085
Db 1463 CCTGCAGGCGTGGCCAGCTACTCTTAGGTGACTAGGTACACCAACATGGTCTAGGGCC 1404
QY 1086 AGG-----TG--AGCAA-C-----GGC-----AC-GTCGAGG 1108
Db 1403 AGGCAGAGCAGCATGGAAGCAAGCTAAGAGGCCATCTTGGGAGACAGGACTGACAGG 1344
QY 1109 --AGGGCA--GGTCCGTC--TG--GCTGC-----T--GCC-TCT----- 1137
Db 1343 AAAGGGCAGG--GCCTCAGCTGTGAAGCGCAGGAACTCGTGAGCTTCTGCAGGCGAG 1286
QY 1138 -----TCTGGTCT--TGCACTGTCTCT-----CAAAAT----- 1163

Db 1285 GGCAGAAACTCAGGTCTGTGTGTGACCTGCTCTAAACAGTGTGTGATAGCAATGAA 1226
QY 1164 -TTT--GA--TGGA-----GTGCCACT-----TC-----CCA----- 1187
Db 1225 GTGTCCAGATCTGTGTATCCATTTGTGTCC--CTGCATTTTTCATGCCATCAAGGCCGAGCCA 1167
QY 1188 -----C-----CCGGGAAA-G-GCTGCC-----GCC-----A-----CCA-CCA 1213
Db 1166 AAGGTAAATCTTTGTATCCGAGAAACGTGCT--CTTGAAGGCCCGGGAGGATGGTCCATCCA 1108
QY 1214 C-CACCAAC--ACAACAGCA-----ATGG-C--AAC--ACCGA--C-A-GC----- 1247
Db 1107 CTGACCAACGAA--AGCATGTTGATGTTTGTGATCGGGCCGATGCTGATGCACTT 1050
QY 1248 --AACCA--ATCAG-----ATAT--ATACA-----A-----A- 1267
Db 1049 AGTGAACAGTCATCAGCTGCAATGTGTTATACAGCATCTGACGGCCCACTTCCGCGAG 990
QY 1268 -----AT-GAAA-----TT-AGAG--AAACA-----CA 1287
Db 989 GCTGCTGTATGGAACGCTTCATACAGGTTGAGGAGTCCATACACACATGCAGCAGCCA 930
QY 1288 GC-----CTCAT--GGGACA--GAAATT--TG--AGG----- 1311
Db 929 GCTGTGTGGCGTGTACATCTCATCGGGGACAGTTG--TTCTCTGGCTGGCCCAATC 873
QY 1312 GA--GG-G-----GAACAAAGATACTTTGGGGGA-----AAAGAGT-- 1346
Db 872 GATGCTGCGCTAAATCTCTGCACATAGAGTTCT--GGCGAGGCTCTGAACAGTGGGTCC 815
QY 1347 -T--TTA--A-----AAAGAAAT--GAAAT--TGCC--T 1372
Db 814 TCTGAGCACTTAGCCGAGTGGCGTAGCACTAATCATGGCAGATAGACTGCGCGCAG 755
QY 1373 TG--CAGA-----T--ATTAGGTA--CA-AT--GG 1394
Db 754 TGACACAGAGAGTGGAGGGGTGCGTGTGTACCCATTCAGAAACAGCCACATCTCAGGG 695
QY 1395 A--GT-TT--TCTTTTCCC-----AAAC-----GGGAAGAACACAGCACACCCCG 1434
Db 694 AATAGGCTGTGTAGTC--CTTCCAGCTATAAACAATTACAG--ACAGC-CAGCAG 644
QY 1435 --CTTGACCCACTGCAA--GCTG--CATCGTGA--ACCTCTTTGGT--CC 1477
Db 543 AACTT--CCCCAGGAGGAGTGGCCACC--GCACACACCTTTTGTGAAGACGTTCC 589
QY 1478 -AGTGTGGCAAGGCG-----TCAG--CC--T--C--TCTG--CCACAGAGT 1514
Db 588 GAGCGGCAACAGGTCAAGGATCATCAGGCCCAATACCCAGGATCTTGAGAGCCACATAGT 529
QY 1515 --GC--CCC--CAC-GTGAACATY--CT----- 1534
Db 528 TCAGGCGAGTCCCAACACTGTGG-AC-TTGTCTCGATGTGCAAGCCCGCCGCAATC 471
QY 1535 --GGAGCT-----GG-----CCATC--CCAAATTCATCAG--TCCA--T-- 1566
Db 470 AGGAGCTGCATGACCGCAGGATACCGCACTCTC--TC-TCTGTATCCAGCTGG 417
QY 1567 -AGAGACGA-----ACAG--AAT--GAGACT--TC-----CGGCC 1595
Db 416 CAGAGA-GATGTGTGATATGTACAGGTAATCAGGAGACTTGGCAAGAGAGAGCGGAC 358
QY 1596 CA-----AGC--GTGGC--GCT--GCGGGCACTTTGG--TA--G--ACT- 1627
Db 357 CACCATAATCACAGCCAGTGTCTCATCTCAGCCTGCACTTGGCATAAAAGTTACTC 298
QY 1628 -----GTCCCAACCAC--GGC-GTGTG--TTGTGAAA--CGTGAATAA----- 1663
Db 297 CATTCAGGGCCCCCTCATTTGGCTGTTTGGCTTTTG-GTAAAGTCGTGAATAACTTCTT 239
QY 1664 -----AAAGAG 1669
Db 238 GTGTCCAGTCCCAAGAG 221

Db 813 GCAGGTCAGAAAGAGGGACA-CGTACAGAGGAGCCCTCAAGAACGGGAGGCCCT 871
QY 308 ATG-ACA---ACC---GGG---TCA---CCCGGG----- 329
Db 872 AGTGACAGGTCAACCCAGAGGGGCTCGCTCAGGGGCTCTCAGGGACCATCCAGACT 931
QY 330 T---GGCTG--GCT-AA--ACC-GCAGCACCATCT--CTATGCT-GGGAA-- 370
Db 932 TGGAGGCTGTTCTTGAAGCACCAGCA---CCTGAGCTTTGCTGGGAATGGCCCA 987
QY 371 -----GAC---AAG---TGGT-----GCCCTGGATC 389
Db 988 CCATGCCACCTCCAGCAGTGAAGACAGGAGATGATGTTCCAGTAGGCCGGGTC 1047
QY 390 -----CTCG-C-GTGG-----TC-C-TTCTGA 407
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QY 408 -----GCA---ACA-----C-----CCAA----- 418
Db 1108 CCAGAGTGTGACAGACAGATGCTGCTGCTTTCAGGTGTTCCAGAGGGGAGATTCTC 1167
QY 419 --AC--GCAG-----TA-----CAGC---ATC---GA----- 435
Db 1168 TGACCCAGCAGCCAGCGTGCMAACCTTAACAACACAGCTGAAACAAAGAGGGGTACCT 1227
QY 436 -----GA---TCCAG-----AA-CGTG-GA---TG----- 452
Db 1228 GGCTGCATGAACATCCAGGCTCTCCCTGATAAGGGTGAGAGTTGCTTAAGCAATCCA 1287
QY 453 -----TGATACAG--AG-----GGCCT-T-----AC-----ACCT-- 476
Db 1288 GGCTTGGAGAGCGACTCAGTGTCTGGCTCTCTCCCAAGCAAGGCACTAAAGAGAA 1347
QY 477 -----GCTCGGTG--CAGA-CAGA-CAAC--CAACCAGAA-----CCTCT- 511
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QY 512 A--GGGT-----CCA-----CCTCAT--TG--TGCAAG-TATCT-- 538
Db 1406 CACTGTGTACTCCAGGCCCTTCCAGGCCCTCATCCAGCGCTGCAAGCTCTCTAGGA 1465
QY 539 -----C-CCA-AAAT--GTAG--AG--ATTCTTCAG-----ATAT 567
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QY 568 -----CTCCAT-----TAATGAAGGAAACAAT--ATT--AGCC-----TCACCTGC 604
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QY 605 AT-----AG-----C-----AACTG--GTAGACCAG-AG-CCTA-C-GGTTA 635
Db 1584 ATCGGTCACTGAAGTCTTGTCCGGGTGAACAGCAGTAG--CAGAGACCCAGCTG-- 1638
QY 636 CTTGGAG--ACACAT--CT-CT-C-CCA-AAGC-GG--TTGGC-----TT--TGTG-- 673
Db 1639 CTTGAGGTCCTTGTCTACTGACAGAGCAGGCAATTAGCCTGTGTACTGTGAGGGA 1698
QY 674 -AGT--GAAG--AC-----GA--ATA-----CTT--GGAA--ATTG-- 698
Db 1699 AAGTCAGAGCCACAAGGAGGATCTGCGGATGATATGGGTTAGGAAGACTCTGAC 1758
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QY 730 -CGA-----GTGCACTGCC--TCC--AATGAC-----GTG----- 754
Db 1818 GCGAGCTGTGAGTGGCTTTTCAAGAAATGACTCTCTCTCTCTTACTTCCAGTGGAAAC 1877
QY 755 -----GCGCGC--CCGTGGT-----AC-GGA-----G-AGTAAAG-- 785
Db 1878 TGATGCTGTGCCCGCTTCCCTGATCCATCACTGAGNAGCAAGATGAGAAACGTGTAA 1937

QY 786 CC-----G--T--GAA-CTATC-C-ACCAT----- 803
Db 938 CCAGCAACAGACTCAGAATCTATCTCTACCATGGGCCAAACCGAGTCGGACGCAAAAG 1997
QY 804 -----ACAT-----TTCAAGAGCAAGG-G----- 822
Db 1998 TACTCTCTACGTATGACATCGTATTAATACTTACAGCCTTCTG--GCCAAGAGATTCC 2055
QY 823 TACA-----GG--TGTCCCGTGGGA-CAAA-----AGGGGA----- 851
Db 2056 TACAACGAAGCAAGAGGGGAGAGTCCC---AGGAGCAAACTCAGTGTGGGGTACCTC 2112
QY 852 --CAC--TGC-----AGT-----G-TGAAGCTCAGCA-GT-- 876
Db 2113 AGCACCTTTGCTTTCAGTAGTCTGGGCTCGGATCATTTTGGATGAAG-CTCATACGTGA 2171
QY 877 --CCCTC-AG--CAGA-----ATTCCAGTG-GTA-----CAA-----GG 905
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Db 2467 GCTGCACCGGTTAAAGCTTTCTGAGGACAAGCGGGCGCTTATGACATCTTTCTGCAAG 2526
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Db 2527 GTCAAGGTGAGCTCTCCAGTCCCTATCTAAGAGACAAGAGGTAGAGGAGCCACC-ATG 2585
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QY 1074 -----GCG-----CCGT-----CAGC-- 1084
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QY 1085 -GAGG-----TG-A-----GC-AA--CGGCAC--GTC-----G 1105
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QY 1138 -----TCT-----GGT-----CTT-----GCACCTGCTTCTCAA 1161
Db 2826 CCAAGTCGATGTCAGAGGCAATCACCACCGTTAGCCTTAATGGCACATG-TT-TCAA 2883
QY 1162 -----A-----TTTTGATG-----TCAGTGCCA-----CTTC----- 1183
Db 2884 GCGCGAGCTTTTGTATGACACAGAGAGGACCAAGGTGTCTTCTGTGTCGAGAACT 2943
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QY 3064 TGGCTGTCAACCCCAACAGAGAAATGGACCTGCTGGAGCATTAAACCACTCCAGGG 3123
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Db |||||
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Db |||||
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QY 1547 ---CC-----CAATTC-ATCAGT-----CCATAG 1568
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Db |||||
QY 1669 -----G-CAAAA-----AAA 1678
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Db 4063 CCCTGTGTGTCAAAACAGCCTCAAA 4086

RESULT 28

AY402248

LOCUS

DEFINITION

AY402248

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

ORIGIN

Query Match

Best Local Similarity

Matches 1401; Conservative

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QY 53 AGCA--A-----CACA--A--TC-TAT--CAGG-----AA-AGA-----AAG----- 79

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QY 80 AAAGAAAAAACCCGACCT--G-ACA-----AAAAAGA-AGAAAAAG--AAG 120

Db 1513 AAAGCAATAAAC--ACCTCCCGTACAGGGAGGATCCCAACACAGCAAGCCATG 1569

QY 121 A-----AGAAAAAATCA-----TG-AAAAACA-----TCCAG--CCAA-----AA 154

Db 1570 ACTTATGTCAGAGAGAAAT-ATTGTGCGCAACAAAGGTTCCAGAACGACGATACGAA 1628

QY 155 ---ATG-----CACA-AT-----TCTATC--T-CTT---GGG----- 176

Db 1629 GGTGATGATTCTCATCAGATGGAAGTC-ATCAGATGCTTTCAGGGATCCTCTATAA 1687

AY402248 9022 bp DNA linear GSS 15-DEC-2003
Mus musculus COL12A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

AY402248 GI:39758234

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 9022)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 9022)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..9022

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>9022

/gene="COL12A1"

/locus_tag="HCM1160"

Query Match 41.5%; Score 696.4; DB 29; Length 9022;

Best Local Similarity 38.7%; Pred. No. 0.031;

Matches 1401; Conservative 0; Mismatches 160; Indels 2056; Gaps 403;

QY 177 ---CA-----ATCTT---CA---CG-----GG---GCTG---GCTGCT--- 199
Db 1688 AACTCAGGAATCCGACGCTGGAGATCTTCGCACTCGGTGTAAGGAGCGCTGTC---GCTCA 1746
QY 200 ---CTG---TG---TCTCTTCCAG---GAGTGCC---CGTG---CGCAGCGGA----- 235
Db 1747 GNACTGGAGCCATTTGCCCTCTCTCTCC---TGCTGAGACCCACGCTGTTTCAAGTGAGGATTT 1805
QY 236 ---GATGCC-----ACC---TT---C---CCCAAAG-----CT-----ATGGA---CA 263
Db 1806 TGATSCCTTTTCAGAGATATCATTTGAACTCACAGATCCATCTCTCTTAGAATTTGAGCA 1865
QY 264 AGTGACGCTCCGCGAG-----GGGAGAG---CG---CGACC----- 295
Db 1866 A---GA---GT---TGGCAGCTATAAGAAAGAAAGCTTTACGTTCCACCAAGAGATCTGAGGTT 1919
QY 296 ---CTCAGG---TGC---ACTA---TTGACAA---CCG---GGTACCCGGCTGGCTGGCTAA 341
Db 1920 TACTCAGTAACTGCTAATAGTTT---CAAGCTGAATGCTCTCC---T---CCTGG---AG 1969
QY 342 AC-----CGCAGCAC---CATCTCTA---TGC---TGG---GA---ATGA---CA 374
Db 1970 ACAATGTCTTTTCGTATCACGTACATAC---AAGGATGCTAATGCTGATGATGAGTCA 2026
QY 375 ---AGTGGT---GCCTGGATCCTC---GC---GTGGTCTCTTGAGCAACACCC----- 416
Db 2027 CAGTGGTGGGCC---AGCCTTCCAGCACTAGT---GTTGTTCT---CAACAACTCAGGCGCA 2079
QY 417 ---AAACGCGAGT-----ACGATCTGAG---ATCCAGAACGTTGAT---GTG--- 454
Db 2080 GAAACCTGTACTTGGTGAATGTACAGC---CGAGTAT---GAGGAC---GGCTTCAGTGTTC 2134
QY 455 ---TATGAC---GAGG---GCCC-----TT---AC---ACCTGCTCGGTG 484
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QY 516 ---TC-----C---ACC---TCAATGT-----GCA-----AGTAT 536
Db 2251 TTAAGGTATCGGATTAGATACAGACCACTTTC---TGGTGGAGAAAGCAAGAGTGAGTA--- 2308
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Db 2309 C---CCAGCCAAT---CAGAGGAGGAAACA---CTGGAGA---ATCTGAGCGCCGACACAAA 2361
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Db 2476 ACACAT-----CAACGCTGAAGTTGTC---TTG---GAGTAGGGCACCAGAAAGGTGAAGC 2527
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Db 2528 AATATCTTG---TCA---CATACCCAGCAGAGGAGGTGAAGTCAAGAGGTGCAC 2579
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QY 833 CCCGTGG-----GAC---AAA---AGG---G---GACA-----CTGCAG---TG- 861
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Db 2931 A---ACTTACAGCAGTGG---AGMAGGAGAGCCCGTGTACCCGAGATGCCACACTGATTTATCT 2988
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Db 2989 CAGATTTCCAAATCTTAAAGATGGATGAAGAAACAGAACACA---CGATGAGAGTTACCTG 3047
QY 947 GAAACACAG-----ACC---TT---TC---CTCTCA----- 968
Db 3048 GAAAGCAGACCCGGGAAAGTCTGCACTACCGTGTGTGTATCGCCCTCAAGGGGGTGG 3107
QY 969 -----A---AC---TCATCTT-----CTTC 982
Db 3108 GAGGCAGATGTTGCTAAGGTGCCACCCACGGTCA---CTTCAACAGTGTCTAAAGAGACTTC 3166
QY 983 A-----ATG-----TCTC---TGAACATGACTATG---GGAA--- 1008
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QY 1009 CTACACTTGGTGGCCTC---CAACAAG---CTG---GCC---ACACC--- 1045
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QY 1127 -----CTG-----CTG---CC-----TCTTCTG-----GTCT 1145
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Db 4043 CTGATCCAGATGACACTCACGCATACAAATGTGGCAGATTTTGTGATCATTTGTC--AA-GA 4099
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QY 1638 -GG--CGTGTG-TTGTGAAA-----CG-----TG--AATA-AAAA----- 1666
Db 4757 GGAACCTGTGCTTG-GAAAGTTTGCAGATGACATTTGTTAGATACAAAACCTCCAGATGAG 4815
QY 1667 GAG--CAAAAA--AAA 1678
Db 4816 GAGTTCAAAGAGGTAGA 4832

RESULT 29
AK086942
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
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AK086942 4379 bp mRNA linear HTC 20-SEP-2003
Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
library, clone:E030013G06 product:hypothetical von Willebrand
factor type A domain containing protein, full insert sequence.

AK086942 GI:26352266
HTC; CAP trapper.
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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99279253
10349636

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20530913
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5

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6 (bases 1 to 4379)

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Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>.

COMMENT

FEATURES

source

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polyA signal

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4378	

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ORIGIN

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Db 362 AAAGTGCAATTTCACCACCCAGACCATCCACCATTCA-AGTCAAGGCTTTCTGACACTAT 420

Qy 61 --AA-TCTATCAG--GA-----A-AGAA-AGAAAGAA-----85
 Db 421 TGAACCTCTATCAGCAGAGGATCGGTGGCTCAGAGAACGACGAAAGGCATTGGCCCT 480

Qy 86 --- AA --- AA-A --- CC --- GA-ACCT --- 98

Df
Qy
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481 CATCAAGGGATCAAGAGTGGGCGCTCCTCTCATAGATTCTTCGACGTCCAGCACGCCGTCTCA 540
99 GACAA-----AAAA-GA-----AG-----A-AAAAGAAG-----AAGAA 125
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
182 T----TCA-C-GGG--GCTG--G-CTGC--TCTG-----TGTCT--CTTC--CA 213
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 AGSAGTGC--CCGTGGCAGCGAG-----ATG--CCACT----- 245
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246 TC-----CCC-----AA-----AG-----CTATGG-----ACAACG 266
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
267 TG--ACGTTCGG--CAG-----G--GGGA-----GAGC-----G-- 290
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291 --CCAC-----CCT--CAGGTGA--CT-----AT-- 309
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1016 ACCCAAGGCTCAAGGCGCTCTCAGCCAGGTGCAAGCCCTGTGCCACAACAACCCATGT 1075
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
310 -----TGA-CAA-----CC---GGG-----TCACC 325
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1076 GAAGAGCTGTCTCATGATCAAGAGATCTCCATAGAGATTGCCAAGGCGCGTTCAAC 1135
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326 CGGGTGGCTTGGCTAAACCGC--AGACCA--TCCTCT--AT-----G--C 363
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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364 TGGCAATGACAAG--TG--GTGCTTG--GATC-----CT--CGC----- 394
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395 --GT-----GGT-----CCTT-----CTGAGCAACA-----CCCCA- 417
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1249 AAGTCTTTATCAGTTCTGGCACCCACGCTTTAATCTGTGGAGAAATTTGTGCCCAT 1308
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
418 -----AACGCAGTA-CAGC--ATC--GAGA-----TCCA--GAACGTGG 449
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1309 TCTCCAGAAACAGTAGCAGCTACTATCCATGAGAAAGCAATGGTCAAAATTTGAA--TGS 1366
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
450 -ATG-TGTA--TGACGA-----GGGCCC-----TT-A----- 471
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1367 CATTATGGAACAGTGAAGATATCCATGTGGACCCACCGCTCTCTTTGAGTACCAGAAG 1426
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
472 CACCTG-----CTCGGTGCAGACA--GA-CA-----A-----CC-ACC- 500
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1427 CAACTGGGAAAGCT--GTGCAGATATGAGCATCGGCTCCAGTGGCTCTCCCTGACCA 1484
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
501 -CA-AGACCTCTAGGTTCAAC-----TC-----ATTG-TGCAAGTAT 536
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1485 GCAGAAGA-ATCTGGGG--CACCGTCTGTCAAAGAAGGGTGGTTATATTGCTGGA--TGT 1539
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
537 CTC-----CCAAAT--TGTAGATTTCTTCAGATAT-----CTCC-----ATTAA 576
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1540 CTGCGTGACC--AAITCCANGTACA--TTATTC--ATATCAGACATCTCCCTGCAGTAC 1592
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Db	1652	ATTGAGAGCTGG-AGGCCGGAG--ATGGTTGCTGTGAGCCATGACAACT-T-ACAAAGA 1705
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Db	1706	GCCTGCGCGTGGGCCCTGGGCGCTGCAGTGTCAAGGAAGCAGAAATGTCTCTGGAGCGCCTC 1765
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Db	1826	CTCTTACCGGGGTATCCCTGACCAAGATGTGCACATACTCAGCGCGCTATGTGGCAGAG 1885
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Db	1886	GCCTATGGGGGTGGGACCTCCAGCTAAATGTCTGTCTCTTATGTGGGCGCAACCCACAG 1945
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Db	1946	ATGGACACCACACCCCTGCCTGCTACGCCAGCGTACTGCACCTGTACTTGCCTACAA 2005
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Db	2006	GAGATCACCCAGGCTGCCGTGGTTCCTCACTGGTTTGGAGAG-ACAGGTATTATGA 2064
QY	786	CCGTGA--ACTATC--CACCATACATTC-----AG--AAGC--CAAGGGTAC-----825
Db	2065	AAGTGATGA-TATCAA-GCCAT-CGTATCTGAGATAGAGAAAGCCCTCAA-CTACTCCC 2120
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Db	2121	AAAAGTGTGCTTCTCTTTGTGGCCTCTCTGAAGAACCACTTCAGAAAA--GA-CTTGCAG 2176
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Db	2237	TATCCTCCCAAGCCACAGCCCTCTCGTGGCAGAAATGAGCATTAAGATGGCTTAGAT 2296
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Db	2476	TCAAGGAAAATCTATTAGAAGGATTAATTTCTCCAT--CCAGCTGCCAGGAGAGACACA 2533
QY	1015	--TTGC-----GTG-----GCC--TCCA-----AC--AAGCTGG-----1037
Db	2534	GTTTGTCAAGTCAAGAGTGGACAGCCACTTGCAGGCTGAAGAGACTGAAGCTGGAGCTC 2593
QY	1038	-----GCC-----AC-----ACCAA-----T-----GCCAGCA-T-----1056
Db	2594	TCCAAATGCTTGGTCCCACTGTAGATATCAAAAGTCAGTACGGGGGCTCCAGCACTGGCG 2653

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Db	2654	GAAC	CTG	CAC	TCT	CTCT	CCCC	AGT	ATAG	AGAT	CAAT	GGG	AGT	AGT	AGT	2713
QY	1075	-CGC	----	----	----	CGT	----	CA	GC	----	GAG	----	GTGA	----	----	1092
Db	2714	ACACT	TGTGG	GAGATGG	AAACGTACAT	CA	TG	AGTGG	AGAG	AGTGG	AC	AGT	TGCTAT	GTG	----	2773
QY	1093	CA	A	----	CGGCAC	----	GTCC	AGG	AG	----	GGCAGGCT	----	G	----	CGTC	1126
Db	2774	CAGAG	CGTGC	ACTGCTGCT	TGCGG	AGCGCG	CGAGGCTAT	TT	GG	CA	CACTTT	TTGG	AAAG	2833	----	2833
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Db	2834	AATGT	GTGCAT	CTCTGCT	GTGAC	ACCTCTGGGT	TCAT	TGG	CGCC	CCCC	CACTTGC	AGTGG	ATAA	AG	----	2893
QY	1149	AC	----	CTGCTTCT	CAAA	TTTT	----	TGA	----	TTGTG	----	AG	----	----	----	1176
Db	2894	ACAGAG	CTCGTT	CTACTG	ATTTGG	GAGAGCT	TG	AG	AAAG	CAC	TGTG	CCAG	GTTC	AACTG	----	2953
QY	1177	C	CA	----	CTT	----	CC	----	C	----	CAC	CCGG	----	GAA	----	1200
Db	2954	CTCAG	CTTGG	CAGAG	CACTAC	AGCTGTG	GCAG	CA	CGCTGTG	TAG	AAAG	CAC	AGG	CT	----	3013
QY	1201	GC	----	C	----	GC	----	CA	----	CCACC	----	ACCAC	----	----	----	1218
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QY	1219	----	----	AACACAA	----	CAG	----	CA	----	ATG	GC	AA	----	----	----	1244
Db	3074	TTAGC	AGCAT	T	TAACGA	AGCCTTCAG	CTTTCAG	ATG	TGC	AG	ATG	TGC	AG	ATG	TT	3133
QY	1245	----	AG	CA	AC	CAA	----	T	CAG	----	ATATAT	CAAA	----	A	----	1280
Db	3134	GATGG	AAAGC	CAG	ACAA	CGTGC	AGCTTAT	ACT	CA	CACTCTCC	AAAGCTT	CCAG	AG	3193	----	3193
QY	1281	----	AAA	----	C	AC	AGC	CTC	ATG	----	G	GA	CAG	AA	----	1304
Db	3194	GAGAG	GGCGTGA	AAAGTG	CA	TACTAT	CTCTC	TG	ACC	AG	CGAG	CA	GA	CAAC	AG	3252
QY	1305	TT	----	TCAGGGA	----	GGG	GA	CAAG	----	AATACT	----	TT	----	----	----	1332
Db	3253	GTTC	CTCAG	GGAGCTGG	CTCC	CTCAG	TGGGGC	----	GT	TACC	ACTG	CCCTGT	TAG	CGA	3309	3309
QY	1333	----	GG	----	G	GGGA	----	AA	----	AGA	----	GT	TT	AAAA	AAAA	1363
Db	3310	CAAGG	CCCTCAG	TGGGAT	CAAG	GT	TGCTC	ACC	AGAG	GT	TTCAT	CAG	AA	AGG	ATCC	3369
QY	1364	AAAT	TGCC	----	TTGCA	----	GAT	A	TT	TAGG	----	TACA	AT	----	----	1399
Db	3370	CAAA	TG	CCACT	CTTTGA	AGGCGAT	CACTTG	AG	GT	TAC	----	TTAC	CCAG	TT	CCACC	3427
QY	1400	TC	----	TTTCC	CAAA	GGG	GA	CA	CAC	AG	----	CACA	CCGG	CT	----	1439
Db	3428	GGCT	AG	AAATCT	CTCT	CAA	----	GCAAG	----	CCC	AG	GTCTT	CAC	AT	CCAG	3482
QY	1440	ACC	CA	CTG	----	CAA	----	GTGCA	----	TC	----	GTG	CA	AA	----	1468
Db	3483	ACT	AA	CATGA	ATCAA	AGGTTACT	CTTCTG	CT	CAC	AG	ATG	TTCT	CC	AGT	----	3540
QY	1469	TT	----	TGGT	----	GCCA	----	----	----	----	----	----	----	----	----	1487
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QY	1488	----	----	AGG	----	GC	----	TCAG	----	CCCTCT	----	----	----	----	----	1501
Db	3601	CCC	AT	CC	AGG	CTCTAG	GAAG	ATCG	ATG	CTTCTG	GGCTT	CTCT	CT	CTG	TTG	3660
QY	1502	----	C	----	TGC	----	C	----	CAG	AG	TTG	----	CCCC	CA		

Db 218 TGGAGGCTGTTCTTCCGATGTGCTAGAACCAAGCGGAGGGGAAGCAGTGTGTGGAAAC 277
QY 24 -----GGAT--T-----TAAA-----TCTCTTTG-----CA-CAAGCTTGAG- 52
Db 278 GTCCCATGGCGGAGGATCTTAACCTTAAGAACTCTC--TGTAACCAAGTAAGCCTCAGC 335
QY 53 AGC-----A--ACA-----CAATCTATCAGGAA-----AGAAA-----G--A 80
Db 336 AGCCATCTGAGTCACAGCTTCACTCTCCAGCCAGCCGAGAAACCCATTAGGTGTCTTA 395
QY 81 A--AGA-----AAAAAC-----CGAAGCTGACAAA-----AGA-----AGAAA--- 114
Db 396 ACAAGATCAAAAACACTCGAA--TGAATAACAGTTTGTGCAAGAGAGGTGAGAGAAAGAC 453
QY 115 -----AAGAA--GA-AGAAAAA-----ATC-----ATGAA-----AA 140
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QY 141 --CC--ATC-----CAGCCAAAATGACAAA-----T--TCT-ATCT-----CT--- 172
Db 514 GCCCAATCTAACAGC--AGGATGGAGAGACCCCTCATCTGACCTTGGTGGCAACTAGA 571
QY 173 -----TGG-----GCATC-----TTC-----AC-----GGG- 189
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QY 190 GC-----TGCT-----GCTCT-----GTGTCTCTT-----CCAAG 215
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QY 216 -----GAGTG-----GAGTG-----CCCG-----TGCGCAGCG-----G 234
Db 689 GGTCTCTACATGTACAGAGAGTGAGAGTCGAGGGGTCCCGAACCAAGC-CAGAGACTCTGAG 747
QY 235 AGA-----TGCCA-----CCT--TC-----CCC--AAAGCTATGG 260
Db 748 AGAAAGGAACCCAGCTTTTGTGCAAGTGTCTTGTGTCAGACCCAGAAAGC- AAGG 806
QY 261 AC-----AAGTGACGTC-CG-----GCAGGGGAGAGCGCACCTCA-----GGTG-- 303
Db 807 TCCAGAAA-----GAGGGACAGTCAGCAGG--GAGC-----CCCTCAAGAACGGGAGGC 855
QY 304 CACTATTG-ACA-----ACC-----GGG-----TCA-----CCCGG----- 329
Db 856 CCTAGTGACAGGTCAACCAAGAGGGGCTCGCTCAGGGGCTCTCCAGGGACCATCCAA 915
QY 330 ---T---GGCCTG--GCT-AA--ACC-GCAGCACCATCCT--CTATGCT-GGGAAT-- 370
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QY 419 -----AC--GCAG-----TA-----CAGC--ATC-----GA----- 435
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QY 436 -----GA-----TCCAG-----AA-GTGG-GA--TG----- 452
Db 1212 CCCTGGCTGCAGTGAACATCCAGGCTCTCCCTGATAAGGGTGAGAGTTGCTTAAGCAAA 1271
QY 453 -----TGTATAGC-----AG-----GGCCCT-T-----AC-----ACCT--- 476
Db 1272 TCCAGGCTTTGGAGGAGCGCACTCAGTGTCTTGGCTCTCTCCCCAGACAGAGCACTAAG 1331

QY 477 -----GCTGGTG--CAGA-CAGA-CAAC--CACCCAAAGA-----CC 508
Db 1332 AGAAGTGCAGCGCTCAG-GAACCAAGAGCAGAGCAACATCA-CCAAAGCTGCTGCTGCCCC 1389
QY 509 TCT--A--GGGT-----CCA-----CCTCAT--TG--TSCAAG-TATCT 538
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QY 539 -----C-CCA--AAATT-----GTAG--AG--ATTTCTTCAG----- 563
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QY 632 GTTACTTGGAG--ACACAT-CT-CT-C-CCA-AAAGC-GG--TTGGC--TT--TGTG-- 673
Db 1626 G---CTTGAAGTCCCTTGTACTGCAACAGAGCAGGCATTAGCTGTCTTACTGTGGA 1682
QY 674 ---AGT--GAAG--AC-----GA--ATA---CTT-GGA--ATTG 698
Db 1683 GGGAAAGTCAGAGCCACAGGAGGATCCTGGCGGATGATATGGGCTTAGGAAGACTC 1742
QY 699 ---AGG--GCA-TCAACC-----G--GGAGCAGTCAG-----GG-G 725
Db 1743 TGAATGATTGCACTCATCTTAACCAAGAGATCAG-CAGAAAGCAGAGAAAGGAG 1801
QY 726 ACTA-CGA---GTGCAGTGCC--TCC---AATGAC-----GTG-- 754
Db 1802 AGAAGCGAGCTGTGACGTGGGCTTTCCAAAGATGACTCTCTGTCTTTACTTCCAGTGGA 1861
QY 755 -----GCCGCGC--CCGTGGT---AC-GGA-----G-AGTAAG----- 781
Db 1862 AACTGATCGTCTGCCCCCTTCCCTGATCCATCTGGAAGAACGAAGTAGAAGT 1921
QY 782 GTCACC-----G--T--GAA-CTATC-C-ACCAT-----AC---ATTTGAG-AAAGC 816
Db 1922 GTAACCAAGCAAGACTCAGAACTCTATCTTACCATGGGCCAAACCGGA-GTGGCAGCG 1980
QY 817 CAGG-----GT---ACA-GGTG-----T---CC-----CCGTGGG----- 840
Db 1981 AAAAGTACTCTCTAGTATGACATCTGTATTACTTACTACGCTTCTGGCC-TAGGAGA 2039
QY 841 -----ACAA-----AAG-GGGA-----CA---CTGCAGTGTGAAG---CC 868
Db 2040 TTTCTACAAGCAAGCAAGGAGAGGTCCCAAGAGCAAACTT-CAGTGTGAGGGTACC 2098
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Db 2099 TCAGCACCCTTCTTCCAGGTAGTCTGGGCTCGGATCATTTTGGATGAAGCTCATTAACGTG 2158
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QY 927 -----GA-----AAGA--AAGG-----GG----- 938
Db 2279 CTCCTGTGCTCCCATTTTGAATGAGTTTCACTTTTGGAGAGCAGGTTGACAAATGTTCA 2338
QY 939 -TGAA---AGTGGAA-----AAC--AGA--CTTTTCT-CT-----CAA 968
Db 2339 ATGAAGAGGGGGAACGGTTAAGCATTTTAAACCAAGAGCCTTT--TGCTGAGGAGAACAA 2396

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 14:04:04 ; Search time 4221.99 Seconds
(without alignments)
10625.327 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 0.1

Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0
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Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1035	100.0	1679	6	AX358872	Sequence
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3	1035	100.0	1679	6	AX403748	Sequence
4	1035	100.0	1679	6	AX454470	Sequence
5	1035	100.0	1679	6	AX464242	Sequence
6	1035	100.0	1679	6	AX490948	Sequence
7	1035	100.0	1679	6	AX358331	Homo sapi
8	979.3	94.6	1839	9	AX665342	Sequence
9	973.9	94.6	1839	9	AF126426	Sequence
10	973.9	94.1	1068	6	AX665344	Sequence
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12	966.7	93.4	1140	6	AX665348	Sequence
13	910.3	88.0	1325	9	BC050716	Homo sapi
14	833.7	80.6	2040	10	RNU16845	Sequence
15	829	80.1	1615	10	BC023307	Sequence
16	814.4	78.7	1410	10	AF282980	Mus muscu
17	690	66.7	1257	5	GGCEPUI	Sequence
18	681.3	65.8	1638	12	AF271233	Synthetic
19	673	65.0	1035	5	AB011810	Gallus ga
20	669.6	64.7	1058	5	AF292935	Gallus ga
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22	636.9	61.5	6380	9	HSM805672	Sequence
23	633.8	61.2	1478	9	HUMORCAM	Sequence
24	633.8	61.2	3110	6	AX665340	Sequence
25	632.4	61.1	3216	5	GGCEPUS	Sequence
26	629.5	60.8	2593	4	BTBOCAM	Sequence
27	628.7	60.7	2935	12	AF271618	Synthetic
28	619.1	59.8	2179	10	RATCALMB	Sequence
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30	616.2	59.5	3069	10	RATCALMA	Sequence
31	613.5	59.3	1533	5	FFNINH55A	Sequence
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46	481.1	46.5	1757	6	AX704805	Sequence
47	481	46.5	191071	9	AP004248	Homo sapi
48	479.9	46.4	184716	2	AC018368	Homo sapi
49	476.8	46.1	1017	9	HSU41901	Sequence
50	471.5	45.6	248329	2	AC109989	Sequence
51	471.2	45.5	187203	2	AP000832	Sequence
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53	470	45.4	202505	2	AP000912	Homo sapi
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55	469.2	45.3	176676	2	AC012234	Homo sapi
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63	461.5	44.6	2455	5	AF241637	Danio rer
64	458.5	44.3	170006	9	AP005122	Homo sapi
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C	66	456.2	44.1	186110	2	AC102204	AC102204 Mus muscu
	67	455.9	44.0	1809	10	AB017139	AB017139 Rattus no
	68	453.7	43.8	945	6	AR030580	AR030580 Sequence
	69	452.7	43.7	258847	2	AC112746	AC112746 Rattus no
	70	452.1	43.7	110000	2	AC110642	Continuation (3 of
	71	451.9	43.7	156795	9	AC105267	AC105267 Homo sapi
	72	451.9	43.7	170302	9	HSJ402N21	AL049553 Human DNA
	73	451.9	43.7	171181	9	AC104190	AC104190 Homo sapi
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	76	451.4	43.6	8405	10	AF221622	AF221622 Rattus no
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	79	450.3	43.5	5117	6	AX880897	AX880897 Sequence
	80	450.3	43.5	5117	6	BD158655	BD158655 Primer fo
	81	450.3	43.5	5117	9	AK023836	AK023836 Homo sapi
	82	450.3	43.5	183252	2	AC023637	AC023637 Homo sapi
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	86	450.1	43.5	3492	9	HSU34227	U34227 Human myosi
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	88	450.1	43.5	4510	9	MACAPOA	U04635 Rhesus monk
	89	450.1	43.5	7368	9	HSU5208	U55208 Human myosi
	90	450	43.5	4376	8	DSU77059	U77059 Dunaliella
	91	450	43.5	186792	2	AC116523	AC116523 Mus muscu
	92	449.9	43.5	348517	1	EX248354	EX248354 Corynebac
	93	449.4	43.4	8461	10	AB035201	AB035201 Rattus no
	94	449.4	43.4	214732	10	AC114005	AC114005 Mus muscu
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	96	449.3	43.4	163475	9	AC092619	AC092619 Homo sapi
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ALIGNMENTS

RESULT 1	AX358872	Sequence 125 from Patent WO0193983.	1679 bp	DNA	linear	PAT 13-FEB-2002
LOCUS	AX358872					
DEFINITION	AX358872					
ACCESSION	AX358872					
VERSION	AX358872.1	GI:18675337				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						

Query Match	100.0%;	Score 1035;	DB 6;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 3.6e-06;		
Matches 1035;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAAACCATCCAGGCAAAATTCATCTCTTGGGCAATCTTACGCGGGCTG	60	
DB	134	ATGAAAACCATCCAGGCAAAATTCATCTCTTGGGCAATTCACGCGGGCTG	193	

QY	61	GCTGCTCTGTGTCTCTTCCAAAGAGATGCGCGTGGCAGCGGAGATGCCACCTTCCCAAA	120
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QY	121	GCTATGACAAACGTGACGCTCCGCGAGGGGAGGCGCCACCTCTCAGGTGCATTTGAC	180
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QY	181	AACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTCTATGCTGGGAATGAC	240
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QY	301	GAGATCCAGAACGCTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	360
DB	434	GAGATCCAGAACGCTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
QY	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG	420
DB	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG	553
QY	421	ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTACCTGCTAGCAACT	480
DB	554	ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTACCTGCTAGCAACT	613
QY	481	GCTAGACCAAGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTTG	540
DB	614	GCTAGACCAAGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTTG	673
QY	541	AGTGAAGACGAATACHTTGAATTTAGGGATCAACCGGGAGACGTCAGGGGACATACGAG	600
DB	674	AGTGAAGACGAATACHTTGAATTTAGGGATCAACCGGGAGACGTCAGGGGACATACGAG	733
QY	601	TGCAGTGGCTTCCAAATGACCTGGCGCGCGCTGGTACGGAGAGTAAGTACCGTGAAC	660
DB	734	TGCAGTGGCTTCCAAATGACCTGGCGCGCGCTGGTACGGAGAGTAAGTACCGTGAAC	793
QY	661	TATCCACCATATATTTTCAAGCAAGGTAAGGTGTCCCGTGGGACAAAGGGGACA	720
DB	794	TATCCACCATATATTTTCAAGCAAGGTAAGGTGTCCCGTGGGACAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAA	780
DB	854	CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAA	913
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QY	841	ATCTTCTTCAATGTCTCTGAAACATGACTATGAGAACTACATTTGGTGGCTTCCCAACAG	900
DB	974	ATCTTCTTCAATGTCTCTGAAACATGACTATGAGAACTACATTTGGTGGCTTCCCAACAG	1033
QY	901	CTGGGGCCACCAATGCGCAGCATCATGCTATTGGTTCAGGGCGCGTCAAGCGGTGAGC	960
DB	1034	CTGGGGCCACCAATGCGCAGCATCATGCTATTGGTTCAGGGCGCGTCAAGCGGTGAGC	1093
QY	961	AACGGCAGCTCGAGGAGGCGCGCTCGCTCTGGCTGGCTCTTCTGTCTTGGTCTTGGCCTG	1020
DB	1094	AACGGCAGCTCGAGGAGGCGCGCTCGCTCTGGCTGGCTCTTCTGTCTTGGTCTTGGCCTG	1153
QY	1021	CTTCTCAAAATTTGA	1035
DB	1154	CTTCTCAAAATTTGA	1168

RESULT 2
AX362365
LOCUS

AX362365 1679 bp DNA linear PAT 15-FEB-2002

DEFINITION Sequence 125 from Patent WO0208288.
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1035; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTGGCAATCTTCACGGGGCTG 60
DB 134 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTGGCAATCTTCACGGGGCTG 193
QY 61 GCTGCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
DB 194 GCTGCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGGACAGTGCAGCGTCCGCGAGGGAGAGCGCCACCTCAGTGCACTATTGAC 180
DB 254 GCTATGGACAGTGCAGCGTCCGCGAGGGAGAGCGCCACCTCAGTGCACTATTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCCTCTATCTGCGGAATGAC 240
DB 314 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCCTCTATCTGCGGAATGAC 373
QY 241 AAGTGTGCTGTGATCTCTGCGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
DB 374 AAGTGTGCTGTGATCTCTGCGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAG 360
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAG 493
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DB 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATGTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
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LOCUS Sequence 103 from Patent WO0077037.
DEFINITION AX403748
ACCESSION AX403748
VERSION AX403748.1 GI:21437184
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Gurney, A., Kljavin, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;
Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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Sequence 55 from Patent WO0208284.
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GI:21713859
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 55 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US);
Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
I. (US)

FEATURES

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Best Local Similarity 100.0%; Fred. No. 3.6e-06;
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DEFINITION Sequence 375 from Patent W00140466.
ACCESSION AX464242
VERSION   AX464242.1 GI:21899137
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE
AUTHORS   Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
            Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
            Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
            Wood, W.L. and Zhang, Z.
            Secreted and transmembrane polypeptides and nucleic acids encoding
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TITLE
JOURNAL   Patent: WO 0140466-A 375 07-JUN-2001;
            Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
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DEFINITION Sequence 55 from Patent W00200690.
ACCESSION AX490948
VERSION   AX490948.1 GI:22323811
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ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
            Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
            Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
            and Ye, W.
            Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
            Patent: WO 0200690-A 55 03-JAN-2002;
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
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ACCESSION AY358331
VERSION AY358331.1 GI:37181786
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,B., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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DEFINITION	Homo sapiens neurotrophin (HNT) mRNA, complete cds.
ACCESSION	AF126426
VERSION	AF126426.1 GI:7158997
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE	1 (bases 1 to 1839)
AUTHORS	Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
TITLE	Cloning and identification of human neurotrophin full length cDNA
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1839)
AUTHORS	Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
TITLE	Direct Submision
JOURNAL	Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
	Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
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DEFINITION Sequence 106 from Patent WO03002765.
ACCESSION AX665348
VERSION AX665348.1 GI:29290467
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
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AUTHORS Sellar, G.C. and Gabra, H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 106 09-JAN-2003;
Cancer Research Technology Limited (GB)
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LOCUS Rattus norvegicus neurotrimin mRNA, complete cds.
DEFINITION Rattus norvegicus neurotrimin mRNA, complete cds.
ACCESSION U16845
VERSION U16845.1 GI:755184
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 2040)
Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
and Salzer,J.B.
Cloning of neurotrimin defines a new subfamily of differentially
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JOURNAL expressed neural cell adhesion molecules
MEDLINE J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
PUBMED 95198094
REFERENCE 2 (bases 1 to 2040)
AUTHORS Salzer,J.B.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
Center, 550 First Avenue, New York, NY 10016, USA
FEATURES
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IMAGE:4480983), complete cds.
ACCESSION BC023307.1 GI:23958300
VERSION MGC.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1615)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
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Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
PUBMED
2 (bases 1 to 1615)
Strausberg, R.
Direct Submission
TITLE

JOURNAL

REMARK
COMMENT

Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcaps-x@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loughsseg, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, R.G., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAX Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it
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Query Match 80.1%; Score 829; DB 10; Length 1615;
Best Local Similarity 85.4%; Pred. No. 0.0087;
Matches 908; Conservative 0; Mismatches 101; Indels 54; Gaps 13;
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Db 40 GAGAAATGGGGGTCTGTGGGTACTCTTCTCCCTCGGAAGTGC-----CTCGTGG 89
QY 43 ----GCAATCT--TCACGGGGCTGCTGTGTGTCTTCTT-----CCA-AGGAGTCCCGT 92
Db 90 TCGTG---TCCTCTCA-----GGCTGTAT---TC-CTTGATCCACAGGATGCCGT 135

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DB 196 GAGCGCCACCTCAGGTGCACTATTCACAACCGGGTCACCGGGTGGCTGCTTAACCG 255
QY 213 CAGCACCATCTCTATGCTGGGAATGACAAGTGGTGGCTGGATCTCTGGTGGTCTTCT 272
DB 256 CAGTACCACCTCTATGCTGGGAATGACAAGTGGTGGCTGGATCTCTGGTGGTCTTCT 315
QY 273 GAGCACACCAACGAGTACAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAG 332
DB 316 GAGTAAACCCAGACCCAGTACAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAG 375
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QY 753 AGAATTCAGTGTGACAGATGACAAAGACTGATTTGAAGGAAAGAGGTGAAGT 812
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DB 976 TGGTCCAGGCGCTGCTGAGGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1035
QY 993 GCTGCTGCTCTTCTGCTTGTGACCTGCTTCTCAAAATTTGA 1035
DB 1036 GCTGCTGCTCTTCTGCTTGTGACCTGCTTCTCAAAATTTGA 1078
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RESULT 16
AF282980 LOCUS 1410 bp mRNA linear ROD 01-FEB-2001
DEFINITION Mus musculus neurotrophin mRNA, complete cds.
ACCESSION AF282980
VERSION AF282980.1 GI:12642539
KEYWORDS
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1410)
AUTHORS Kim.T.H., Choi.S.C., Kim.J., Jeon.J.W., Kim.K.D. and Lee.S.H.
TITLE Cloning and expression of mouse neurotrophin gene in the developing nervous system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1410)
AUTHORS Kim.T.H., Choi.S.C., Kim.J., Jeon.J.W., Kim.K.D. and Lee.S.H.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea University, 1-5 Ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea
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ORIGIN
    Query Match 78.7%; Score 814.4; DB 10; Length 1410;
    Best Local Similarity 85.6%; Pred. No. 0.013;
    Matches 897; Conservative 0; Mismatches 113; Indels 38; Gaps 11;
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QY 53 CGGGGCTGCTGCTCTGTCTCTT-----CCA-AGGAGTCCCGTCCGCGAGCGGAGATCC 107
DB 59 -----GGCTGCTAT---TC-CTTGATCCACAGGAGTCCCGTGGTGGAGATGC 107
QY 108 CACCTTCCCAAGCTATGGAACAACGTGACGGTCCGCGAGGGGGAGAGCGCCACCTCAG 167
DB 108 TACCTTCCCAAGCTATGGAACAACGTGACGGTCCGCGAGGGGGAGAGCGCCACCTCAG 167
QY 168 GTGCATATGACAACCGGGTCAACCGGGTGGCTTAAACCGGAGCACCCTCTCTA 227
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QY 228 TGTGGAATGACAAGTGGTGGCTGATCTCTCGGTGGTCTTCTGAGCAACACCCAAAC 287
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QY 528 GGTGGCTTTGTGAGTAGAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 587
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RESULT 17
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LOCUS G.gallus mRNA for CEPU-1. 1257 bp mRNA linear VRT 29-APR-1998
DEFINITION G.gallus mRNA for CEPU-1.
ACCESSION Z72497
VERSION Z72497.1 GI:1325950
KEYWORDS Brain; CEPU-1; glycoprotein; GPI-anchor protein.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1257)
CEPU-1, a novel immunoglobulin superfamily molecule, is expressed
by developing cerebellar Purkinje cells
J. Neurosci. 16 (5), 1770-1779 (1996)
96370549
MEDLINE 877445
PUBMED 877445
2 (bases 1 to 1257)
Bruemmendorf, T.
Direct Submission
AUTHORS Bruemmendorf T., Max-Planck-Institute for
Developmental Biology, Molecular Biology, Spemannstrasse 35,
Tuebingen, Germany, 72076
JOURNAL Location/Qualifiers
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Best Local Similarity 76.9%; Pred. No. 1.4;
Matches 835; Conservative 0; Mismatches 178; Indels 73; Gaps 31;

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Db 141 GCGCGACTCTT-CTTCTCCAAAGAGTCCCGTGGCAGCGAGATGCCACCTTCCCCA 199
QY 119 AAGCTATGACAAAGTACGCTCCGCGAGGGGAGAGCGCCCTCAGGTGCAATATTG 178
Db 200 AAGCTATGACAAAGTACGCTCCGCGAGGGGAGAGTCCACGCTCAGGTGCTCCGTTG 259
QY 179 AACACCGGCTCACCAGGCTGGCTTAACCCGAGCAGCATCTCTATGCTGGAGT 238
Db 260 AACACCGGCTCACCAGGCTGGCTGAACCCGAGCAGCATCTCTATGCTGGAGT 319
QY 239 AACAGTGTGCTGATCCTCGCTGGTCTTCTTGAG-CAACACCAACAGCAGTACAGC 297
Db 320 AACAGTGTGCTGATGAGCCGAGGCTGGTCTCTTG-GCCAACAACCAACAGCAGTACAGC 378
QY 298 ATCGAGATCCAGAGCGTGGATGTGTATGACG-AGGGCCCTTACACCTGCTCGGTGACAG 356
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QY 357 AGACAAACCAACCAAGACCTCTAGGCTCCACCTCAATTTGTGCAAGTATCTCCCAAAATGT 416
Db 438 AGACAAATCACCCCAAGACATCTCGGTGACCTTATTTGTGCAAGTGTCCGCAAAAT--T 495
QY 417 A--GAGATTCTTTCAGATATCTCCATTAATGAAG--GGAAACAATATTAGCCTCACCTGCA 472
Db 496 ACCGAGACCTCTTCTGACATCTCCATCAATGAGTGG--CAACGTACAGCTCACCTGCA 553
QY 473 TAGCAACTGGTAGACAGAGCTACGGTACTTGGAGACACATCTTCTCCAAAGCGGTG 532
Db 554 TAGCACCGGCGAGGCGAGACCCCAATCACTCGTGGAGACATCTCGCCCAAGGTG 613
QY 533 GCTTTGTGAGTGAAGACGAATACCTTGGAAATTC-GGGCATCACCCGGGAGCAGTCAAGG 591
Db 614 GCTTCATCAGGAGGACGAGTACCTCCAAAGAGTGGAGA-TCAAGGSCATCAGAGGAGCAGTCCGGGC 672
QY 592 GACTACAGTGCAGTGCCTTCCAATGAGCTGGCGCGCCGCTGGTGTGCTACGAGAGTAAAGTGC 651
Db 673 GAGTACAGTGCAGTGCCTCCAAAGAGTGGAGA-TCAAGGSCATCAGAGGAGCAGTCAAGTGC 732
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QY 890 CTTCCAAAGCTGGGCGACACCAATCCAGCATCATGCTATTG-----G 935
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QY 1030 TTTTGA 1035
Db 1144 TTCTGA 1149

RESULT 18
AF271233 1638 bp DNA linear SYN 21-MAY-2001
LOCUS Synthetic construct secretory IgCEPUS-GFP fusion protein
DEFINITION (IgCEPUS-GFP) gene, complete cds.
ACCESSION AF271233
VERSION AF271233.1 GI:14161268
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1. (bases 1 to 1638)
AUTHORS Kim, D.-S. and Moss, D.J.
TITLE Secretory IgCEPUS-GFP fusion protein expressions in transfected
cell lines
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 1638)
AUTHORS Kim, D.-S. and Moss, D.J.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea

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ORIGIN

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Best Local Similarity 71.1%; Pred. No. 2.4;
Matches 841; Conservative 0; Mismatches 167; Indels 175; Gaps 42;

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Db 55 GCGGCACTCTCTCTTCTCAAGAGTGGCGTGGCAGCGAGATGCCACCTTCCCCAAA 114
QY 121 GCTATGACAACTGAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
Db 115 GCTATGACAACTGAGCTGTGGCGCAAGGGGAGTGCACCGCTCAGGTGCTCCGTGGAC 174
QY 181 AACCGGCTCAACCGCGGTGCGCTGCTTAAACCGCAGCACCCTCTCTATGCTGGGAATGAC 240
Db 175 AACCGGCTCAACCGCGGTGCGCTGCTTAAACCGCAGCAGCATCTCTATGCGGCAATGAC 234
QY 241 AAGTGTGCTGGATCCTCGCGTGGTCTTCTAGCAACACCCAAACGAGTAGCAGCATC 300
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QY 418 GAGATTTCTCAGATATCTCAATTAATGAAG--GGAACTAATATTAGCTCAGCTGCAATGAG 475
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QY 536 TTGTGAGTGAAGACGAATATTGAAATTTCA--GGGCATCACCCGGGAGCAGTCAGGGGAC 594
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QY 655 GTGAATATCCACCATACATTTTCAAGGCAAGGGGTACAGGTGTCCCTGGGACAAAAG 714
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QY 773 ATGACAAAAGCTGATTGAAGGAAAGAGGGGTGAAGTGAAGAAACAGACCTTTCCTCT 832
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LOCUS AF292935 1058 bp mRNA linear VRT 24-AUG-2000
DEFINITION Gallus gallus CEPU-Se alpha 2 isoform (CEPU-Se) mRNA, complete cds.
ACCESSION AF292935
VERSION AF292935.1 GI:9887384
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1058)
Lodge,A.P., McNamee,C.J., Howard,M.R., Reed,J.E. and Moss,D.J.
Characterisation of CEPU-Se, a secreted isoform of the IglON family
protein CEPU-1
Unpublished
2 (bases 1 to 1058)
Lodge,A.P. and Moss,D.J.
Direct Submission
Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK
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ORIGIN
Query Match 64.7%; Score 669.6; DB 5; Length 1058;
Best Local Similarity 77.1%; Pred. No. 2.5;
Matches 808; Conservative 0; Mismatches 169; Indels 71; Gaps 30;
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Db 48 GAATATGGCC---CAGGCGAAAAATGCAGACCCCGTCTCATGGGTGATCTTCGCCGGGAT 104
Qy 60 GGCTGCTCT-GTGCTCTTCCAAAGAGTGGCCGTCGCGAGGAGATGCCACCTTCCCA 118
Db 105 GGCCGACTCT-CTCTTCCAAAGAGTGGCCGTCGCGAGGAGATGCCACCTTCCCA 163
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Db 164 AAGCTATGGACAACGTCAGCTGCGGCAAGGGAGAGTGCCACGCTCAGGTGCTCCGTGG 223
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Qy 474 AGCAACTGGTAGACAGGAGCTAGGTTACTTTGGAGACATCTTCCCAAGGGTTGG 533
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Qy 534 CTTTGTGAGTGAAGACGAATACCTTGAATTTCA--GGGCATCACCCGGGAGCAGTCAGGGG 592
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Qy 998 TG--CCTCTTCTGCTTTCG--ACCTGC 1021
Db 1030 TGACCAACCACTG---TGCAAGACGTGC 1053
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AF292936 1013 bp mRNA linear VRT 24-AUG-2000
DEFINITION Gallus gallus CEPU-Se alpha 1 isoform (CEPU-Se) mRNA, complete cds.
ACCESSION AF292936
VERSION AF292936.1 GI:9887386
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1013)
Lodge,A.P. and Moss,D.J.
Direct Submission
Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK
Location/Qualifiers
FEATURES

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659 ACTACCCACGTCATCTCGGATGCGAAGAGCACCGGTGTGCCGGTGGGGCAGAAGGG-- 716

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897 CAAGCTGGGGCCACCAATGCCAGCATCATGCTATTTTGGTCCAGGGCGCGCTCAGCGAGGT 956

897 CGAGCTAGGAAACACCAACGCCAGCATGATCC--TTT-----T-----GGT 936

957 GAGCAACGGCAC-----GTCAGAGA--GGG--CAGG--CTGCGT--CTGCGTGTCTG--CCT 1002

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1003 CTTCGTGCTCTTGC---ACCTGC 1021

991 CCACGTG---TGCAAGACGTGC 1008

RESULT 22

HSR05672 6380 bp mRNA linear PRI 16-JUN-2003

LOCUS Homo sapiens mRNA; cDNA DKFP686H1949 (from clone DKFP686H1949); complete cds.

ACCESSION BX537377.1 GI:31873255

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (base 1 to 6380)

AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

TITLE Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

JOURNAL Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

ABSTRACT This clone (DKFP686H1949) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.

FEATURES

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137. 1153

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Db 579 T--GCTGTGTC--TTGCTATTGGCAGACAGAGCCTCACTGTGACATGGAGACAC--CTGTC 633
Qy 521 ---CCA--AAG--CGGTTGGCTTCTGTAGTGAAGCAATCTTGGAAAT--TCAGGGCAT 572
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Qy 748 TCA--GCAGAAATCCAGTGGTACAAAGGATGACAA--A--AG--ACTGAT--T-GAAGA 795
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Db 1086 C--C--TCCA--GA--GCATCTGGCTGTCTCTGGCTATCAGGACCTCTTAGCCACTTCTT 1140
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Qy 1031 ---TTTGA 1035
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RESULT 23
HUMOBAM
LOCUS
DEFINITION Human (clone PHOM) opioid-binding cell adhesion molecule mRNA,
complete cds.
ACCESSION L34774
VERSION L34774.1 GI:514373
KEYWORDS opioid-binding cell adhesion molecule.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1478)
AUTHORS Shark, K.B. and Lee, N.M.
TITLE Cloning, sequencing and localization to chromosome 11 of a cDNA
encoding a human opioid-binding cell adhesion molecule (OBAM)
JOURNAL Unpublished (1994)
COMMENT Original source text: Homo sapiens (library: Stratagene brain)
occipital cortex cDNA to mRNA.
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PIKF"
CDS
ORIGIN
Query Match 61.2%; Score 633.8; DB 9; Length 1478;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 817; Conservative 0; Mismatches 145; Indels 205; Gaps 77;
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Db 143 GCGCAGCGAGATGCCACCTTCCCCAAAGCTATGGACAACGTCGACGGTCCGGCAGGGGGA 202
QY 153 GAGCGCACCTCAGGTGACATATTGACAACCGGGTCACCCGGTGGCTGCTGCTGCTAAACCG 212
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DEFINITION Sequence 98 from Patent WO03002765.
ACCESSION AX665340
VERSION AX665340.1 GI:29290463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
SELLAR,G.C. and GABRA,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 98 09-JAN-2003;
Cancer Research Technology Limited (GB)
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Query Match 61.2%; Score 633.8; DB 6; Length 3110;
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QY 3 GA-AA-----ACC--ATCAGCC--AAAAATGCACAATCTATCTCTTGG 42
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DEFINITION Gallus gallus CEPU gene.
ACCESSION AJ225897
VERSION AJ225897.1 GI:2897596
KEYWORDS CEPU gene; neural secreted glycoprotein.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1
REFERENCE
1 Kim,D.S., Rhee,T.H., Moss,D.J. and Kim,J.Y.
AUTHORS cDNA cloning of the CEPU, a secreted type of neural glycoprotein
TITLE belonging to the immunoglobulin-like oploid binding cell adhesion
molecule (OBAM) subfamily
JOURNAL Mol. Cells 9 (3), 270-276 (1999)
MEDLINE 99347334
PUBMED 10420985
REFERENCE
2. (bases 1 to 3216)
AUTHORS Kim,D.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-1998) Pukyong National University, Microbiology,
599-1 Daeyeon-3dong, Nam-gu, Pusan 608-737, KOREA (ROK)
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exon

intron

exon

ORIGIN

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Query Match 61.1%; Score 632.4; DB 5; Length 3216;
Best Local Similarity 48.3%; Pred. No. 29;
Matches 871; Conservative 0; Mismatches 155; Indels 776; Gaps 68;
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Db 341 ACCCGCTCTCATGGTGTCTTTCGGGGATGCGCGACTCC-TCTCTTCCAGAGTG 399
QY 88 CCGTGGCAGCGGAGATGCCCTTCCCAAGACTATGGACAACGTGACGCTCGGCGAG 147
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QY 148 GGGGAGAGCGCCACCTCTCAGGTGCACTATTGACAACCGGCTCACCGGCTGGCTGGCTA 207
Db 460 GGGGAGAGTGCACAGCTCAGGTGCTCCGTGGACAACCGGCTCACCGGCTGGCTG 519
QY 208 AACCGAGACACCATCTCTATGCTGGGAATGACAAGTGGTGGCTGATCTCGCGTGGTC 267
Db 520 AACCGAGACACCATCTCTATGCGGCAATGACAAGTGGTGGCTGATCTCGCGTGGTC 579
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Db 580 CTCTGGCAACACCAAAACCCAGTACAGATCCAGATCCAGATCCAGATCCAGAT 639
QY 328 G-AGGCGCCTTACCTCTCGTTCGTCAGACAGACACCCCAAGACCTCTAGGGTCCA 386
Db 640 GAAGGGCCC-TACACCTGCTCGTCGTCAGACAGACATCACCCCAAGACATCTCGCTGCA 698
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QY 445 GAAG--GGAAACAATATTAGCCTCACCTGATAGCACTGATAGCAGAGCCTACGGTTA 502
Db 757 GAAGTGG--CAACGTGACGCTCACCCTGATAGCAGCAGGCGGCGAGACCCCAATCA 814
QY 503 CTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTTGTAGTGAAGACGAATATCTGGAAA 562
Db 815 CTTGGAGACACATCTCTCCCAAGCGTGTGGCTTTTGTAGTGAAGACGAATATCTGGAAA 874
QY 563 TTCA-GGGCATCAACCGGAGAGAGTACAGGGAGTACAGTGTGCTCTCCCAATGACGTG 621
Db 875 -TCACAGGCATCACGAGGGAGAGTACAGGGAGTACAGTGTGCTCTCCCAACGAGTGTG 933
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QY 646 -----A-----AGG-----TCACC----- 654
Db 994 GGGACAGCCAGGGCCACATTGTCACCCGAGGGGATGCACCGTTCACCTGCCCTTGG 1053
QY 655 -----GTG----- 657
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QY 658 -----AA----- 663
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QY 664 CCACC-----ATA----- 671
Db 1174 CAACCTGAGTTTCTGCTGCTGAGATGCTGTGTGATACCTCAGGGGAGAGGG 1233
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QY 683 -----GTT-----GTT----- 690
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QY 691 ---A---CA-----GTTCC----- 701
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QY 702 -----CG-----TGGG-- 707
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Db 2073 GA 2074

RESULT 26
BTOBCAM
LOCUS Bovine mRNA for opioid binding protein/cell adhesion molecule
DEFINITION BTOBCAM 2593 bp mRNA linear MAM 31-MAR-1995
ACCESSION X12672
VERSION X12672.1 GI:585
KEYWORDS cell adhesion molecule; glycoprotein; immunoglobulin superfamily;
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2593)
AUTHORS Schofield, P.R., McFarland, K.C., Hayflick, J.S., Wilcox, J.N.,
Cho, T.M., Roy, S., Lee, N.M., Loh, H.H. and Seeburg, P.H.
TITLE Molecular characterization of a new immunoglobulin superfamily
protein with potential roles in opioid binding and cell contact
JOURNAL EMBO J. 8 (2), 489-495 (1989)
MEDLINE 89251576
PUBMED 2721489
AUTHORS Schofield, P.R.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-1988) Schofield P.R.
COMMENT Data kindly reviewed (19-may-1989) by Schofield P.R.
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polyA_site

ORIGIN
Query Match 60.8%; Score 629.5; DB 4; Length 2593;
Best Local Similarity 70.5%; Pred. No. 27;
Matches 802; Conservative 0; Mismatches 161; Indels 174; Gaps 61;
QY 8 CCA--TCAGCC--AAAATGCAACAATCTATCTCTTGG-----GCAATCT--TCACGGGGC 58
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RESULT 27

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LOCUS
DEFINITION Synthetic construct secretory IgCEPUS-GFP fusion protein
(gIgCEPUS-GFP) gene, complete cds.
ACCESSION AF271618
VERSION AF271618.1 GI:14161270
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 2935)
AUTHORS Kim,D.-S. and Moss,D.J.
TITLE Neuronal-specific secretory IgCEPUS-GFP fusion protein expression
in transfected cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2935)
AUTHORS Kim,D.-S. and Moss,D.J.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea
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FEATURES

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ORIGIN

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Query Match 60.7%; Score 628.7; DB 12; Length 2935;
Best Local Similarity 47.6%; Pred. No. 31;
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D 705 ACCCGCTCATGGGTGATCTTTCGCGGGATGGCGCACTCC--TCTCTTCAAGAGATG 763
QY 88 CCGTGGCAGCGAGATGCCACTTCCCAAGCTTATGCAACAGCTGACGCTGCGGCGAG 147
D 764 CCGTGGCAGCGAGATGCCACTTCCCAAGCTTATGCAACAGCTGACGCTGCGGCGAA 823
QY 148 GGGGAGAGCGCAACCTCTCAGGTGCACTATTGCAACCGGGTCAACCGGGTGCCTGGCTA 207
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Db 824 GGGAGAGTGTCCACGCTCAGTGTCTCCGTGGCAACACCGCGTCCACCGCGTGGCGCTGCTG 883
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QY 658 -----AA-----ATAT 663
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QY 702 -----CG-----TGGG-- 707
Db 1838 AGAGCTGCAGGAGTGGGCATAAGCTCGGAGATGATTTTCTCTCTTGTGAGATGGGA 1897
QY 708 -ACAAAGG-----GGA--CAC----- 721
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QY 722 -----TGC-----AG----- 726
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QY 727 TGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAAGACTG 786
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Db 2312 GAGGCGAGGGGCGATGCCACCTACGCGAGCTGACCTGAAAGTTTCTCTGACACACCGCGC 2371
QY 993 --GCTGC--TGCTCTTCTTGG-----TCTTG-CACC-----TG 1020
Db 2372 AAGCTGCCGTGCC---CTGGCCACACCTCTGTGACCACTTACCTAGCGGTGCAGTG 2427
QY 1021 CTT-----CT-----GAAATTTTGA 1035
Db 2428 CTTACGCGCTACCCCGACCA---TGA 2453

RESULT 28

RATCALMB
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source
CDS

RATCALMB
Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
M88710.1 GI:203247
cell adhesion-like molecule; opiod binding protein.
Rattus norvegicus (Norway rat)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Rattus.
1 (bases 1 to 2179)
Lippman,D.A., Lee,N.M. and Loh,H.H.
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Original source text: Rattus norvegicus (strain Simonsen ICR) brain
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ORIGIN

Query Match 59.8%; Score 619.1; DB 10; Length 2179;
Best Local Similarity 70.8%; Pred. No. 34;
Matches 809; Conservative 0; Mismatches 169; Indels 165; Gaps 72;

QY 3 GA-AA--ACCATCCAGC--CAAAATGC-A-CAA-TT-----CTATC-----TCT 39
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QY 190 ACCCGGTGGCTGGCTTAAACCGGAGCACCATCTCTATCTGCTGGGAATGACAAGTGGTC 249
Db 487 ACCGAGTAGCTGGCTTAAACCGGAGCACCATCTCTAGCTGGGAATGACAAGTGGTC 546
QY 250 CTGGATCTCGGTGGTC--CTTCTGAGCAACACCCAAACGAGTACAGCATCGAGATCC 307
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QY 368 CAAGACCTCTAGGTCCACCTCATTTGCAAGTATCTCCAAAT--TGTAGAGATTTC 425
Db 665 CCAAACTCCCGGTCCACTCATGTGCAAGTCTCTCCAGATATG-A-ACATCTC 722
QY 426 TTCAGATATCTCAATTAATGAAGGAACAATATTAGC---CTCACC-----TGCATAGC 476
Db 723 TTCAGA-----CATTACT--GTGAATGAGATAGCAGTGTGACCTTGTTATGCTCGC 773
QY 477 AACTGGTAGACAGAGCCTACGGTTTACTTGGAGACACATCTTC---CCA--AAG--CGG 529
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RESULT 29
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DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
ACCESSION M88711
VERSION M88711.1 GI:203249
KEYWORDS cell adhesion-like molecule; opiod binding protein.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2337)
Lippman,D.A., Lee,N.M. and Loh,H.H.
Opioid-binding cell adhesion molecule (OBCM)-related clones from a
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Gene 117 (2), 249-254 (1992)
MEDLINE 92347701
PUBMED 1339369
COMMENT Original source text: Rattus norvegicus brain cDNA to mRNA.
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RESULT 30

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ACCESSION M88709
VERSION    M88709.1 GI:203245
KEYWORDS   cell adhesion-like molecule; oploid binding protein.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 3069)
AUTHORS   Lippman,D.A., Lee,N.M. and Loh,H.H.
TITLE      Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
            rat brain cDNA library
JOURNAL    Gene 117 (2), 249-254 (1992)
MEDLINE    92347701
PUBMED     1339369
COMMENT    Original source text: Rattus norvegicus (strain Simonsen ICR)
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ORIGIN

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Matches 794; Conservative 0; Mismatches 176; Indels 120; Gaps 63;

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Job time : 4251.99 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:40:25 ; Search time 495.763 Seconds

(without alignments)
9496.706 Million cell updates/sec

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Searched: 2960401 seqs, 227450654 residues

Total number of hits satisfying chosen parameters: 5920802

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1035	100.0	1679	9	US-09-999-832A-522
5	1035	100.0	1679	10	US-09-978-189-522
6	1035	100.0	1679	10	US-09-978-608A-522
7	1035	100.0	1679	10	US-09-978-585A-522
8	1035	100.0	1679	10	US-09-978-191A-522
9	1035	100.0	1679	10	US-09-978-403A-522
10	1035	100.0	1679	10	US-09-978-564A-522
11	1035	100.0	1679	10	US-09-999-833A-522
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16	1035	100.0	1679	10	US-09-978-193A-522	Sequence 522, App
17	1035	100.0	1679	10	US-09-999-830A-522	Sequence 522, App
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; PRIOR APPLICATION NUMBER: 60/085697									
Query Match 100.0%; Score 1035; DB 9; Length 1679;									
Best Local Similarity 100.0%; Pred. No. 3 6e-09;									
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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RESULT 2

US-09-978-697-522
Sequence 522, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322

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Best Local Similarity 100.0%; Pred. No. 3 6e-09;			
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
PRIOR FILING DATE: 1998-04-28			
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PRIOR APPLICATION NUMBER: 60/085704			
PRIOR FILING DATE: 1998-05-15			
PRIOR APPLICATION NUMBER: 60/085697			

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Db	254	GCTATGGA CAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC	313
Qy	181	AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGACCACTCTCTATGTGGGAATGAC	240
Db	314	AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGACCACTCTCTATGTGGGAATGAC	373
Qy	241	AAGTGGTGCCTGGATCCTTCGCGTGGTCTCTTGAGCACACCCCAACCGCAGTACAGATC	300
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Qy	301	GAGATCCAGAAACGTTGGATGTATGAAGAGGCGCTTTACCTCTCGGTGAGACAGAC	360
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Qy	361	AACCAACCAAGACCTCTAGGTCCTCCTGCTCACTGCAAGTATCTCCAAAATTTGAGAG	420
Db	494	AACCAACCAAGACCTCTAGGTCCTCCTGCTCACTGCAAGTATCTCCAAAATTTGAGAG	553
Qy	421	ATTTCTTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGATAGCACT	480
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Db	794	TATCCACCATACATTTGAGAAAGCGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	853
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; Sequence 522, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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/ PRIOR APPLICATION NUMBER: 60/085573
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1035; DB 9; Length 1679;
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QY 61 GCTGCTCTGTGCTCTTCCAAAGAGTCCCGTGGCGAGGAGATGCCACCTTCCCAA 120
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DB 254 GCTATGGACAAAGTACCGGTCCCGAGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGCCTGGATCCTCGCTGCTCTTCTGAGCAACCCAAACCGCAGGTACAGCATC 300
DB 1153 AAGTGGTGCCTGGATCCTCGCTGCTCTTCTGAGCAACCCAAACCGCAGGTACAGCATC 300
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DB 374 AAGTGGTGCCTGGATCCTCGCTGCTCTTCTGAGCAACCCAAACCGCAGGTACAGCATC 433
QY 301 GAGATCCAGAAAGTGGATGTGTATGACGAGGGCCCTTACACTCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAAAGTGGATGTGTATGACGAGGGCCCTTACACTCTGCTCGGTGAGACAGAC 493
QY 361 AACACCCCAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACACCCCAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGATACCAACT 480
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGATACCAACT 613
QY 481 GGTAGACAGAGCCCTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
DB 614 GGTAGACAGAGCCCTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
QY 541 AGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTTACGAG 600
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QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 780
DB 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGGAAACACAGACCTTCTCTCAAACTC 840
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; Sequence 522, Application US/09999832A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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1	APPLICANT: Grimaldi, J. Christopher	1	PRIOR APPLICATION NUMBER: 60/080199
2	APPLICANT: Gurney, Austin L.	2	PRIOR FILING DATE: 1998-03-31
3	APPLICANT: Hillan, Kenneth J.	3	PRIOR APPLICATION NUMBER: 60/080327
4	APPLICANT: Kijavin, Ivar S.	4	PRIOR FILING DATE: 1998-04-01
5	APPLICANT: Kuo, Sophia S.	5	PRIOR APPLICATION NUMBER: 60/080328
6	APPLICANT: Napier, Mary A.	6	PRIOR FILING DATE: 1998-04-01
7	APPLICANT: Pan, James	7	PRIOR APPLICATION NUMBER: 60/080333
8	APPLICANT: Paoni, Nicholas F.	8	PRIOR FILING DATE: 1998-04-01
9	APPLICANT: Roy, Margaret Ann	9	PRIOR APPLICATION NUMBER: 60/080334
10	APPLICANT: Shelton, David L.	10	PRIOR FILING DATE: 1998-04-01
11	APPLICANT: Stewart, Timothy A.	11	PRIOR APPLICATION NUMBER: 60/081070
12	APPLICANT: Tumas, Daniel	12	PRIOR FILING DATE: 1998-04-08
13	APPLICANT: Williams, P. Mickey	13	PRIOR APPLICATION NUMBER: 60/081049
14	APPLICANT: Wood, William I.	14	PRIOR FILING DATE: 1998-04-08
15	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	15	PRIOR APPLICATION NUMBER: 60/081071
16	TITLE OF INVENTION: Acids Encoding the Same	16	PRIOR FILING DATE: 1998-04-08
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19	CURRENT FILING DATE: 2001-10-24	19	PRIOR APPLICATION NUMBER: 60/081203
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22	PRIOR APPLICATION NUMBER: 60/062250	22	PRIOR FILING DATE: 1998-04-09
23	PRIOR FILING DATE: 1997-10-17	23	PRIOR APPLICATION NUMBER: 60/081955
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29	PRIOR FILING DATE: 1997-11-21	29	PRIOR APPLICATION NUMBER: 60/081952
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36	PRIOR APPLICATION NUMBER: 60/077649	36	PRIOR FILING DATE: 1998-04-21
37	PRIOR FILING DATE: 1998-03-11	37	PRIOR APPLICATION NUMBER: 60/082704
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39	PRIOR FILING DATE: 1998-03-12	39	PRIOR APPLICATION NUMBER: 60/082804
40	PRIOR APPLICATION NUMBER: 60/078004	40	PRIOR FILING DATE: 1998-04-22
41	PRIOR FILING DATE: 1998-03-13	41	PRIOR APPLICATION NUMBER: 60/082700
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600

		Query Match		100.0%; Score 1035; DB 10; Length 1679;	
		Best Local Similarity		100.0%; Pred. No. 3.6e-09;	
		Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGAAACCATCCAGCAAAATGCAATTTCTATCTTTGGCAATCTTACGGGGCTG	60		
DB	134	ATGAAACCATCCAGCAAAATGCAATTTCTATCTTTGGCAATCTTACGGGGCTG	193		
QY	61	GCTGCTCTGTCTCTTCCAAAGAGTGCCTGGCGAGCGGAGATGCCACCTTCCCAAA	120		
DB	194	GCTGCTCTGTCTCTTCCAAAGAGTGCCTGGCGAGCGGAGATGCCACCTTCCCAAA	253		
QY	121	GCTATGGCAACGTGACGCTCCGGAGGGGAGAGGCCACCTCAGGTGCATTTGAC	180		
DB	254	GCTATGGCAACGTGACGCTCCGGAGGGGAGAGGCCACCTCAGGTGCATTTGAC	313		
QY	181	AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATCTGGGAATGAC	240		
DB	314	AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATCTGGGAATGAC	373		
QY	241	AAGTGTGCTGTGATCCTCGTGTGCTCTTCTGAGCAACACCCAAACGCGATCAGCATC	300		
DB	374	AAGTGTGCTGTGATCCTCGTGTGCTCTTCTGAGCAACACCCAAACGCGATCAGCATC	433		
QY	301	GAGATCCAGAACGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC	360		
DB	434	GAGATCCAGAACGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC	493		
QY	361	AACACCCAAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCCAAAATTTAGAG	420		
DB	494	AACACCCAAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCCAAAATTTAGAG	553		
QY	421	ATTCTCTCAGATATCTCCATTAAAGGGAACAATATTAGCTCACCCTGCATAGCACT	480		
DB	554	ATTCTCTCAGATATCTCCATTAAAGGGAACAATATTAGCTCACCCTGCATAGCACT	613		
QY	481	GGTAGACAGAGCTCAGGTTACTTTGAGACACATCTCTCCAAAGCGGTGGCTTTTG	540		
DB	614	GGTAGACAGAGCTCAGGTTACTTTGAGACACATCTCTCCAAAGCGGTGGCTTTTG	673		
QY	541	AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG	600		
DB	674	AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG	733		
QY	601	TGCAGTGCCTCAATGACGTGGCGCGCGCTGGTACGGAGATGAAGGTACCGTGAAC	660		
DB					
DB	734	TGCAGTGCCTCAATGACGTGGCGCGCGCTGGTACGGAGATGAAGGTACCGTGAAC	793		
QY	661	TATCCACCATATATTTCAAGAGCCAAAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA	720		
DB	794	TATCCACCATATATTTCAAGAGCCAAAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA	853		
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAGGATGACAAA	780		
DB	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAGGATGACAAA	913		
QY	781	AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGGAAAAACAGACCTTTCTCTCAAACTC	840		
DB	914	AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGGAAAAACAGACCTTTCTCTCAAACTC	973		
QY	841	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATCTACTTGGTGGCTTCCAAACAG	900		
DB	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATCTACTTGGTGGCTTCCAAACAG	1033		
QY	901	CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGGCCGCTCAGCGAGGTGAGC	960		
DB	1034	CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGGCCGCTCAGCGAGGTGAGC	1093		
QY	961	AACGGCACGTGAGAGGGGAGGCTGCTGTGGCTGTGCTTCTTGTGGTGTGACCTG	1020		
DB	1094	AACGGCACGTGAGAGGGGAGGCTGCTGTGGCTGTGCTTCTTGTGGTGTGACCTG	1153		
QY	1021	CTTCTCAAAATTTGA	1035		
DB	1154	CTTCTCAAAATTTGA	1168		
RESULT 6					
US-09-978-608A-522					
; Sequence 522, Application US/09978608A					
; Publication No. US20030045462A1					
; GENERAL INFORMATION:					
; APPLICANT: Ashkenazi, Avi					
; APPLICANT: Baker Kevin P.					
; APPLICANT: Botstein, David					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Eaton, Dan					
; APPLICANT: Ferrara, Napoleon					
; APPLICANT: Filvaroff, Ellen					
; APPLICANT: Fong, Sherman					
; APPLICANT: Gao, Wei-Qiang					
; APPLICANT: Gerber, Hanspeter					
; APPLICANT: Gerritsen, Mary E.					
; APPLICANT: Goddard, Audrey					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Grimaldi, J. Christopher					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Hillan, Kenneth J.					
; APPLICANT: Kljavin, Ivar J.					
; APPLICANT: Kuo, Sophia S.					
; APPLICANT: Napier, Mary A.					
; APPLICANT: Pan, James;					
; APPLICANT: Paoni, Nicholas F.					
; APPLICANT: Roy, Margaret Ann					
; APPLICANT: Shelton, David L.					
; APPLICANT: Stewart, Timothy A.					
; APPLICANT: Tumas, Daniel					
; APPLICANT: Williams, P. Mickey					
; APPLICANT: Wood, William I.					
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic					
; FILE REFERENCE: P2630PIC22					
; CURRENT APPLICATION NUMBER: US/09/978,608A					
; NUMBER OF SEQ ID NOS: 624					
; Prior Application removed - See File Wrapper or Palm					
; SEQ ID NO 522					
; LENGTH: 1679					
; TYPE: DNA					

Db 374 AAGTGTGCTGGATCCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACGTGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
Db 434 GAGATCCAGAACGTGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACCCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAG 420
Db 494 AACCCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAG 553
QY 421 ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
Db 554 ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 481 GTGAGACCAAGCCTAGCTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
Db 614 GTGAGACCAAGCCTAGCTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG 600
Db 674 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG 733
QY 601 TGCACTGCTCCATACACGTGGCGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 660
Db 734 TGCACTGCTCCATACACGTGGCGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTCAAGCCAGGCTACAGGTGTCCTCCGTTGGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTTCAAGCCAGGCTACAGGTGTCCTCCGTTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGACAGAAATTCAGTGGTACAAAGATGACAAA 780
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGACAGAAATTCAGTGGTACAAAGATGACAAA 913
QY 781 AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAACTC 840
Db 914 AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAACTC 973
QY 841 ATCTCTTCAATGCTCTCAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG 900
Db 974 ATCTCTTCAATGCTCTCAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG 1033
QY 901 CTGGGCCACCAATGCCAGCATCATGCTATTGTTCCAGGGCCCTCAGCGAGGTGAGC 960
Db 1034 CTGGGCCACCAATGCCAGCATCATGCTATTGTTCCAGGGCCCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGCTCAGAGAGGCGAGGCTGCGTCTGCTGCTCTTCTGCTCTTGTGACCTG 1020
Db 1094 AACGGCAGCTCAGAGAGGCGAGGCTGCGTCTGCTGCTCTTCTGCTCTTGTGACCTG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 8

US-09-978-191A-522
; Sequence 522, Application US/09978191A
; Publication No. US2003005039A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-05

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; PRIOR FILING DATE: 1998-05-06
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.6e-09;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCAAATGCAATTTCTTGGCAATCTTGGCAATCTTGGGGCTG 60

Db 134 ATGAAACCATCCAGCCAAATGCAATTTCTTGGCAATCTTGGGGCTG 193

Qy 61 GCTGCTCTGTGTCTTCCAGGAGTGCCGCGCAGCGGAGATGCCACCTTCCCAAA 120

Db 194 GCTGCTCTGTGTCTTCCAGGAGTGCCGCGCAGCGGAGATGCCACCTTCCCAAA 253

Qy 121 GCTATGGACAACTGACCGGTCCGCGCAGCGGAGAGCCCACTCAGGTGCACTATTGAC 180

Db 254 GCTATGGACAACTGACCGGTCCGCGCAGCGGAGAGCCCACTCAGGTGCACTATTGAC 313

Qy 181 ACCCGGTTCACCGGGTGGCTGGCTAAACCGCAGACCATCTCTATCTCTGGGATGAC 240

Db 314 ACCCGGTTCACCGGGTGGCTGGCTAAACCGCAGACCATCTCTATCTCTGGGATGAC 373

Qy 241 AAGTGTGCTTGGATCCTCGCGTGGTCTTTCAGCAACACCCAAACGAGTACAGCATC 300

Db 374 AAGTGTGCTTGGATCCTCGCGTGGTCTTTCAGCAACACCCAAACGAGTACAGCATC 433

Qy 301 GAGATCCAGAACTGGATGTGTATGAGAGGCCCTTACACCTGTCTGGTGAGACAGAC 360

Db 434 GAGATCCAGAACTGGATGTGTATGAGAGGCCCTTACACCTGTCTGGTGAGACAGAC 493

Qy 361 ACCACCCAAAGACCTCTAGGTTCCACCTCAATTTGTGCAAGTATCTCCCAAAATTTAGAG 420

Db 494 ACCACCCAAAGACCTCTAGGTTCCACCTCAATTTGTGCAAGTATCTCCCAAAATTTAGAG 553

Qy 421 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT 480

Db 554 ATTCTTCAGATATCTCCATTAATGAGGACACATATATAGCTCCTCACCCTGCATACCAACT 613
QY 481 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db 614 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
QY 541 AGTGAAGACGAAATCTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTTACGAG 600
Db 674 AGTGAAGACGAAATCTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTTACGAG 733
QY 601 TGCAGTGGCTCCAATGACGTGCGCGCCGCGTGTGACGAGAGTAAAGGTCAACCTGTAAC 660
Db 734 TGCAGTGGCTCCAATGACGTGCGCGCCGCGTGTGACGAGAGTAAAGGTCAACCTGTAAC 793
QY 661 TATCCACCATATCTTCAGAGCCCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Db 794 TATCCACCATATCTTCAGAGCCCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCTCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTACAGGATGACAAA 780
Db 854 CTGAGTGTGAAGCTCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTACAGGATGACAAA 913
QY 781 AGACTGATTTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAACTC 840
Db 914 AGACTGATTTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAACTC 973
QY 841 ATCTCTCTCAATGCTCTGAAATGACTATGGGAACTACTGCTGGGCTCTCCACAG 900
Db 974 ATCTCTCTCAATGCTCTGAAATGACTATGGGAACTACTGCTGGGCTCTCCACAG 1033
QY 901 CTGGGCCACACCAATGCGAGCAGTATGCTATTTGGTCCAGCGCGCTCAGCGAGGTGAGC 960
Db 1034 CTGGGCCACACCAATGCGAGCAGTATGCTATTTGGTCCAGCGCGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGTCTAGAGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1094 AACGGCAGTCTAGAGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY 1021 CTCTCTCAATTTGA 1035
Db 1154 CTCTCTCAATTTGA 1168

RESULT 9

US-09-978-403A-522

; Sequence 522, Application US/09978403A

; Publication No. US2003050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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;	PRIOR APPLICATION NUMBER:	60/085697

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Qy	61	GCTGCTCTGTGTCCTTCCAAAGAGTGCCCGTGGCGAGCGGAGATGCCAC	CTTCCCCCAA	120
Db	194	GCTGCTCTGTGTCCTTCCAAAGAGTGCCCGTGGCGAGCGGAGATGCCAC	CTTCCCCCAA	253
Qy	121	GCTATGGAACAACGTGACGCTCCGGCAGGGGAGAGCGCCACCTC	CAGGTGCATATTGAC	180
Db	254	GCTATGGAACAACGTGACGCTCCGGCAGGGGAGAGCGCCACCTC	CAGGTGCATATTGAC	313
Qy	181	AACCGGTCACCGGGTGGCTGTGCTAAACCGGAGACCATCTCTATG	CTGGGATGAC	240
Db	314	AACCGGTCACCGGGTGGCTGTGCTAAACCGGAGACCATCTCTATG	CTGGGATGAC	373
Qy	241	AAGTGTGTGCTGGATCTCTCGGTGTGTCCTTCTGAGCAACACCCAA	ACGCAGTACAGATC	300
Db	374	AAGTGTGTGCTGGATCTCTCGGTGTGTCCTTCTGAGCAACACCCAA	ACGCAGTACAGATC	433
Qy	301	GAGATCCAGAACGTGGATGTGTATGACGAGGCGCCTTTACACCTG	CTGGTGCAGACAGAC	360
Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGCGCCTTTACACCTG	CTGGTGCAGACAGAC	493
Qy	361	AACCACCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTACTCC	CAAAATTTGTAGAG	420
Db	494	AACCACCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTACTCC	CAAAATTTGTAGAG	553
Qy	421	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTC	CACCTGCATAGCAACT	480
Db	554	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTC	CACCTGCATAGCAACT	613
Qy	481	GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAG	CGGTTGGCTTTGTG	540
Db	614	GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAG	CGGTTGGCTTTGTG	673
Qy	541	AGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAG	TACGGGACTACGAG	600
Db	674	AGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAG	TACGGGACTACGAG	733
Qy	601	TGCAGTGCCTCCAAATGAGCTGGCGCGCCGTGGTACGGAGAGTAA	AGGTACCGGTGAAC	660

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QY 721 CTGCAGTGTGAAGCTTCCAGCAGTCCCTCCAGCAGATTCAGTGTGTACAGATGACAAA 780
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QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 840
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 973
QY 841 ATCTTCTTCAATGTTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCAAACAG 900
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QY 901 CTGGCCACACCAATGCCAGCATATGCTATTGTTCCAGGCGCGTCCAGGAGTGCAGC 960
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QY 961 AACGSCAGTCCAGGAGGCGAGGTCGGTCTGGCTCTTCTGCTTCTTGACCTG 1020
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; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/085697

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Db      194 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCCGTCGCGAGGGAGATGCCACCTTCCCAA 253
QY      121 GCTATGGACAAAGTGAAGTCCGGTCCGGCAGGGGAGAGGCCACCTCTAGGTGCACTATTGAC 180
Db      254 GCTATGGACAAAGTGAAGTCCGGTCCGGCAGGGGAGAGGCCACCTCTAGGTGCACTATTGAC 313
QY      181 AACCGGGTCACCCGGGTGGCTGGCTTAAACCGGAGCACCATCCTCTATGCTGGGAATGAC 240
Db      314 AACCGGGTCACCCGGGTGGCTGGCTTAAACCGGAGCACCATCCTCTATGCTGGGAATGAC 373
QY      241 AAGTGTGCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
Db      374 AAGTGTGCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY      301 GAGATCCAGAACCTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGACAGACAGAC 360
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QY      361 AACCAACCCAAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
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QY      421 ATTTCTTCAGATATCTCCATTTAATGAAGGGAACAATATTAGCCTCACCTGCTAGCAACT 480
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Db      674 AGTGAAGACGAATACTTTGGAATTTAGGGCATCACCCGGGAGCAGTACAGGGGACTAGGAG 733
QY      601 TGCAGTGCCTCCCAATGACGTCGGCCGGCCGGTGGTACGGAGAGTAAGGTCAACCGTGAAC 660
Db      734 TGCAGTGCCTCCCAATGACGTCGGCCGGCCGGTGGTACGGAGAGTAAGGTCAACCGTGAAC 793
QY      661 TATCCACCATACATTTTCAGAGCCAAAGGTTACAGGTGTCTCCCGTGGGACAAAGGGGACA 720
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QY 1021 CTCTCTCAAAATTTGA 1035
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; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PLC65
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; PRIOR FILING DATE: 1998-05-15

Query Match      100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 134 ATGAAACCATCCAGCCAAATGCAATTTCTTCTTTGGGCAATTTTACGGGGCTG 193
Qy 61 GCTGCTCTGTCTCTTCCAGGAGTCCGCTGGGAGGAGATGCCACCTTCCCAAA 120
Db 194 GCTGCTCTGTCTCTTCCAGGAGTCCGCTGGGAGGAGATGCCACCTTCCCAAA 253
Qy 121 GCTATGGACAAACGTGACGGTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 254 GCTATGGACAAACGTGACGGTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
Qy 181 AACGGGTACCCGGGTGGCTGGCTAAACGGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 314 AACGGGTACCCGGGTGGCTGGCTAAACGGGAGGAGGAGGAGGAGGAGGAGGAG 373
Qy 241 AAGTGTGCTCTGATCTCTGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGATC 300
Db 374 AAGTGTGCTCTGATCTCTGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGATC 433
Qy 301 GAGATCCAGAAACGTGGATGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 434 GAGATCCAGAAACGTGGATGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
Qy 361 AACCAACCAAGACCTTAGGGTCCAGCTCATTTGTCAGAGTATCTCCAAAATTGTAGAG 420
Db 494 AACCAACCAAGACCTTAGGGTCCAGCTCATTTGTCAGAGTATCTCCAAAATTGTAGAG 553
Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCTCACCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCTCACCTGCATAGCAACT 613
Qy 481 GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
Db 614 GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
Qy 541 AGTGAAGACGAATACCTTGGAAATTCAGGGCAGTCCAGGGGAGGAGGAGGAGGAG 600
Db 674 AGTGAAGACGAATACCTTGGAAATTCAGGGCAGTCCAGGGGAGGAGGAGGAGGAG 733
Qy 601 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGGTACGGAGAGTAAAGGTACCGTGAAC 660
Db 734 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGGTACGGAGAGTAAAGGTACCGTGAAC 793
Qy 661 TATCCACCATACATTTTCAAGCAAGGAGTACAGGTGTCCTGGGAGCAAAAGGGGACA 720
Db 794 TATCCACCATACATTTTCAAGCAAGGAGTACAGGTGTCCTGGGAGCAAAAGGGGACA 853
Qy 721 CTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGGTACAGGAGTACAAA 780
Db 854 CTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGGTACAGGAGTACAAA 913
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Qy 841 ATCTTCTTCAATGTCTCTGAAATGACTATGGAACTACACTTGGTGGCTCCCAACAG 900
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Qy 901 CTGGGCGCACCAATGCCAGCATCATGTATTGTTGGTCCAGGGCGCTCAGCGAGGTGAGC 960
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
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1 ATGAAACCATCCAGCCAAATGCAAAATCTATCTCTTTGGGCAATCTTTCAGGGGCTG 60
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Qy

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RESULT 13

US-09-978-824-522

; Sequence 522, Application US/09978824

; Publication No. US20030055216A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Hillan, Kenneth J.
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APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
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Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCAAATGCAAAATCTCTCTGGCAATCTTCACGGGCTG 60
Db 134 ATGAAACCATCCAGCCAAATGCAAAATCTCTCTGGCAATCTTCACGGGCTG 193
Qy 61 GCTGCTGTGTCTCTTCCAAAGAGTGCCCGTGGCGAGCGGAGATGCCACTTCCCAAA 120
Db 194 GCTGCTGTGTCTCTTCCAAAGAGTGCCCGTGGCGAGCGGAGATGCCACTTCCCAAA 253
Qy 121 GCTATGACACAGTGACGTCGCGAGCGGAGCGGAGCGGAGATGCCACTTATTTGAC 180
Db 254 GCTATGACACAGTGACGTCGCGAGCGGAGCGGAGCGGAGATGCCACTTATTTGAC 313
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Db 314 AACCGGCTCACCCGGGTGGCTTAAACCGGAGCGGAGCGGAGATGCCACTTATTTGAC 373

241 AAGTGGTGCTGGATCCTCGCGTGGTCTCTTCGAGCAACACCCAAACGCGAGTACAGATC 300
Db 374 AAGTGGTGCTGGATCCTCGCGTGGTCTCTTCGAGCAACACCCAAACGCGAGTACAGATC 433
Qy 301 GAGATCCAGAACGCTGGATGTATGAGAGGGGCCCTTACACCTGCTGGTGGAGACAGAC 360
Db 434 GAGATCCAGAACGCTGGATGTATGAGAGGGGCCCTTACACCTGCTGGTGGAGACAGAC 493
Qy 361 AACCAACCCAAAGACCTCTAGGCTCCACCTCATTTGTCAGAGTATCTCCAAATTTAGAG 420
Db 494 AACCAACCCAAAGACCTCTAGGCTCCACCTCATTTGTCAGAGTATCTCCAAATTTAGAG 553
Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCCTCACCTCATAGCAACT 480
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RESULT 14
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; Sequence 522, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/084414

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9 PRIOR FILING DATE: 1998-05-07
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12 PRIOR APPLICATION NUMBER: 60/084600
13 PRIOR FILING DATE: 1998-05-07
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16 PRIOR APPLICATION NUMBER: 60/084643
17 PRIOR FILING DATE: 1998-05-07
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37 PRIOR FILING DATE: 1998-05-15
38 PRIOR APPLICATION NUMBER: 60/085697
39 PRIOR FILING DATE: 1998-05-15
40 PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1035; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.6e-09;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCAAAATGCAATCTATCTCTTGGCAATCTTCACGGGCTG 60
DB 134 ATGAAACCATCCAGCAAAATGCAATCTATCTCTTGGCAATCTTCACGGGCTG 193
QY 61 GCTGCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCCAAA 120
DB 194 GCTGCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGACACAGTGCCTGCGCAGCGAGATGCCACCTTCCAGTGCATTTGAC 180
DB 254 GCTATGACACAGTGCCTGCGCAGCGAGATGCCACCTTCCAGTGCATTTGAC 313
QY 181 AACCGGCTCAACCGGCTGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 314 AACCGGCTCAACCGGCTGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGCCTGGATCTCTGCTGGTCTCTTCTGAGCAACCCAAACGAGTACGATC 300
DB 374 AAGTGGTGCCTGGATCTCTGCTGGTCTCTTCTGAGCAACCCAAACGAGTACGATC 433
QY 301 GAGATCCAGACAGTGGATGTTATGACAGGGCCCTTACACCTGCTCGGTGCGACAGAC 360
DB 434 GAGATCCAGACAGTGGATGTTATGACAGGGCCCTTACACCTGCTCGGTGCGACAGAC 493
QY 361 AACCAACCAAGACCTCTAGGGTCCACCTATCTGCAAGTACTCTCCAAATTTGAGAG 420
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTATCTGCAAGTACTCTCCAAATTTGAGAG 553

QY 421 ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTCACCTGCATAGCACT 480
DB 554 ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
QY 481 GGTAGACACAGAGCTACGGGTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
DB 614 GGTAGACACAGAGCTACGGGTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATATCTTGGAAATTCAGGCGATCACCAGGAGCAGTCAAGGAGTACGAG 600
DB 674 AGTGAAGACGAATATCTTGGAAATTCAGGCGATCACCAGGAGCAGTCAAGGAGTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACCTGCGCGCGCGGTGTAAGGAGTAAAGTCAACCGTGAAC 660
DB 734 TGCAGTGCCTCCAAATGACCTGCGCGCGCGGTGTAAGGAGTAAAGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAAGGCAAGGCTACAGGTGTCCCGGTGGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTTTCAAGGCAAGGCTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
QY 721 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAA 780
DB 854 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAA 913
QY 781 AGACTCATTTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAACTC 840
DB 914 AGACTCATTTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAACTC 973
QY 841 ATCTTCTTCAATGTCTCTGAAACATGACTATGGAACTACACTTTGGTGGCTTCCAAACAG 900
DB 974 ATCTTCTTCAATGTCTCTGAAACATGACTATGGAACTACACTTTGGTGGCTTCCAAACAG 1033
QY 901 CTGGGACACCAATCCAGCATCATGCTATTGCTCAGGCGCGCTCAGCAGGTGAGC 960
DB 1034 CTGGGACACCAATCCAGCATCATGCTATTGCTCAGGCGCGCTCAGCAGGTGAGC 1093
QY 961 AACGGCACGTCGAGGAGGCGAGCTGCGTCTGGCTGCTGCTCTTCTGCTTTCACCTG 1020
DB 1094 AACGGCACGTCGAGGAGGCGAGCTGCGTCTGGCTGCTGCTCTTCTGCTTTCACCTG 1153
QY 1021 CTTCTCAAAATTTGA 1035
DB 1154 CTTCTCAAAATTTGA 1168

RESULT 15

US-09-978-423A-522

; Sequence 522, Application US/09978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC21
 ; CURRENT APPLICATION NUMBER: US/09/978,423A
 ; CURRENT FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR APPLICATION NUMBER: 60/066364
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 ; PRIOR FILING DATE: 1998-04-01
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 ; PRIOR FILING DATE: 1998-04-01

Query Match 100.08; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.08; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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134 ATGAAACCATCCAGCCAAATGCAATCTATCTCTGGCAATCTTCAACGGGGTG 193
61 GCTGCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 120
194 GCTGCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 253
121 GCTATGACACAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 180
254 GCTATGACACAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 313
181 AACCGGTTCACCGGGTGGCTGCTAAACCGCAGCACCCTCTCTATGCTGGGAATGAC 240
314 AACCGGTTCACCGGGTGGCTGCTAAACCGCAGCACCCTCTCTATGCTGGGAATGAC 373
241 AAGTGTGCTGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
374 AAGTGTGCTGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
301 GAGATCCAGAACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
434 GAGATCCAGAACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
361 AACACCCAAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
494 AACACCCAAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
421 ATTCTTTCAGATCTCTCATTAATGAGGAAACAAATTTAGCTTACCTGCTGCTGCTGCTG 480
554 ATTCTTTCAGATCTCTCATTAATGAGGAAACAAATTTAGCTTACCTGCTGCTGCTGCTG 613
481 GGTAGACAGAGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
614 GGTAGACAGAGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
541 AGTGAAGACGAATCTTTGAAATTCAGGGCATCACCGGGAGAGTCCAGGGGACTACGAG 600
674 AGTGAAGACGAATCTTTGAAATTCAGGGCATCACCGGGAGAGTCCAGGGGACTACGAG 733

QY 601 TGCAGTGCCTCCAAATGAGTGGCGCGCCCGTGTGTACGAGAGTAAAGGTCAACCGTGAAC 660
DB 734 TGCAGTGCCTCCAAATGAGTGGCGCGCCCGTGTGTACGAGAGTAAAGGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAGAAAGCCAAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
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QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTCCTCAGTGGTAAAGGATGACAAA 780
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QY 781 AGACTGATTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 914 AGACTGATTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973
QY 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCTCCAAACAG 900
DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCTCCAAACAG 1033
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DB 1034 CTGGGCCACACCAATGCGCAGATCATCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
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DB 1094 AACGGCACGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
QY 1021 CTCTTCAAAATTTTGA 1035
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RESULT 16

US-09-978-193A-522
; Sequence 522, Application US/09978193A
; Publication No. US20030073624A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC6
; CURRENT APPLICATION NUMBER: US/09/978,193A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

1 PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGAACCATCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTCACGGGCTG 60
Db      |||
Qy      134 ATGAACCATCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTCACGGGCTG 193
Db      |||
Qy      61  GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 120
Db      |||
Qy      194 GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 253
Db      |||
Qy      121 GCTATGACAAACGTGACGGTCCGAGGGGAGAGCGCCACCTTCAGGTGACATTTGAC 180
Db      |||
Qy      254 GCTATGACAAACGTGACGGTCCGAGGGGAGAGCGCCACCTTCAGGTGACATTTGAC 313
Db      |||
Qy      181 AACGGGTGTCACCCGGGTGGCTGCTAAACCGAGAGCCATCTCTATGTCTGGAAATGAC 240
Db      |||
Qy      314 AACGGGTGTCACCCGGGTGGCTGCTAAACCGAGAGCCATCTCTATGTCTGGAAATGAC 373
Db      |||
Qy      241 AAGTGGTGCCTTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 300
Db      |||
Qy      374 AAGTGGTGCCTTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 433
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Qy      301 GAGATCCAGAACGTGGATGTATGAGAGGGCCCTTACCTGCTCGGTGCAGACAGAC 360
Db      |||
Qy      434 GAGATCCAGAACGTGGATGTATGAGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
Db      |||
Qy      361 AACCAACCAAGACCTCTAGGGTCCACTCATCTGCAAGTATCTCCCAAAATGTAGAG 420
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Qy      494 AACCAACCAAGACCTCTAGGGTCCACTCATCTGCAAGTATCTCCCAAAATGTAGAG 553
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Qy      421 ATTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Qy      554 ATTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCAACT 613
Db      |||
Qy      481 GGTAGACAGAGCTAGGTACTTCTGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
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Qy      614 GGTAGACAGAGCTAGGTACTTCTGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
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Qy      541 AGTGAAGACGAATCTTGGAAATTCAGGGCATACCCGGGAGAGTCCAGGGGACTAGAG 600
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Qy      674 AGTGAAGACGAATCTTGGAAATTCAGGGCATACCCGGGAGAGTCCAGGGGACTAGAG 733
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Qy      601 TGCAGTGCCTCCATGATAGTGGGCCGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAAC 660
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Qy      734 TGCAGTGCCTCCATGATAGTGGGCCGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAAC 793
Db      |||
Qy      661 TATCCACCATATCTTCCAGAGCCAGGGTACAGGTGTCCTCCGGAGCAAAAGGGGACA 720
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Qy      794 TATCCACCATATCTTCCAGAGCCAGGGTACAGGTGTCCTCCGGAGCAAAAGGGGACA 853
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Qy      721 CTCAGTGTGAAGCCTTCAGCAGTCCCTCTCAGCAAAATTCAGTGGTACAGGATGACAA 780
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Qy      854 CTCAGTGTGAAGCCTTCAGCAGTCCCTCTCAGCAAAATTCAGTGGTACAGGATGACAA 913
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; Sequence 522, Application US/09999830A
; Publication No. US2003007700A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C70
; CURRENT APPLICATION NUMBER: US/09/999,830A
; CURRENT FILING DATE: 2001-08-31
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QY	121	GCTATGGACAAAGTGAAGCTCCGGCAGGGGAGAGCGCACCTCAGGTGCACTATTGAC	180
Db	254	GCTATGGACAAAGTGAAGCTCCGGCAGGGGAGAGCGCACCTCAGGTGCACTATTGAC	313
QY	181	AACCGGCTCACCGGGTGGCTTGAACCGCAGCAACAATCTATGTGGGAATGAC	240
Db	314	AACCGGCTCACCGGGTGGCTTGAACCGCAGCAACAATCTATGTGGGAATGAC	373
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QY	301	GAGATCCAGAAAGTGGATGTATGACGAGGGCCCTTACACCTGTCTCGGTGCAGACAGAC	360
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Db	734	TGCAGTGCCCTCCAATGACGTGGCCCGCTGGTACGGAGGTAAAGGTCACCGTGNAC	793
QY	661	TATCCACCATACATTTTCAGAAAGCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA	720
Db	794	TATCCACCATACATTTTCAGAAAGCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA	853
QY	721	CTCAGGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA	780
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QY	781	AGACTGATTGAAGGAAGAAAGGGTGAAGAGTGGAAAAAGAGCTTTCTCTCAAAATCTC	840
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QY	841	ATCTTCTTCAATGTCTTGAAACATGACTATGGGAATCTACATTGCGTGGCTCCAAACAG	900
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QY	901	CTGGGGCCACACCAATGCCAGCATCATGCTATTTGGTTCAGCGCGCTGACGAGGTGAGC	960
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Query Match 100.0%; Score 1035; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.6e-09; Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGGACAAGTGAAGCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
Db GCTATGGACAAGTGAAGCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGCGGAATGAC 240
Db AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGCGGAATGAC 373
QY 241 AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGAGCAACACCCAAAGCAGTACAGCATC 300
Db AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGAGCAACACCCAAAGCAGTACAGCATC 433
QY 301 GAGATCCAGACGCTGATGTATGACAGAGGGCCCTTACCTGCTGCTGTCAGACAGAC 360
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QY 421 ATTTCTTCAGATATCTCAATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Db TGCAGTGCCTCAATGATGCTGGCGCGCGCGTGTGACGAGAGTAAAGGTCACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAGAGCCAAAGGTCAGTGTCTCCCGTGGGACAAAGGGGACA 720
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RESULT 19

US-09-978-187B-522

; Sequence 522, Application US/09978187B

Publication No. US20030096744A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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7	PRIOR APPLICATION NUMBER: 60/085580	
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7	PRIOR APPLICATION NUMBER: 60/085573	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085704	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085697	

181 AAACGGGTCACCCGGGTGGCTTGGCTAAACCCGAGCAC

Qy	1	ATGAAACCATCCAGCCAAAAATGCACAAATCTATCTCTTGGGCAATCTTTCACGGGGCTG	60
Db	134	ATGAAACCATCCAGCCAAAAATGCACAAATCTATCTCTTGGGCAATCTTTCACGGGGCTG	193
Qy	61	GCTGCTCTGTGTCCTTCCAGGAGTGCCCTGGCGACGCGAGATGCCACTTTCGCCAAA	120
Db	194	GCTGCTCTGTGTCCTTCCAGGAGTGCCCTGGCGACGCGAGATGCCACTTTCGCCAAA	253
Qy	121	GCTATGGACCAACGTCACGCTCGGCGAGGGGAGAGCGCACCTTCAGGTGCATTTATGAC	180
Db	254	GCTATGGACCAACGTCACGCTCGGCGAGGGGAGAGCGCACCTTCAGGTGCATTTATGAC	313
Qy	181	AACCGGGTCACCCGGTGGCTGGCTAAACCGCAGCACCAATCTCTATGTCTGGGAATGAC	240
Db	314	AACCGGGTCACCCGGTGGCTGGCTAAACCGCAGCACCAATCTCTATGTCTGGGAATGAC	373

241 AAGTGTGTCCTGGATCCTCGGTGGTCTTCTGAGCAACACCCAAAGCAGTACAGATC 300
Db |||||
374 AAGTGTGTCCTGGATCCTCGGTGGTCTTCTGAGCAACACCCAAAGCAGTACAGATC 433
QY |||||
301 GAGATCCAGACGTCGATGATGATGAGAGAGGCGCTTACCTGCTGGTGCAGACAGAC 360
Db |||||
434 GAGATCCAGACGTCGATGATGATGAGAGAGGCGCTTACCTGCTGGTGCAGACAGAC 493
QY |||||
361 AACCAACCAAGACCTCTAGGGTCCACCTATTGCAAGTATCTCCCAAAATGTTAGAG 420
Db |||||
494 AACCAACCAAGACCTCTAGGGTCCACCTATTGCAAGTATCTCCCAAAATGTTAGAG 553
QY |||||
421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
Db |||||
554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY |||||
481 GGTAGACAGAGCCTACGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db |||||
614 GGTAGACAGAGCCTACGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
QY |||||
541 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCCGGGAGAGTACAGGAGTACAGAG 600
Db |||||
674 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCCGGGAGAGTACAGGAGTACAGAG 733
QY |||||
601 TGCAGTGCCTCCATGACGTGGCGCGCGCTGTGTACGAGAGTAAAGGTACCGTGAAC 660
Db |||||
734 TGCAGTGCCTCCATGACGTGGCGCGCGCTGTGTACGAGAGTAAAGGTACCGTGAAC 793
QY |||||
661 TATCCACCATACATTTCCAGAAAGCCAGGGTACAGGTGTCCTCCGAGCAAAAGGGGACA 720
Db |||||
794 TATCCACCATACATTTCCAGAAAGCCAGGGTACAGGTGTCCTCCGAGCAAAAGGGGACA 853
QY |||||
721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGAGTACAGAA 780
Db |||||
854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGAGTACAGAA 913
QY |||||
781 AGACTGATTCAGGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATC 840
Db |||||
914 AGACTGATTCAGGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATC 973
QY |||||
841 ATCTTCTCAATGCTCTGAACATGACTATGGGAACTACACTTGGCTGGCTCCCAACAG 900
Db |||||
974 ATCTTCTCAATGCTCTGAACATGACTATGGGAACTACACTTGGCTGGCTCCCAACAG 1033
QY |||||
901 CTGGGCAACCAATGCTGAGCAGTATGCTATTTGGTCCAGGCGCGTACAGAGGTGAGC 960
Db |||||
1034 CTGGGCAACCAATGCTGAGCAGTATGCTATTTGGTCCAGGCGCGTACAGAGGTGAGC 1093
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961 AACGGCACGTCGAGGAGGCGAGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db |||||
1094 AACGGCACGTCGAGGAGGCGAGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY |||||
1021 CTTCTCAAAATTTGA 1035
Db |||||
1154 CTTCTCAAAATTTGA 1168

RESULT 20

US-09-978-643A-522
; Sequence 522, Application US/09978643A
; Publication No. US20030104998A1
; GENERAL INFORMATION:
; APPLICANT: Aekhenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C16
; CURRENT APPLICATION NUMBER: US/09/978,643A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-643A-522

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAATGCAATTTCTTCTTGGCAATCTTCAAGGCTG 60
Db 134 ATGAAACCATCCAGCCAAATGCAATTTCTTCTTGGCAATCTTCAAGGCTG 193
QY 61 GCTGCTCTCTGCTCTTCCAGAGGTGCGCGTGGCGAGAGATGCCACCTTCCCAA 120
Db 194 GCTGCTCTCTGCTCTTCCAGAGGTGCGCGTGGCGAGAGATGCCACCTTCCCAA 253
QY 121 GCTATGGAACAAGTGAAGTCCCGGAGGGGAGAGCGCCCTCAGGTGCACTATTGAC 180
Db 254 GCTATGGAACAAGTGAAGTCCCGGAGGGGAGAGCGCCCTCAGGTGCACTATTGAC 313
QY 181 AACCGGTCACCGGGTGGCTTAAACCGAGAGACCATCTCTATGCTGGGAATGAC 240
Db 314 AACCGGTCACCGGGTGGCTTAAACCGAGAGACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGGCTTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAAGCAGTACAGCATC 300
Db 374 AAGTGGTGGCTTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAAGCAGTACAGCATC 433
QY 301 GAGATCCAGACGTCGATGATGATGAGAGGCGCTTACACTGCTCGGTGCAGACAGAC 360
Db 434 GAGATCCAGACGTCGATGATGATGAGAGGCGCTTACACTGCTCGGTGCAGACAGAC 493
QY 361 AACCAACCAAGACCTCTAGGGTCCACCTATTGCAAGTATCTCCCAAAATGTTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTATTGCAAGTATCTCCCAAAATGTTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 481 GGTAGACAGAGCCTACGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db 614 GGTAGACAGAGCCTACGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
QY 541 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCCGGGAGAGTACAGGAGTACAGAG 600
Db 674 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCCGGGAGAGTACAGGAGTACAGAG 733

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;; PRIOR FILING DATE: 1998-04-27
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;; PRIOR APPLICATION NUMBER: 60/085580
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAACCATCCAGCAAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG 60
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Db	134	ATGAAAACCATCCAGCAAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG	193
QY	61	GCTGCTCTGTGTCTCTTCCAGAGAGTGCCTGCGGAGGAGATCCACCTTCTCCCAAA	120
Db	194	GCTGCTCTGTGTCTCTTCCAGAGAGTGCCTGCGGAGGAGATCCACCTTCTCCCAAA	253
QY	121	GCTATGGACAACGTGACGGTCCGGAGGGAGAGGCCACCTCAGGTGCACTATTGAC	180
Db	254	GCTATGGACAACGTGACGGTCCGGAGGGAGAGGCCACCTCAGGTGCACTATTGAC	313
QY	181	AACCGGTCACCCGGTGGCTTAAACCGCAGCACCATCTCTATCTGGGATGAC	240
Db	314	AACCGGTCACCCGGTGGCTTAAACCGCAGCACCATCTCTATCTGGGATGAC	373
QY	241	AGTGGTGCCTGGATCTCTCGGTGTCTTCTGAGGAAACCCAAACGAGTACAGCATC	300
Db	374	AGTGGTGCCTGGATCTCTCGGTGTCTTCTGAGGAAACCCAAACGAGTACAGCATC	433
QY	301	GAGATCCAGAACGTGGATGTGTATCAGCAGGGCCCTTACCTGCTCGGTGCGAGACAG	360
Db	434	GAGATCCAGAACGTGGATGTGTATCAGCAGGGCCCTTACCTGCTCGGTGCGAGACAG	493
QY	361	AACCAACCAAGACCTTAGGGTCCACCTCAATGTGCAAGTATCTCCAAATTTAGAG	420
Db	494	AACCAACCAAGACCTTAGGGTCCACCTCAATGTGCAAGTATCTCCAAATTTAGAG	553
QY	421	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCTGCATGACAACT	480
Db	554	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCTGCATGACAACT	613
QY	481	GGTAGACCAGACCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG	540
Db	614	GGTAGACCAGACCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG	673
QY	541	AGTGAAGCAATCTTGGAAATTCAGGGCAATCAACCGGGAGCAGTCAAGGGGACTACGAG	600
Db	674	AGTGAAGCAATCTTGGAAATTCAGGGCAATCAACCGGGAGCAGTCAAGGGGACTACGAG	733
QY	601	TGCAGTGCCTCCAATGACGTGGCGCCGCGCTGCTGAGAGTAAAGGTACCGTGAAC	660
Db	734	TGCAGTGCCTCCAATGACGTGGCGCCGCGCTGCTGAGAGTAAAGGTACCGTGAAC	793
QY	661	TATCCACATACATTTTCAGAAAGCCAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	720
Db	794	TATCCACATACATTTTCAGAAAGCCAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA	913
QY	781	AGACTGATTGAAGGAAAGAGGGTCAAGTGGAAACTACATTTGGGAGGCTTCCAACTC	840
Db	914	AGACTGATTGAAGGAAAGAGGGTCAAGTGGAAACTACATTTGGGAGGCTTCCAACTC	973
QY	841	ATCTTCTCAATGTCTCTGAACATGACTATGGAACTACATTTGGGAGGCTTCCAACTC	900
Db	974	ATCTTCTCAATGTCTCTGAACATGACTATGGAACTACATTTGGGAGGCTTCCAACTC	1033
QY	901	CTGGGACACCAATGCGCAGCATATGCTATTGGTTCAGGCGCGTCAAGGAGGTGAGC	960
Db	1034	CTGGGACACCAATGCGCAGCATATGCTATTGGTTCAGGCGCGTCAAGGAGGTGAGC	1093
QY	961	AACGGACGTCGAGGAGGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
Db	1094	AACGGACGTCGAGGAGGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1153
QY	1021	CTTCTCAAAATTTGA	1035
Db	1154	CTTCTCAAAATTTGA	1168

RESULT 23

US-09-978-188A-522

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: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Guney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2630P1C8
: CURRENT APPLICATION NUMBER: US/09/978,188A
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATGACAAATCTATCTTGGGCAATCTTACGGGGCTG 60
DB 134 ATGAAACCATCCAGCCAAAATGACAAATCTATCTTGGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTGCTCTTCCAGGAGTGCCGTCGCGAGGAGTGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTGCTCTTCCAGGAGTGCCGTCGCGAGGAGTGCCACCTTCCCAAA 253
QY 121 GCTATGGCAACGTCGAGCGGTCCGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGGCAACGTCGAGCGGTCCGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCACCGGGTGGCTGCTAAACGCGAGCACTCTTATGCTGGGATGAC 240

DB 314 AACCGGGTCACCGGGTGGCTGAAACCGGAGCAACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGTGCTTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTAGACATC 300
DB 374 AAGTGTGCTTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTAGACATC 433
QY 301 GAGATCCAGAACGTCGATGTATGAGAGGGGCTTACACCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAACGTCGATGTATGAGAGGGGCTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACCACCCAAAGACCTCTAGGCTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCACCCAAAGACCTCTAGGCTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTCTCAGATATCTTCCATTAATGAAGGAAACAATATTAGCTTCACTGCTAGCAACT 480
DB 554 ATTCTCTCAGATATCTTCCATTAATGAAGGAAACAATATTAGCTTCACTGCTAGCAACT 613
QY 481 GGTAGACAGAGCTTACGTTTACCTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
DB 614 GGTAGACAGAGCTTACGTTTACCTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATACTTTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGACGAATACTTTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCCATGACGTCGCGCCGCGGTGAGTAAAGGTAAAGGTCAACCGTGAAC 660
DB 734 TGCAGTGCCTCCATGACGTCGCGCCGCGGTGAGTAAAGGTAAAGGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAGAGCCAGGTCAGGTGTCCTCCGTCGGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTTTCAGAGCCAGGTCAGGTGTCCTCCGTCGGGACAAAGGGGACA 853
QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAAGGATCACAAA 780
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAAGGATCACAAA 913
QY 781 AGACTGATGAAGGAAAGAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAACTC 840
DB 914 AGACTGATGAAGGAAAGAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAACTC 973
QY 841 ATCTTCTTCAATGCTCTGACATGACTATGGGACTACATTTGGTGGGCTCCACAAAG 900
DB 974 ATCTTCTTCAATGCTCTGACATGACTATGGGACTACATTTGGTGGGCTCCACAAAG 1033
QY 901 CTGGGCCACACCAATGCCAGCATCATGCTATTGCTCCAGGCGCGCTCAGCGAGGTGAGC 960
DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGCTCCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGTCGAGAGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1094 AACGGCAGTCGAGAGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY 1021 CTCTCAAAATTTTGA 1035
DB 1154 CTCTCAAAATTTTGA 1168

RESULT 24
US-09-978-681A-522
; Sequence 522, Application US/09978681A
; Publication No. US20030195148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630FIC18
CURRENT APPLICATION NUMBER: US/09/578,681A
CURRENT FILING DATE: 2002-03-19
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742

1 PRIOR FILING DATE: 1998-04-30
 2 PRIOR APPLICATION NUMBER: 60/084366
 3 PRIOR FILING DATE: 1998-05-05
 4 PRIOR APPLICATION NUMBER: 60/084414
 5 PRIOR FILING DATE: 1998-05-06
 6 PRIOR APPLICATION NUMBER: 60/084441
 7 PRIOR FILING DATE: 1998-05-06
 8 PRIOR APPLICATION NUMBER: 60/084637
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 10 PRIOR APPLICATION NUMBER: 60/084639
 11 PRIOR FILING DATE: 1998-05-07
 12 PRIOR APPLICATION NUMBER: 60/084640
 13 PRIOR FILING DATE: 1998-05-07
 14 PRIOR APPLICATION NUMBER: 60/084598
 15 PRIOR FILING DATE: 1998-05-07
 16 PRIOR APPLICATION NUMBER: 60/084600
 17 PRIOR FILING DATE: 1998-05-07
 18 PRIOR APPLICATION NUMBER: 60/084627
 19 PRIOR FILING DATE: 1998-05-07
 20 PRIOR APPLICATION NUMBER: 60/084643
 21 PRIOR FILING DATE: 1998-05-07
 22 PRIOR APPLICATION NUMBER: 60/085339
 23 PRIOR FILING DATE: 1998-05-13
 24 PRIOR APPLICATION NUMBER: 60/085338
 25 PRIOR FILING DATE: 1998-05-13
 26 PRIOR APPLICATION NUMBER: 60/085323
 27 PRIOR FILING DATE: 1998-05-13
 28 PRIOR APPLICATION NUMBER: 60/085582
 29 PRIOR FILING DATE: 1998-05-15
 30 PRIOR APPLICATION NUMBER: 60/085700
 31 PRIOR FILING DATE: 1998-05-15
 32 PRIOR APPLICATION NUMBER: 60/085689
 33 PRIOR FILING DATE: 1998-05-15
 34 PRIOR APPLICATION NUMBER: 60/085579
 35 PRIOR FILING DATE: 1998-05-15
 36 PRIOR APPLICATION NUMBER: 60/085580
 37 PRIOR FILING DATE: 1998-05-15
 38 PRIOR APPLICATION NUMBER: 60/085573
 39 PRIOR FILING DATE: 1998-05-15
 40 PRIOR APPLICATION NUMBER: 60/085704
 41 PRIOR FILING DATE: 1998-05-15
 42 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3,6e-09;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAACCATCCAGCCAAATGCAATCTATCTCTTGGGCAATCTTCCAGGGGCTG 60
 134 ATGAAACCATCCAGCCAAATGCAATCTATCTCTTGGGCAATCTTCCAGGGGCTG 193
 61 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGGCGAGGAGATGCCACCTTCCCAAA 120
 194 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGGCGAGGAGATGCCACCTTCCCAAA 253
 121 GCTATGACAACTGACGGTCCGGAGGGGAGAGCGCCCTCAGTGCACTATTGAC 180
 254 GCTATGACAACTGACGGTCCGGAGGGGAGAGCGCCCTCAGTGCACTATTGAC 313
 181 AACCGGTCACCGGGTGCTGCTAAACCGAGCACTCTCTATGTGCGGAATGAC 240
 314 AACCGGTCACCGGGTGCTGCTAAACCGAGCACTCTCTATGTGCGGAATGAC 373
 241 AAGTGGTGCTGCTGCTCTCTGAGCACTCTCTGAGCACTCTCTATGTGCGGAATGAC 300
 374 AAGTGGTGCTGCTGCTCTCTGAGCACTCTCTGAGCACTCTCTATGTGCGGAATGAC 433
 301 GAGATCAGAACTGAGTGATGAGCGAGGGGCTTACACCTGCTGCTGCGTGACAGAC 360
 434 GAGATCAGAACTGAGTGATGAGCGAGGGGCTTACACCTGCTGCTGCGTGACAGAC 493
 361 AACCAACCAAGACCTTAGGGTCCACTATTGTGCAAGTATCTCCAAAATTTAGAG 420

Db 494 AACCAACCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 553
 Qy 421 ATTTCTTCAGATATCTCCATTAAAGGGAACAATATTAGCTCCTCAGCTGCAATAGCACT 480
 Db 554 ATTTCTTCAGATATCTCCATTAAAGGGAACAATATTAGCTCCTCAGCTGCAATAGCACT 613
 Qy 481 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAAGCGTTGGCTTTG 540
 Db 614 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAAGCGTTGGCTTTG 673
 Qy 541 AGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTACGGGACCTACAG 600
 Db 674 AGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTACGGGACCTACAG 733
 Qy 601 TGCAGTGCTCTCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 660
 Db 734 TGCAGTGCTCTCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 Qy 661 TATCCACCATACATTTGAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
 Db 794 TATCCACCATACATTTGAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
 Qy 721 CTGAGTGTAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGGTACAAAGGATGACAAA 780
 Db 854 CTGAGTGTAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGGTACAAAGGATGACAAA 913
 Qy 781 AGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAACACAGACCTTCTCTCAAACTC 840
 Db 914 AGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAACACAGACCTTCTCTCAAACTC 973
 Qy 841 ATCTTCTCAATGTCTCTGAACATGATATGGGAACTACACTTGGTGGCTTCCAAACAG 900
 Db 974 ATCTTCTCAATGTCTCTGAACATGATATGGGAACTACACTTGGTGGCTTCCAAACAG 1033
 Qy 901 CTGGGCGACACCAATGCCAGCATCATCTATTGGTCCAGGCGCGGTACGGAGGTGAGC 960
 Db 1034 CTGGGCGACACCAATGCCAGCATCATCTATTGGTCCAGGCGCGGTACGGAGGTGAGC 1093
 Qy 961 AACGGCACGTGAGAGGGGAGGCTGGCTCTGGCTGCTGCTCTCTTCTGCTTTCACCTG 1020
 Db 1094 AACGGCACGTGAGAGGGGAGGCTGGCTCTGGCTGCTGCTCTCTTCTGCTTTCACCTG 1153
 Qy 1021 CTCTCAAAATTTGA 1035
 Db 1154 CTCTCAAAATTTGA 1168

RESULT 25
 US-09-978-194A-522
 ; Sequence 522, Application US/09978194A
 ; Publication No. US2003019533A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillen, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C10
CURRENT APPLICATION NUMBER: US/09/978,194A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640

Db	674	AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTTCAGGGGACTACGAG	733
QY	601	TGCAGTGCCTCCAAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC	660
Db	734	TGCAGTGCCTCCAAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC	793
QY	661	TATCCACATACATTTTCAGAAAGCCAAAGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA	720
Db	794	TATCCACATACATTTTCAGAAAGCCAAAGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCCCTCAGCAGAAATTCACAGTGGTACAAAGGATGACAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCCCTCAGCAGAAATTCACAGTGGTACAAAGGATGACAA	913
QY	781	AGACTGATTTCAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACTTTTCCTCTCAAAATC	840
Db	914	AGACTGATTTCAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACTTTTCCTCTCAAAATC	973
QY	841	ATCTTCTTCAATGTCTCTGAAACATGACTATGGGAACTACACTTGCCTGCGCTCCAAACAG	900
Db	974	ATCTTCTTCAATGTCTCTGAAACATGACTATGGGAACTACACTTGCCTGCGCTCCAAACAG	1033
QY	901	CTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCCTCAGCGAGGTGAGC	960
Db	1034	CTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCCTCAGCGAGGTGAGC	1093
QY	961	AACGGCAGCTCGAGGAGGGCAGGCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
Db	1094	AACGGCAGCTCGAGGAGGGCAGGCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1153
QY	1021	CTTCTCAAAATTTTGA	1035
Db	1154	CTTCTCAAAATTTTGA	1168

RESULT 26

US-09-999-829A-522

; Sequence 522, Application US/09999829A

; Publication No. US20030195344A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gottard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PIC61

; CURRENT APPLICATION NUMBER: US/09/999,829A

; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 624

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATCTCTATCTCTTGGCAATCTTCACGGGGCTG 60

Db	134	ATGAAACCATCCAGCCAAAATGACAAATTCCTCTCTGGGCAATCTTCACGGGGCTG	193
QY	61	GCTGCTCTGTGTCCTTCCAAGAGTGCOCGTGCGCAGCGGAGATGCCACCTTCCCCAA	120
Db	194	GCTGCTCTGTGTCCTTCCAAGAGTGCOCGTGCGCAGCGGAGATGCCACCTTCCCCAA	253
QY	121	GCTATGGCAACGTCACCGTCCGGCAGGGGAGAGCCACCCTCAGGTGCATATTGAC	180
Db	254	GCTATGGCAACGTCACCGTCCGGCAGGGGAGAGCCACCCTCAGGTGCATATTGAC	313
QY	181	AACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTCGGGAATGAC	240
Db	314	AACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTCGGGAATGAC	373
QY	241	AAGTGGTGGCTGGATCTCTCGGTGGTCTCTTTCTGAGGAACACCCAAACGAGTACAGCATC	300
Db	374	AAGTGGTGGCTGGATCTCTCGGTGGTCTCTTTCTGAGGAACACCCAAACGAGTACAGCATC	433
QY	301	GAGATCCAGAAACGTCGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGC	360
Db	434	GAGATCCAGAAACGTCGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGC	493
QY	361	AACCAACCCAAAGACCTCTAGGGTCCACCTCTATTTGCAAGTATCTCCAAAATTGTAGAG	420
Db	494	AACCAACCCAAAGACCTCTAGGGTCCACCTCTATTTGCAAGTATCTCCAAAATTGTAGAG	553
QY	421	ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCTCACCTGCATAGCAACT	480
Db	554	ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCTCACCTGCATAGCAACT	613
QY	481	GGTAGACGAGGCCTACGGTTACTTTGGAGACACATCTCTCTCCAAAGCGGTTGGCTTTGTG	540
Db	614	GGTAGACGAGGCCTACGGTTACTTTGGAGACACATCTCTCTCCAAAGCGGTTGGCTTTGTG	673
QY	541	AGTGAAGACGAATACTTTGGAATTTCAAGGCATCACCCGGGAGCAGTCAAGGGAATACAG	600
Db	674	AGTGAAGACGAATACTTTGGAATTTCAAGGCATCACCCGGGAGCAGTCAAGGGAATACAG	733
QY	601	TGCAGTGCCTCCAAATGACGTGGCCGCGCCGCTGGTACGGAGGTAAAGGTCACCGTGAAC	660
Db	734	TGCAGTGCCTCCAAATGACGTGGCCGCGCCGCTGGTACGGAGGTAAAGGTCACCGTGAAC	793
QY	661	TATCCACATACATTTTCAGAGCCAAAGGTTACAGGTGTCCCGGTGGGACAAAAGGGGACA	720
Db	794	TATCCACATACATTTTCAGAGCCAAAGGTTACAGGTGTCCCGGTGGGACAAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA	913
QY	781	AGACTGATTCAAGGAAGAGGGGTGAAAGTGAAGAACAGACCTTTCTCTCAAAATCTC	840
Db	914	AGACTGATTCAAGGAAGAGGGGTGAAAGTGAAGAACAGACCTTTCTCTCAAAATCTC	973
QY	841	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTCGCTGGCTCCAAACAG	900
Db	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTCGCTGGCTCCAAACAG	1033
QY	901	CTGGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCAAGGAGGTGAGC	960
Db	1034	CTGGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCAAGGAGGTGAGC	1093
QY	961	AACGGCACGTCGAGGAGGGCAGGCTGGCTGCTGCTGCTGCTCTCTCTGCTCTGACCTG	1020
Db	1094	AACGGCACGTCGAGGAGGGCAGGCTGGCTGCTGCTGCTGCTCTCTCTGCTCTGACCTG	1153
QY	1021	CTTCTCAAAATTTGA	1035
Db	1154	CTTCTCAAAATTTGA	1168

US-09-978-544A-522

Sequence 522, Application US/09978544A
Publication No. US20030199436A1

GENERAL INFORMATION:

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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

FILE REFERENCE: P2630PIC13

CURRENT APPLICATION NUMBER: US/09/978,544A

CURRENT FILING DATE: 2002-03-19

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.6e-09;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 134 ATGAAACCATCCAGCCAAAATGCACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193
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QY 61 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAAA 120
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Db 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAAA 253
|||
QY 121 GCTATGGACAACGTGACCGTCCGCGAGGGGAGAGCGGCAACCTCAGTGCACTATTGAC 180
|||
Db 254 GCTATGGACAACGTGACCGTCCGCGAGGGGAGAGCGGCAACCTCAGTGCACTATTGAC 313
|||
QY 181 AACCGGGTCACCCGGGTGCGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
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Db 314 AACCGGTCAACCGGTGGCTGCTAAACCGAGACCATCTCTATCTGGAATGAC 373
QY 241 AAGTGGTCTGGATCTCGGTGCTCTTCTGAGCAACCCAAAGCGAGTACAGATC 300
Db 374 AAGTGGTCTGGATCTCGGTGCTCTTCTGAGCAACCCAAAGCGAGTACAGATC 433
QY 301 GAGATCCAGAACGTTGATGTATGACAGAGGCGCTTACACCTGCTCGGTGAGACAGAC 360
Db 434 GAGATCCAGAACGTTGATGTATGACAGAGGCGCTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACACCCAAAGACCTTACGCTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 420
Db 494 AACACCCAAAGACCTTACGCTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTTACCTGCTCATAGCACT 480
Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTTACCTGCTCATAGCACT 613
QY 481 GGTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db 614 GGTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCAAAGCGTTGGCTTTGTG 673
QY 541 AGTGAAGACGAATCTTGGAAATTCAGGCGCATCACCGGAGAGTCAAGGAGTACGAG 600
Db 674 AGTGAAGACGAATCTTGGAAATTCAGGCGCATCACCGGAGAGTCAAGGAGTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGGTACGAGAGTAAAGTCAACCGTGAAC 660
Db 734 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGGTACGAGAGTAAAGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAAGCAAGGTAAGGTGTCCTCCGTCGGGCAAAAGGGGACA 720
Db 794 TATCCACCATACATTTTCAAGCAAGGTAAGGTGTCCTCCGTCGGGCAAAAGGGGACA 853
QY 721 CTGCACTGTAAGCTTCAGAGTCCCTTCAGAGATTCAGTGTGTACAGATGACAAA 780
Db 854 CTGCACTGTAAGCTTCAGAGTCCCTTCAGAGATTCAGTGTGTACAGATGACAAA 913
QY 781 AGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGAAAGGTAAGTGAAGTGAAGTGAAG 913
Db 914 AGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGAAAGGTAAGTGAAGTGAAGTGAAG 973
QY 841 ATCTTCTCAATGTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 974 ATCTTCTCAATGTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1033
QY 901 CTGGGCAACACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGTGA 960
Db 1034 CTGGGCAACACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGTGA 1093
QY 961 AACGCGAGTTCAGAGGCGAGGCTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1094 AACGCGAGTTCAGAGGCGAGGCTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 29

US-09-978-665A-522
; Sequence 522, Application US/09978665A
; Publication No. US20030199437A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC19
; CURRENT APPLICATION NUMBER: US/09/978,665A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAACCATCCAGCCAAATGCAATTCCTCTCTTTGGGCAATCTTTCAGGGGCTG	60
Db	134	ATGAAACCATCCAGCCAAATGCAATTCCTCTCTTTGGGCAATCTTTCAGGGGCTG	193
Qy	61	GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGGAGATGCCACTTCCCAAA	120
Db	194	GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGGAGATGCCACTTCCCAAA	253
Qy	121	GCTATGAGCAACCTGAGCGGTCCCGGAGGGGAGCGGCCCTCAGGTGCATATTGAC	180
Db	254	GCTATGAGCAACCTGAGCGGTCCCGGAGGGGAGCGGCCCTCAGGTGCATATTGAC	313
Qy	181	AACCGGCTCACCCGGGTGGCTGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	240
Db	314	AACCGGCTCACCCGGGTGGCTGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	373
Qy	241	AAGTGTGCTGGATCCTCGGTGCTCTTCTGAGCAACCAACCAACGAGTACAGATC	300
Db	374	AAGTGTGCTGGATCCTCGGTGCTCTTCTGAGCAACCAACCAACGAGTACAGATC	433
Qy	301	GAGATCCAGAACCTGAGTGTATGAGGAGGGCCCTTACCTGCTCGGTGAGAGAC	360
Db	434	GAGATCCAGAACCTGAGTGTATGAGGAGGGCCCTTACCTGCTCGGTGAGAGAC	493
Qy	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGAG	420

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Query Match 100.0%; Score 1035; DB 10; Length 1679;

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QY	1	ATGAACACCATCCAGCCAAATGCAATTCCTCTTTGGGCAATCTTCAGGGGCTG	60
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Db	434	GAGATCCAGAACTGTGATGACGAGGGCCCTTACCTGCTCGGTGAGACAGAC	493
QY	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAGATATCTCCCAAAATTTAGAG	420
Db	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAGATATCTCCCAAAATTTAGAG	553
QY	421	ATTTCTTCAGATATCTCCATTAAAGGGAACAATATTAGCTCACCTGCATAGCAACT	480
Db	554	ATTTCTTCAGATATCTCCATTAAAGGGAACAATATTAGCTCACCTGCATAGCAACT	613
QY	481	GGTAGACGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTTTGTG	540
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QY	541	AGTGAAGACGAATACTTTGGAATTCAGGGCATCAACCGGAGCAGTCAGGGGACTACGAG	600


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674 AGTGAAGACGAAATCTTGGAAATTCAGGSCATCACCCGGAGCAGTCAGGGGACTACGAG 733
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794 TATCCACCATACATTTCAAGAGCCAAAGGGTACAGGTGTCCCCTGGGACAAAAGGGGACA 853
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721 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGCAATTCAGTGGTACAGGATGACAAA 780
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Db
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974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGCGTGGCTCCAAACAG 1033
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901 CTGGGCCACACCAATGCAGCATCATGTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 960
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Db
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1094 AACGGCACGTGAGGAGGGCAGGCTGCGTCTGGCTGCTGCTCTTCTGGTCTTGGCACCTG 1153
QY
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Db
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1154 CTTCTCAAAATTTGA 1168
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Search completed: May 28, 2004, 21:31:31
Job time : 500.763 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:09:09 ; Search time 458.39 Seconds

(without alignments)

9592.021 Million cell updates/sec

Title: US-10-017-084A-522_COPY_134_1168

Perfect score: 1035

Sequence: 1 atgaaaccatccagccaaa.....acctgcttcctcaaatgtga 1035

Scoring table: IDENTITY_NUC

Gapop 1.0 , Gapext 0.1

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_29Jan04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	100.0	1679	2	Aaz34324 Human PRO
2	1035	100.0	1679	3	Aac78590 Human PRO
3	1035	100.0	1679	4	Aac87037 Nucleotid
4	1035	100.0	1679	4	Aas21431 Human cDN
5	1035	100.0	1679	6	ABK33598
6	1035	100.0	1679	6	ABL88099
7	1035	100.0	1679	6	ABL95588
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9	1035	100.0	1679	7	ACD24040 Novel hum
10	1035	100.0	1679	7	ACA66903 cDNA enco
11	1035	100.0	1679	7	ACD42387
12	1035	100.0	1679	7	ACD68655
13	1035	100.0	1679	7	ACA67181
14	1035	100.0	1679	7	ACA63892
15	1035	100.0	1679	7	ACA03790
16	1035	100.0	1679	7	ACA04996
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19	1035	100.0	1679	7	ABK33598
20	1035	100.0	1679	7	ABK33598
21	1035	100.0	1679	7	ABK33598
22	1035	100.0	1679	7	ACA04516
23	1035	100.0	1679	7	ACA66437

24	1035	100.0	1679	7	ACA68559	Novel hum
25	1035	100.0	1679	7	ACA04211	Human cDN
26	1035	100.0	1679	8	ACA65657	Human cDN
27	1035	100.0	1679	8	ADA45894	Novel hum
28	1035	100.0	1679	8	ADA76325	Human PRO
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30	1035	100.0	1679	8	ADA18975	Human PRO
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33	1035	100.0	1679	8	ADB27924	cDNA enco
34	1035	100.0	1679	8	ADA86403	Novel hum
35	1035	100.0	1679	8	ADB15967	Human PRO
36	1035	100.0	1679	8	ADA47753	Human PRO
37	1035	100.0	1679	8	ADA67548	Human PRO
38	1035	100.0	1679	8	ADB30555	cDNA enco
39	1035	100.0	1679	8	ADA85851	Novel hum
40	1035	100.0	1679	8	ADA97063	Human PRO
41	1035	100.0	1679	8	ADA79367	Human PRO
42	1035	100.0	1679	8	ADA87506	Novel hum
43	1035	100.0	1679	8	ADB16708	Human PRO
44	1035	100.0	1679	8	ADA91800	Novel hum
45	1035	100.0	1679	8	ADB14863	Human PRO
46	1035	100.0	1679	8	ADA25061	Novel hum
47	1035	100.0	1679	8	ADA47275	Human sec
48	1035	100.0	1679	8	ADB18824	Novel hum
49	1035	100.0	1679	8	ADA94039	Human PRO
50	1035	100.0	1679	8	ADB19935	Novel hum
51	1035	100.0	1679	8	ADB13247	Novel hum
52	1035	100.0	1679	8	ACD98611	Novel hum
53	1035	100.0	1679	8	ACD30038	Novel hum
54	1035	100.0	1679	8	ADA12722	Human cDN
55	1035	100.0	1679	8	ADA74501	Human PRO
56	1035	100.0	1679	8	ADB24734	Human PRO
57	1035	100.0	1679	8	ADA82258	Human PRO
58	1035	100.0	1679	8	ADA75221	Human PRO
59	1035	100.0	1679	8	ADA85299	Novel hum
60	1035	100.0	1679	8	ADA84747	Novel hum
61	1035	100.0	1679	8	ADB30003	cDNA enco
62	1035	100.0	1679	8	ADA80531	Human PRO
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64	1035	100.0	1679	8	ADA46998	Human PRO
65	1035	100.0	1679	8	ADB25294	Human PRO
66	1035	100.0	1679	8	ADA93470	Human PRO
67	1035	100.0	1679	8	ADB26820	cDNA enco
68	1035	100.0	1679	8	ADB31107	cDNA enco
69	1035	100.0	1679	8	ABT44571	Human PRO
70	1035	100.0	1679	8	ADA61035	Homo sapi
71	1035	100.0	1679	8	ADB24182	Human PRO
72	1035	100.0	1679	8	ADA96511	Human PRO
73	1035	100.0	1679	8	ADA81083	Human PRO
74	1035	100.0	1679	8	ADA95959	Human PRO
75	1035	100.0	1679	8	ADB26268	cDNA enco
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77	1035	100.0	1679	8	ACD82238	Human sec
78	1035	100.0	1679	8	ACD29453	Novel hum
79	1035	100.0	1679	8	ADA77552	Human PRO
80	1035	100.0	1679	8	ADB18272	Human PRO
81	1035	100.0	1679	8	ADA86955	Novel hum
82	1035	100.0	1679	8	ADA88058	Novel hum
83	1035	100.0	1679	8	ADA46446	Novel hum
84	1035	100.0	1679	8	ADB28476	cDNA enco
85	1035	100.0	1679	8	ADB29028	cDNA enco
86	1035	100.0	1679	8	ADA76980	Human PRO
87	1035	100.0	1679	8	ADA88610	Novel hum
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89	1035	100.0	1679	8	ADB27372	cDNA enco
90	1035	100.0	1679	8	ADB22305	Novel hum
91	1035	100.0	1679	8	ACD30273	Human cDN
92	1035	100.0	1679	8	ABT43944	Human mem
93	1035	100.0	1679	8	ADA66996	Human PRO
94	1035	100.0	1679	8	ADB22857	Human PRO
95	1035	100.0	1679	8	ADB23630	Human PRO
96	1035	100.0	1679	8	ADA92352	Novel hum

Adh15415 Human PRO
Adh83615 Novel hum
Adh80721 Novel hum
Adh73262 Novel hum

97 1035 100.0 1679 8 ADB15415
98 1035 100.0 1679 8 ADB83615
99 1035 100.0 1679 8 ADB80721
100 1035 100.0 1679 8 ADB73262

ALIGNMENTS

RESULT 1

AAZ34324
ID AAZ34324 standard; cDNA; 1679 BP.

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AC AAZ34324;

XX
DT 07-DEC-1999 (first entry)

XX
DE Human PRO337 nucleotide sequence.

XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.

XX
OS Homo sapiens.

XX
PN WO9946281-A2.

XX
PD 16-SEP-1999.

XX
XX 08-MAR-1999; 99WO-US005028.

XX
PR 10-MAR-1998; 98US-0077450P.

PR
PR 11-MAR-1998; 98US-0077632P.

PR
PR 11-MAR-1998; 98US-0077641P.

PR
PR 12-MAR-1998; 98US-0077649P.

PR
PR 12-MAR-1998; 98US-0077791P.

PR
PR 13-MAR-1998; 98US-0078004P.

PR
PR 17-MAR-1998; 98US-00040220.

PR
PR 20-MAR-1998; 98US-0078886P.

PR
PR 20-MAR-1998; 98US-0078910P.

PR
PR 20-MAR-1998; 98US-0078936P.

PR
PR 20-MAR-1998; 98US-0078939P.

PR
PR 25-MAR-1998; 98US-0079294P.

PR
PR 26-MAR-1998; 98US-0079656P.

PR
PR 27-MAR-1998; 98US-0079663P.

PR
PR 27-MAR-1998; 98US-0079664P.

PR
PR 27-MAR-1998; 98US-0079689P.

PR
PR 27-MAR-1998; 98US-0079728P.

PR
PR 30-MAR-1998; 98US-0079786P.

PR
PR 30-MAR-1998; 98US-0079920P.

PR
PR 31-MAR-1998; 98US-0079923P.

PR
PR 31-MAR-1998; 98US-0080105P.

PR
PR 31-MAR-1998; 98US-0080107P.

PR
PR 31-MAR-1998; 98US-0080165P.

PR
PR 31-MAR-1998; 98US-0080194P.

PR
PR 01-APR-1998; 98US-0080327P.

PR
PR 01-APR-1998; 98US-0080328P.

PR
PR 01-APR-1998; 98US-0080333P.

PR
PR 01-APR-1998; 98US-0080334P.

PR
PR 08-APR-1998; 98US-0081049P.

PR
PR 08-APR-1998; 98US-0081070P.

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PR 08-APR-1998; 98US-0081071P.

PR
PR 09-APR-1998; 98US-0081195P.

PR
PR 09-APR-1998; 98US-0081203P.

PR
PR 09-APR-1998; 98US-0081229P.

PR
PR 15-APR-1998; 98US-0081817P.

PR
PR 15-APR-1998; 98US-0081839P.

PR
PR 15-APR-1998; 98US-0081952P.

PR
PR 15-APR-1998; 98US-0081955P.

PR
PR 21-APR-1998; 98US-0082568P.

PR
PR 21-APR-1998; 98US-0082569P.

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PR 22-APR-1998; 98US-0082700P.

PR
PR 22-APR-1998; 98US-0082704P.

PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 30-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0083742P.
PR 06-MAY-1998; 98US-0084141P.
PR 07-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 13-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 15-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0085704P.
PR 22-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087108P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.

(GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

P-PSDB; AAY41773.

New secreted and transmembrane polypeptides and their polynucleotides,
useful for treating blood coagulation disorders, cancers and cellular
adhesion disorders.

Claim 2; Fig 221; 530pp; English.

The Present invention describes secreted and transmembrane polypeptides
and their polynucleotides. The nucleotide sequences are useful as sources
of probes, primers, for chromosome mapping, and for generation of
antisense sequences. They can also be used to create transgenic animals.
The proteins can be used to treat a variety of diseases and disorders,
depending on their function. Diseases that may be treated include blood
coagulation disorders, cancers and cellular adhesion disorders. They may
also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
AA41774 represent polynucleotide and polypeptide sequence given in the
exemplification of the present invention

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1035;	DB 2;	Length 1679;	
Best Local Similarity	100.0%;	Pred. No. 3.1e-07;			
Matches 1035;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAACCATCCAGCCAAAAATGCACAATTCCTATCTCTTGGGCAAACTTTCACGGGGCTG	60		
DB	134	ATGAAACCATCCAGCCAAAAATGCACAATTCCTATCTCTTGGGCAAACTTTCACGGGGCTG	193		
QY	61	GCTGCTCTGTGTCCTTCCAAAGGAGTGCCGCTGGCCGACGGAGATGCCACCTTCCCCAAA	120		
DB	194	GCTGCTCTGTGTCCTTCCAAAGGAGTGCCGCTGGCCGACGGAGATGCCACCTTCCCCAAA	253		
QY	121	GCTATGGACAACGCTGACGGTCCGGCAGGGGGAGAGCGCACCTCAGGTGCATATTGAC	180		
DB	254	GCTATGGACAACGCTGACGGTCCGGCAGGGGGAGAGCGCACCTCAGGTGCATATTGAC	313		
QY	181	AACCGGGTCACCGGGTGGCTGGCTTCTGAGACAACCCAAAGCGAGTACAGATC	300		
DB	314	AACCGGGTCACCGGGTGGCTGGCTTCTGAGACAACCCAAAGCGAGTACAGATC	433		
QY	241	AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGACAACCCAAAGCGAGTACAGATC	375		
DB	374	AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGACAACCCAAAGCGAGTACAGATC	433		
QY	301	GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACTGCTCGGTGCAGACAGAC	360		
DB	434	GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACTGCTCGGTGCAGACAGAC	493		
QY	361	AACACCCAAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAATTGTAGAG	420		
DB	494	AACACCCAAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAATTGTAGAG	553		
QY	421	ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGGCTCACCTGCATAGCACT	480		
DB	554	ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGGCTCACCTGCATAGCACT	613		
QY	481	GGTAGACGAGGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	540		
DB	614	GGTAGACGAGGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673		
QY	541	AGTCAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCGTACGGGACTACGAG	600		
DB	674	AGTCAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCGTACGGGACTACGAG	733		
QY	601	TGCAGTGCCTCCAAATGACGTGGCGCCCGTGGTACGGAGGTAAAGTTCACCGTGAAC	660		
DB	734	TGCAGTGCCTCCAAATGACGTGGCGCCCGTGGTACGGAGGTAAAGTTCACCGTGAAC	793		
QY	661	TATCCACCATACATTTCCAGAACGCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	720		
DB	794	TATCCACCATACATTTCCAGAACGCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	853		
QY	721	CTGCAGTGTCAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA	780		
DB	854	CTGCAGTGTCAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA	913		
QY	781	AGA CTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAAACAGACTTTCTCTCAAAACTC	840		
DB	914	AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAAACAGACTTTCTCTCAAAACTC	973		
QY	841	ATCTTCTTCAATGTCTCTGAACTATGCTATGGGAACTACATTTGGTGGCCCTCCAAACAG	900		
DB	974	ATCTTCTTCAATGTCTCTGAACTATGCTATGGGAACTACATTTGGTGGCCCTCCAAACAG	1033		
QY	901	CTGGGGCACACCAATGCCAGCATCATGTATTGGTCCAGGGCGCGTCCAGCAGGTGAGC	960		
DB	1034	CTGGGGCACACCAATGCCAGCATCATGTATTGGTCCAGGGCGCGTCCAGCAGGTGAGC	1093		
QY	961	AACGGCACGTTCGAGGAGGGCAGGCTGGCTGCTGGCTCTTGTCTTGCACCTG	1020		
DB	1094	AACGGCACGTTCGAGGAGGGCAGGCTGGCTGCTGGCTCTTGTCTTGCACCTG	1153		
QY	1021	CTTCTCAAAATTTGA	1035		

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.08; Score 1035; DB 3; Length 1679;
Best Local Similarity 100.08; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAACCATCCAGCCAAATGACAAATCTATCTCTGGCAATCTTCACGGGCTG 60
DB |||
QY 134 ATGAAACCATCCAGCCAAATGACAAATCTATCTCTGGCAATCTTCACGGGCTG 193
DB |||
QY 61 GCTGCTCTGCTCTCTCTCAAGGAGTGCCCGTGGCAGCGAGATGCCACCTCCCAAA 120
DB |||
QY 194 GCTGCTCTGCTCTCTCTCAAGGAGTGCCCGTGGCAGCGAGATGCCACCTCCCAAA 253
DB |||
QY 121 GCTATGACAAACGTCAGCGTCCGCGAGGGGAGAGCGCCCTCAGTGCATATTGAC 180
DB |||
QY 254 GCTATGACAAACGTCAGCGTCCGCGAGGGGAGAGCGCCCTCAGTGCATATTGAC 313
DB |||
QY 181 AACCGGTCACCCGGGTGGCTGCTAAACCGCAGCACCACCTCTCTATGCTGGGAATGAC 240
DB |||
QY 314 AACCGGTCACCCGGGTGGCTGCTAAACCGCAGCACCACCTCTCTATGCTGGGAATGAC 373
DB |||
QY 241 AAGTGGTGCCTGCTGATCTCCGCTGGTCTCTGAGCAACACCCAAACGCGATCAGCATC 300
DB |||
QY 374 AAGTGGTGCCTGCTGATCTCCGCTGGTCTCTGAGCAACACCCAAACGCGATCAGCATC 433
DB |||
QY 301 GAGATCCAGAACGTCGATGATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
DB |||
QY 434 GAGATCCAGAACGTCGATGATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
DB |||
QY 361 AACCAACCAAGACCTTGAAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB |||
QY 494 AACCAACCAAGACCTTGAAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
DB |||
QY 421 ATTCTCTCAGATATCTCCATTAATGAGGAAACAAATATTAGCTCATCTGCTAGCAACT 480
DB |||
QY 554 ATTCTCTCAGATATCTCCATTAATGAGGAAACAAATATTAGCTCATCTGCTAGCAACT 613
DB |||
QY 481 GGTAGACCAAGACCTTACGCTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTG 540
DB |||
QY 614 GGTAGACCAAGACCTTACGCTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTG 673
DB |||
QY 541 AGTGAAGAGCAATCTTGAATTTAGGCGATCACCCGGGAGCAGTCAAGGAGTACGAG 600
DB |||
QY 674 AGTGAAGAGCAATCTTGAATTTAGGCGATCACCCGGGAGCAGTCAAGGAGTACGAG 733
DB |||
QY 601 TGCAGTGCCTCCAAATGACGTGCGCGCCGCTGTACGAGAGTAAAGGTCAACCGTGAAC 660
DB |||
QY 734 TGCAGTGCCTCCAAATGACGTGCGCGCCGCTGTACGAGAGTAAAGGTCAACCGTGAAC 793
DB |||
QY 661 TATCCACCAATATTTTCAAGACCAAGGTATACAGGTGTCCCGTGGGACAAAGGGGACA 720
DB |||
QY 794 TATCCACCAATATTTTCAAGACCAAGGTATACAGGTGTCCCGTGGGACAAAGGGGACA 853
DB |||
QY 721 CTGCAAGTGAAGCTTACGAGTCCCTTACGAGAAATTCAGTGTGTAAGAATGACAAA 780
DB |||
QY 854 CTGCAAGTGAAGCTTACGAGTCCCTTACGAGAAATTCAGTGTGTAAGAATGACAAA 913
DB |||
QY 781 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACACAGACCTTCTCTCAAACTC 840
DB |||
QY 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACACAGACCTTCTCTCAAACTC 973
DB |||
QY 841 ATCTTCTTCAATGTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCAAACAG 900
DB |||
QY 974 ATCTTCTTCAATGTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCAAACAG 1033
DB |||
QY 901 CTGGGCCACACCAATGCGAGCATATGCTATTGTCAGGCGCGCTCAGGAGTGAAC 960
DB |||
QY 1034 CTGGGCCACACCAATGCGAGCATATGCTATTGTCAGGCGCGCTCAGGAGTGAAC 1093
DB |||
QY 961 AACGCGACGTCAGGAGGCGAGGCTGCTGCTGGCTGCTGCTTCTTCTGCTTCCACTG 1020
DB |||
QY 1094 AACGCGACGTCAGGAGGCGAGGCTGCTGCTGGCTGCTGCTTCTTCTGCTTCCACTG 1153
DB |||
```

QY 1021 CTCTCAAAATTTGA 1035
DB 1154 CTCTCAAAATTTGA 1168

RESULT 3

AAC87037
ID AAC87037 standard; cDNA; 1679 BP.

XX AAC87037;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of human polypeptide PRO337.

XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 134..1168

FT /*tag= a

FT sig_peptide 134..216

FT /*tag= b

XX WO200077037-A2.

XX 21-DEC-2000.

XX 22-MAY-2000; 2000WO-US014042.

XX 15-JUN-1999; 99US-0139695P.

XX 20-JUL-1999; 99US-0145070P.

XX 26-JUL-1999; 99US-0145698P.

XX 17-AUG-1999; 99US-0149396P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028301.

XX 02-DEC-1999; 99WO-US028565.

XX 07-DEC-1999; 99US-0169495P.

XX 05-JAN-2000; 2000WO-US000219.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 01-MAR-2000; 2000WO-US005601.

XX 20-MAR-2000; 2000WO-US005841.

XX 30-MAR-2000; 2000WO-US007377.

XX 15-MAY-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein DA, Deenoyers L, Eaton DL;
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier WA, Pan J;
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
XX Wood WI, Zhang Z;

XX WPI; 2001-050091/06.

XX P-PSDB; AAB31204.

XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a

transmembrane polypeptide is useful for gene therapy and identification of related polypeptides.

Claim 2; Fig 51; 244pp; English.

The present sequence encodes a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187, PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 4; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACCATCCAGCCAAAATGACAAATCTATCTCTTGGCAATCTTCAAGGGGTG 60
DB 134 ATGAACCATCCAGCCAAAATGACAAATCTATCTCTTGGCAATCTTCAAGGGGTG 193
QY 61 GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAAA 120
DB 194 GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAAA 253
QY 121 GCTATGACACAGTGCAGTGCAGCGGAGGAGAGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGACACAGTGCAGTGCAGCGGAGGAGAGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTACCCGGGTGGCTGCTAAACCGCAGCAGCAATCTCTGCTGGGAATGAC 240
DB 314 AACCGGGTACCCGGGTGGCTGCTAAACCGCAGCAGCAATCTCTGCTGGGAATGAC 373
QY 241 AGTGGTGCCTGATCTCTGCTGGTCTCTTGAGCAACCAACCAAGCAGTACGATC 300
DB 374 AGTGGTGCCTGATCTCTGCTGGTCTCTTGAGCAACCAACCAAGCAGTACGATC 433
QY 301 GAGATCCAGAACGTTGATGACGAGGCGCCCTTACACCTGCTCGGTGCGAGACAG 360
DB 434 GAGATCCAGAACGTTGATGACGAGGCGCCCTTACACCTGCTCGGTGCGAGACAG 493
QY 361 AACCAACCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATGTAG 420
DB 494 AACCAACCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATGTAG 553
QY 421 ATTCTTTCATATCTCCATATAGAGGAAACAATATTAGCTCCTCCTGATAGCAACT 480
DB 554 ATTCTTTCATATCTCCATATAGAGGAAACAATATTAGCTCCTCCTGATAGCAACT 613
QY 481 GGTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCCAAGGGTGGCTTTGTG 540
DB 614 GGTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCCAAGGGTGGCTTTGTG 673
QY 541 AGTGAAGCAATCTTGGAAATTCAGGGCATCCCGGAGCAGTCAGGGAGTACGAG 600
DB 674 AGTGAAGCAATCTTGGAAATTCAGGGCATCCCGGAGCAGTCAGGGAGTACGAG 733
QY 601 TSCAGTGCCTCCAAATGACGTGGCGCGCGGTGATACGAGAGTAAAGGTCAACCGTGAAC 660
DB 734 TSCAGTGCCTCCAAATGACGTGGCGCGCGGTGATACGAGAGTAAAGGTCAACCGTGAAC 793
QY 661 TATCCACCACATATTTAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720

Db 794 TATCCACCACATATTTAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 780
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAACTC 840
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAACTC 973
QY 841 ATCTTCTTCAATGTCTCTTGAACATGACTATGGAAACTACATCTTGGTGGCTTCCCAACAG 900
Db 974 ATCTTCTTCAATGTCTCTTGAACATGACTATGGAAACTACATCTTGGTGGCTTCCCAACAG 1033
QY 901 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGTTCAGCGAGGTGAGC 960
Db 1034 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGTTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGCTGAGGAGGCGAGGCTGGTCTGGTCTGGTCTTCTTGGTCTTGGACCTG 1020
Db 1094 AACGGCAGCTGAGGAGGCGAGGCTGGTCTGGTCTGGTCTTCTTGGTCTTGGACCTG 1153
QY 1021 CTCTCTCAAAATTTTGA 1035
Db 1154 CTCTCTCAAAATTTTGA 1168

RESULT 4
AAS21431
ID AAS21431 standard; cDNA; 1679 BP.
AC AAS21431;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO337 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy; ss.
OS Homo sapiens.
XX
XX WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US014941.
 PR 05-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000US-0209832P.
 PR 11-AUG-2000; 2000WO-US020710.
 PR 23-AUG-2000; 2000WO-US022031.
 PR 24-AUG-2000; 2000WO-US023522.
 PR 08-NOV-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030952.
 XX 10-NOV-2000; 2000WO-US030873.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Garriksen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-408281/43.
 DR P-PSDB; AAU12359.
 DR
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 3; Fig 375; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 4; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAACCAATCCAGCAAAATGACAAATTCATCTCTTGGCAATCTTCAGGGGCTG 60
 DB 134 ATGAAACCAATCCAGCAAAATGACAAATTCATCTCTTGGCAATCTTCAGGGGCTG 193
 QY 61 GCTGCTCTGTGCTCTTCCAGAGGTGCGCGTGCAGCGGAGATGCCACCTTCCCAA 120
 DB 194 GCTGCTCTGTGCTCTTCCAGAGGTGCGCGTGCAGCGGAGATGCCACCTTCCCAA 253
 QY 121 GCTATGGACACAGTGCAGCGTCCGCGAGGGGAGAGCGCCACCTCAGTGCATATTGAC 180
 DB 254 GCTATGGACACAGTGCAGCGTCCGCGAGGGGAGAGCGCCACCTCAGTGCATATTGAC 313

181 AACCGGTCAACCGGGTGGCTGGCTAAACCGGAGCAACATCTCTTATGTGGGAATGAC 240
 DB 314 AACCGGTCAACCGGGTGGCTGGCTAAACCGGAGCAACATCTCTTATGTGGGAATGAC 373
 QY 241 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCGAGTACGATC 300
 DB 374 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCGAGTACGATC 433
 QY 301 GAGATCCAGAACGCTGGATGATGAGAGGGGCCCTTTACACCTGCTGCGTGACAGACAGAC 360
 DB 434 GAGATCCAGAACGCTGGATGATGAGAGGGGCCCTTTACACCTGCTGCGTGACAGACAGAC 493
 QY 361 AACCAACCAAGACCTCTAGGTTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 420
 DB 494 AACCAACCAAGACCTCTAGGTTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 553
 QY 421 ATTCTCTCAGATATCTCCATTAATGAAGGCAACATATTAGCCTCACCTGCATAGCAACT 480
 DB 554 ATTCTCTCAGATATCTCCATTAATGAAGGCAACATATTAGCCTCACCTGCATAGCAACT 613
 QY 481 GGTAGACGAGGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTGTG 540
 DB 614 GGTAGACGAGGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTGTG 673
 QY 541 AGTGAAGACGATACCTTGAATTCAGGGCATCACCAGGAGCAGTACAGGGHCTACGAG 600
 DB 674 AGTGAAGACGATACCTTGAATTCAGGGCATCACCAGGAGCAGTACAGGGHCTACGAG 733
 QY 601 TGCAGTGCCTCCAATGACGCTGGCGCGCGTGTGACGAGAGTAAAGGTACCGTGAAC 660
 DB 734 TGCAGTGCCTCCAATGACGCTGGCGCGCGTGTGACGAGAGTAAAGGTACCGTGAAC 793
 QY 661 TATCCACCATACATTTTCAGAACCAAGGTAAGGTGTCCCGTGGGACAAAGGGGACA 720
 DB 794 TATCCACCATACATTTTCAGAACCAAGGTAAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACGTGTGACAGGATGACAA 780
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACGTGTGACAGGATGACAA 913
 QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAACTC 840
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAACTC 973
 QY 841 ATCTTCTTCAATGTCTCTGAACATCACTATGGAACATGACATGCGGAACTACCTTGGCGCTCCAAACAG 900
 DB 974 ATCTTCTTCAATGTCTCTGAACATCACTATGGAACATGACATGCGGAACTACCTTGGCGCTCCAAACAG 1033
 QY 901 CTGGGCCACACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 960
 DB 1034 CTGGGCCACACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 1093
 QY 961 AACGCGACGTGAGAGGGCGAGGTGCTCTGCGTGTGCTGCTTCTTGTGCTTGCACCTG 1020
 DB 1094 AACGCGACGTGAGAGGGCGAGGTGCTCTGCGTGTGCTGCTTCTTGTGCTTGCACCTG 1153
 QY 1021 CTCTCAAAATTTTGA 1035
 DB 1154 CTCTCAAAATTTTGA 1168

RESULT 5
 ABK33598
 ID ABK33598 standard; cDNA; 1679 BP.
 XX AC ABK33598;
 XX 08-MAY-2002 (first entry)
 XX cDNA encoding human PRO protein, Seq ID No 125.
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;

KW pericyte cell proliferation; chondrocyte cell proliferation;
 XX tumour necrosis factor-alpha; gene; ss.

OS Homo sapiens.

PN WO200208288-A2.

XX 31-JAN-2002.

PF 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220585P.

PR 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.

PR 25-JUL-2000; 2000US-0220666P.

PR 26-JUL-2000; 2000US-0220893P.

PR 28-JUL-2000; 2000WO-US020710.

PR 01-AUG-2000; 2000US-0222425P.

PR 22-AUG-2000; 2000US-0227133P.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 28-NOV-2000; 2000US-0253646P.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001WO-US017092.

PA (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2002-172001/22.

DR P-PSDB; AAU83654.

DR WPI; 2002-172001/22.

DR P-PSDB; AAU83654.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PI useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.

XX Claim 2; Fig 125; 359pp; English.

PS The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO
 CC protein coding sequences of the invention

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 1035; DB 6; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

	Matches 1035;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAAACCATCCAGCCAAATAATGCAAAATTTCTATCTTTGGGCAATCTTCAAGGGCTG	60		
DB	134	ATGAAAACCATCCAGCCAAATAATGCAAAATTTCTATCTTTGGGCAATCTTCAAGGGCTG	193		
QY	61	GCTGCTGTGTCTCTTCCAAAGGAGTCCCGTGGCGCAGCGAGATGCCACCTTCCCAAA	120		
DB	194	GCTGCTGTGTCTCTTCCAAAGGAGTCCCGTGGCGCAGCGAGATGCCACCTTCCCAAA	253		
QY	121	GCTATGGACAAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATTTGAC	180		
DB	254	GCTATGGACAAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATTTGAC	313		
QY	181	AACCGGCTCACCCGGTGGCTTAAACCGCAGCACCCTCTATCTTGGGAATGAC	240		
DB	314	AACCGGCTCACCCGGTGGCTTAAACCGCAGCACCCTCTATCTTGGGAATGAC	373		
QY	241	AAGTGTGCTGATCTCTCGGCTGGTCTTCTAGACAAACCCAAACGCAATCAGCATC	300		
DB	374	AAGTGTGCTGATCTCTCGGCTGGTCTTCTAGACAAACCCAAACGCAATCAGCATC	433		
QY	301	GAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAG	360		
DB	434	GAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAG	493		
QY	361	AACCAACCAAGACCTCTAGGGTCCACTCATTTGCAAGTATCTCCCAAAATTTGAGAG	420		
DB	494	AACCAACCAAGACCTCTAGGGTCCACTCATTTGCAAGTATCTCCCAAAATTTGAGAG	553		
QY	421	ATTCTTTCAGATATCTCATTAATGAAGGAAACAAATTAAGCTTCACTGCATAGCAACT	480		
DB	554	ATTCTTTCAGATATCTCATTAATGAAGGAAACAAATTAAGCTTCACTGCATAGCAACT	613		
QY	481	GGTAGACACAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG	540		
DB	614	GGTAGACACAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG	673		
QY	541	AGTGAAGACGAATPACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTAG	600		
DB	674	AGTGAAGACGAATPACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTAG	733		
QY	601	TGCAAGTCCCTCCAAATGACGTCGGCGCCCGTGGTAGGGAGTAAGGTACCGGTGAAC	660		
DB	734	TGCAAGTCCCTCCAAATGACGTCGGCGCCCGTGGTAGGGAGTAAGGTACCGGTGAAC	793		
QY	661	TATCCACCATACATTTTCAAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	720		
DB	794	TATCCACCATACATTTTCAAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	853		
QY	721	CTGCAGTGTGAAGCTCTCAGAGTCCCTCAGCAGAATTCAGTGGTACAGGATGACAAA	780		
DB	854	CTGCAGTGTGAAGCTCTCAGAGTCCCTCAGCAGAATTCAGTGGTACAGGATGACAAA	913		
QY	781	AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACACCTTCTCTCAAAATC	840		
DB	914	AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACACCTTCTCTCAAAATC	973		
QY	841	ATCTTCTTCAATGTCTCTGAAACATGACTATGGAACTACACTTGGGTGGCTCCCAACAG	900		
DB	974	ATCTTCTTCAATGTCTCTGAAACATGACTATGGAACTACACTTGGGTGGCTCCCAACAG	1033		
QY	901	CTGGGGCACCAACATGACGATCATGATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC	960		
DB	1034	CTGGGGCACCAACATGACGATCATGATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC	1093		
QY	961	AACGCGCAGTCCAGAGGCGAGGCTCGCTTGGCTGGCTCTTCTTGGTCTTGGACCTG	1020		
DB	1094	AACGCGCAGTCCAGAGGCGAGGCTCGCTTGGCTGGCTCTTCTTGGTCTTGGACCTG	1153		
QY	1021	CTTCTCAAAATTTGA	1035		
DB	1154	CTTCTCAAAATTTGA	1168		

RESULT 6
 ABL88099
 ID ABL88099 standard; cDNA; 1679 BP.
 XX
 AC ABL88099;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO337 cDNA sequence SEQ ID NO:55.
 XX
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vutinary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219566P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709323.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US030873.
 PR 20-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferriar N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-090516/12.
 DR P-ESDB; ABB84844.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 XX Claim 2; Fig 55; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAACCATCCAGCCAAATGCAATTCATCTCTGGGCAATCTTACGGGGCTG 60
 DB 134 ATGAAACCATCCAGCCAAATGCAATTCATCTCTGGGCAATCTTACGGGGCTG 193
 QY 61 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 120
 DB 194 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 253
 QY 121 GCTATGGACAAAGTGAAGTTCGGGAGGAGGAGCGCCCTCAGTGCATTTGAC 180
 DB 254 GCTATGGACAAAGTGAAGTTCGGGAGGAGGAGCGCCCTCAGTGCATTTGAC 313
 QY 181 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCCTCTCTAGTGGGATGAC 240
 DB 314 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCCTCTCTAGTGGGATGAC 373
 QY 241 AAGTGTGCTGTGATCTCTGCGGTGCTCTCTGAGCAACACCCAAACGAGTACGATC 300
 DB 374 AAGTGTGCTGTGATCTCTGCGGTGCTCTCTGAGCAACACCCAAACGAGTACGATC 433
 QY 301 GAGATCCAGAACGTGGATGCTATGACGAGGGCCCTTACACCTGCTGCTGACAGAC 360
 DB 434 GAGATCCAGAACGTGGATGCTATGACGAGGGCCCTTACACCTGCTGCTGACAGAC 493
 QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCATCTGTGCAAGTATCTCCCAAATGTAGAG 420
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATCTGTGCAAGTATCTCCCAAATGTAGAG 553
 QY 421 ATTTCTTCAGATATCTCATTAATGAAGGAAACAATATTAGCCTCCTGCATAGCAACT 480
 DB 554 ATTTCTTCAGATATCTCATTAATGAAGGAAACAATATTAGCCTCCTGCATAGCAACT 613
 QY 481 GGTAGACAGAGCCTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540
 DB 614 GGTAGACAGAGCCTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 541 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 600
 DB 674 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 733
 QY 601 TGCAGTGCCTCCATGACGTGGCGGCCCGCTGCTGAGAGATTAAGGTTCACCGTGAAC 660
 DB 734 TGCAGTGCCTCCATGACGTGGCGGCCCGCTGCTGAGAGATTAAGGTTCACCGTGAAC 793
 QY 561 TATCCACCATACATTTCCAGAACCCAGGGTACAGGTGTCCCCGTGGGACAAAGGGGACA 720

```

Db      794  TATCCACCAATACATTTTCAAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY      721  CTGCACTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGGTACAGGATGACAAA 780
Db      854  CTGCACTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGGTACAGGATGACAAA 913
QY      781  AGACTGATTTGAAGGAAAGAAAGGGGTGAAGGTGGAAGAAAGAGACCTTTCTCTCAAAACTC 840
Db      914  AGACTGATTTGAAGGAAAGAAAGGGGTGAAGGTGGAAGAAAGAGACCTTTCTCTCAAAACTC 973
QY      841  ATCTCTCTCAATGTCTCTGAACATGACTATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 900
Db      974  ATCTCTCTCAATGTCTCTGAACATGACTATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1033
QY      901  CTGGGCGCACCAATGCGCAGCATCATGCTATTGCTCCAGGCGCGCTCAGCGAGGTGAGC 960
Db      1034  CTGGGCGCACCAATGCGCAGCATCATGCTATTGCTCCAGGCGCGCTCAGCGAGGTGAGC 1093
QY      961  AACGCGACGTGAGGAGGCGAGGCTGCGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 1020
Db      1094  AACGCGACGTGAGGAGGCGAGGCTGCGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 1153
QY      1021  CTTCTCAATTTTGA 1035
Db      1154  CTTCTCAATTTTGA 1168

RESULT 7
ABL95588
ID      ABL95588 standard; cDNA; 1679 BP.
AC      ABL95588;
XX      XX
KW      Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW      cardiant; cytosolic; antiangiogenic; hypotensive; vulnerary;
KW      antiarteriosclerotic; gene; ss.
XX      XX
OS      Homo sapiens.
XX      XX
PN      WO200208284-A2.
XX      XX
PD      31-JAN-2002.
XX      XX
PF      09-JUL-2001; 2001WO-US021735.
XX      XX
PR      20-JUL-2000; 2000US-0219556P.
PR      25-JUL-2000; 2000US-0220624P.
PR      25-JUL-2000; 2000US-0220664P.
PR      28-JUL-2000; 2000WO-US020710.
PR      02-AUG-2000; 2000US-0222695P.
PR      17-AUG-2000; 2000US-00643657.
PR      23-AUG-2000; 2000WO-US023522.
PR      24-AUG-2000; 2000WO-US023522.
PR      07-SEP-2000; 2000US-0230978P.
PR      18-SEP-2000; 2000US-00664610.
PR      18-SEP-2000; 2000US-00665350.
PR      24-OCT-2000; 2000US-0242922P.
PR      08-NOV-2000; 2000US-00709238.
PR      08-NOV-2000; 2000WO-US030952.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      20-DEC-2000; 2000WO-US034956.
PR      22-JAN-2001; 2001US-00767609.
PR      28-FEB-2001; 2001WO-US006498.
PR      28-FEB-2001; 2001WO-US006520.
PR      01-MAR-2001; 2001WO-US006666.

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PR      09-MAR-2001; 2001US-00802706.
PR      14-MAR-2001; 2001US-00808689.
PR      22-MAR-2001; 2001US-00816744.
PR      05-APR-2001; 2001US-00828366.
PR      10-MAY-2001; 2001US-00854208.
PR      10-MAY-2001; 2001US-00854280.
PR      25-MAY-2001; 2001US-00866028.
PR      25-MAY-2001; 2001US-00866034.
PR      25-MAY-2001; 2001WO-US017092.
PR      30-MAY-2001; 2001WO-US017443.
PR      01-JUN-2001; 2001WO-US017800.
PR      20-JUN-2001; 2001WO-US019692.
XX      (GETH ) GENENTECH INC.
PA      (BAKE/) BAKER K P.
PA      (FERK/) FERRARA N.
PA      (GERE/) GERBER H.
PA      (GERR/) GERRITSEN M E.
PA      (GODE/) GODDARD A. E.
PA      (GODC/) GODOWSKI P J.
PA      (GURN/) GURNEY A L.
PA      (HILL/) HILLAN K J.
PA      (MARS/) MARSTERS S A.
PA      (PANJ/) PAN J.
PA      (PAON/) PAONI N F.
PA      (STEP/) STEPHAN J F.
PA      (WATA/) WATANABE C K.
PA      (WILL/) WILLIAMS P M.
PA      (WOOD/) WOOD W I.
XX      XX
PI      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      WPI; 2002-171999/22.
DR      P-PSDB; ABB95450.
XX      XX
PT      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT      infarction), endothelial or angiogenic disorders in a mammal.
XX      XX
XX      Claim 1; Fig 55; 567pp; English.
XX      XX
CC      The present invention provides the protein and coding sequences of human
CC      PRO proteins. These are useful for treating or diagnosing a
CC      cardiovascular, endothelial or angiogenic disorder, including cardiac
CC      hypertrophy, trauma, cancer, age-related macular degeneration,
CC      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC      healing. The present sequence is a coding sequence of the invention
XX      XX
SQ      Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
XX      XX
Query Match      100.0%; Score 1035; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  ATGAAACCATCCAGCCAAATGCAATTTCTTTGGCAATCTTATCTTTGGCAATCTTACGGGGCTG 60
Db      134  ATGAAACCATCCAGCCAAATGCAATTTCTTTGGCAATCTTATCTTTGGCAATCTTACGGGGCTG 193
QY      61  GCTGCTCTGTGTCTTCTTCAAGAGTCCCGTGGCAGCGAGATGCCACCTTTCCCAAA 120
Db      194  GCTGCTCTGTGTCTTCTTCAAGAGTCCCGTGGCAGCGAGATGCCACCTTTCCCAAA 253
QY      121  GCTATGGACAAGTGCAGCTCCGCGAGGGGAGAGCGCCACCTTCAGTGCACTATTGAC 180
Db      254  GCTATGGACAAGTGCAGCTCCGCGAGGGGAGAGCGCCACCTTCAGTGCACTATTGAC 313
QY      181  AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTTATGCTGGGATGAC 240

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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US047259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001US-0006520.
PR 01-MAR-2001; 2001US-0006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854280.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00871092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0089692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001US-00887879.
PR 29-JUN-2001; 2001US-00887879.
PR 09-JUL-2001; 2001US-00887879.
PR 18-JUL-2001; 2001US-00887879.
PR 08-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
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PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-341980/32.

P-PSDB; ABO17803.

PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.

Claim 2; Fig 375; 660pp; English.

CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides. The polypeptide encoded by (I) is used to
CC PRO polypeptide, modulate a biological activity of a cell expressing a
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, inhibit the binding of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,

CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAACCATCCAGCCAAAATGCAAAATTTCTATCTCTTGGGCAATCTTCCGGGGCTG 60
DB 134 ATGAAAACCATCCAGCCAAAATGCAAAATTTCTATCTCTTGGGCAATCTTCCGGGGCTG 193
QY 61 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCCAAA 120
DB 194 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGACAAAGTACGCTCCGCGAGGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGACAAAGTACGCTCCGCGAGGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTGGCTTAAACCGGAGCAACCATCTCTATGTGGGAATGAC 240
DB 314 AACCGGGTCAACCGGGTGGCTGGCTTAAACCGGAGCAACCATCTCTATGTGGGAATGAC 373
QY 241 AAGTGGTGCTGGATCTCTGCGTGGTCTTCTAGGCAACCCAAACGCGAGTACAGATC 300
DB 374 AAGTGGTGCTGGATCTCTGCGTGGTCTTCTAGGCAACCCAAACGCGAGTACAGATC 433
QY 301 GAGATCCAGAACTGATGATGACAGGGGCCCTTACACCTGCTCGGTGCGAGACAGAC 360
DB 434 GAGATCCAGAACTGATGATGACAGGGGCCCTTACACCTGCTCGGTGCGAGACAGAC 493
QY 361 AACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAGCTGCACTAGCACT 480
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAGCTGCACTAGCACT 613
QY 481 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
DB 614 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATCTTGGAAATTTAGGGCATCACCCGGAGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGACGAATCTTGGAAATTTAGGGCATCACCCGGAGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCGCGCGGTGTTACGGAGAGTAAAGGTCAACCGTGAAC 560
DB 734 TGCAGTGCCTCCAAATGACGTGGCGCGCGGTGTTACGGAGAGTAAAGGTCAACCGTGAAC 793
QY 661 TATCCACCATATCAATTTGAGAAATTTAGGGCATCACCCGGAGAGCAGTCAGGGGACTACGAG 720
DB 794 TATCCACCATATCAATTTGAGAAATTTAGGGCATCACCCGGAGAGCAGTCAGGGGACTACGAG 853
QY 721 CTGCGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGAGTACACAA 780
DB 854 CTGCGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGAGTACACAA 913
QY 781 AGACTGATTGAAGAGGAAGAAAGGGGTGAAGTGGGAAACAGACACCTTCTCTCAAAATCTC 840
DB 914 AGACTGATTGAAGAGGAAGAAAGGGGTGAAGTGGGAAACAGACACCTTCTCTCAAAATCTC 973
QY 841 ATCTTCTTCAATGTCTCTGAAACATGACTATGGAATCACTATGGAACTACCTTGGCTCCCAACAG 900
DB 974 ATCTTCTTCAATGTCTCTGAAACATGACTATGGAATCACTATGGAACTACCTTGGCTCCCAACAG 1033


```
RESULT 10
ACD42387
ID ACD42387 standard; cDNA; 1679 BP.
AC
AC ACD42387;
DT
DT 05-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antidiabetic;
KW ophthalmological; cytostatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003040014-A1.
XX
PD 27-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066269.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-00591115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0098601P.
PR 10-SEP-1998; 98US-0098803P.
PR 10-SEP-1998; 98US-0098811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.

101-DEC-1999; 99WO-US028301.
102-DEC-1999; 99WO-US028565.
07-DEC-1999; 99US-0169435P.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
09-MAR-2000; 2000WO-US006471.
30-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
15-NOV-2001; 2001US-00002796.

( GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gao W, Gerber H, Gerecht ME, Goddard A;
Godowski P, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
Paoni NF, Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
Wood WI, Zhang Z;

WPI, 2003-503396/47.
P-Psdb; ABC25175.

New secreted and transmembrane PRO polypeptides, useful for treating
diabetes, retinal disorders and stimulating an immune response.

Claim 2; Fig 51; 254pp; English.

The invention describes an isolated polypeptide (I) having at least 80 %
amino acid sequence identity to 30 secreted and transmembrane
polypeptides. PRO polypeptides are also useful for stimulating
hypertrophy of adult heart, for inhibiting vascular endothelial growth
factor stimulated proliferation of endothelial cells, stimulating
proliferation of stimulated T-lymphocytes and for inducing proliferation
of PDB12 pancreatic ductal cells and are thus useful in the treatment of
disorders which involve protein secretion by the pancreas, including
diabetes. PRO polypeptides are useful for inducing vascular permeability
and in enhancing survival of retinal neurons cells and are thus useful
for the treatment of retinal disorders. PRO polypeptides are also useful
for stimulating an immune response and inducing inflammation by inducing
mononuclear cell and eosinophil infiltration at the site of infection of
an animal. The PRO polypeptides are further useful for inducing apoptosis
in endothelial cells for inhibiting neoplastic growth. This sequence
encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACCATCCAGCCAAATTCATCTCTTGGGCAATCTTACCGGGCTG 60
|||||
DB 134 ATGAACCATCCAGCCAAATTCATCTCTTGGGCAATCTTACCGGGCTG 193
```

QY 61 GCTGCTCTGCTGCTCTCTCCAGAGAGTGCCGTCGCGAGCGGAGATGCGACCTTCCCAAA 120
DB 194 GCTGCTCTGCTGCTCTCTCCAGAGAGTGCCGTCGCGAGCGGAGATGCGACCTTCCCAAA 253
QY 121 GCTATGGAACAACGTCAGCGTCCGCGAGGAGGAGCGCCACCCTCAGGTGCACTATTGAC 180
DB 254 GCTATGGAACAACGTCAGCGTCCGCGAGGAGGAGCGCCACCCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCACCCGGGTGGCTGGCTAAACCGGAGCACCCTCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCACCCGGGTGGCTGGCTAAACCGGAGCACCCTCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGCCTGATCCTCGCTGGTCTCTCTGAGCAACACCCAAACGAGTACAGATC 300
DB 374 AAGTGGTGCCTGATCCTCGCTGGTCTCTCTGAGCAACACCCAAACGAGTACAGATC 433
QY 301 GAGATCCAGAACGTCGATGTCATGTCAGGAGGCGCTTACACCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAACGTCGATGTCATGTCAGGAGGCGCTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACCCACCAAGACCTTAGGTCACCTCATTGTCAGATATCTCCCAAAATTTGAGAG 420
DB 494 AACCCACCAAGACCTTAGGTCACCTCATTGTCAGATATCTCCCAAAATTTGAGAG 553
QY 421 ATTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT 480
DB 554 ATTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT 613
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DB 614 GGTAGACGAGCTACGGTTACTTGGAGACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCACTGCTCCCAATGACGTCGGCGCGCCGTCGTAACGAGAGTAAGGTACCCGTGAAC 660
DB 734 TGCACTGCTCCCAATGACGTCGGCGCGCCGTCGTAACGAGAGTAAGGTACCCGTGAAC 793
QY 661 TATCCACCATACATTCAGAGCCAGGTCACAGGTGTCCTCCGTCGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTCAGAGCCAGGTCACAGGTGTCCTCCGTCGGACAAAGGGGACA 853
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DB 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 913
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DB 1034 CTGGGACACCAATGCCAGCATCATCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGTCGAGGAGGAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1094 AACGGCAGTCGAGGAGGAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
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RESULT 11

ACD42857

ID ACD42857 standard; cdna; 1679 BP.

XX

AC ACD42857;
XX 09-SEP-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO337 cDNA.
XX Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW cell death; growth induction cascade; blood coagulation cascade;
KW viral infection; gene; ss.
XX Homo sapiens.
XX US2003050239-A1.
XX 13-MAR-2003.
XX 15-OCT-2001; 2001US-00978191.
XX 17-OCT-1997; 97US-0062250P.
PR 13-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0068364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
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PR 01-APR-1998; 98US-0080333P.
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PR 08-APR-1998; 98US-0081049P.
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PR 29-APR-1998; 98US-0083392P.
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PR 29-APR-1998; 98US-0083496P.

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PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
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PR 05-MAY-1998; 98US-0084366P.
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PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
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PR 22-MAY-1998; 98US-0086430P.
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PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 28-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091010P.
PR 30-JUL-1998; 98US-0091359P.
PR 11-SEP-1998; 98US-0094651P.
PR 07-OCT-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-01068978.
PR 02-NOV-1998; 98US-02021141.
PR 06-NOV-1998; 98US-00184216.
PR 20-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
PR 07-DEC-1998; 98US-02024855.
PR 22-DEC-1998; 98US-02020054.
PR 22-DEC-1998; 98US-00218517.
PR 23-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0113621P.
PR 05-JAN-1999; 98US-0113622P.
PR 05-MAR-1999; 98US-0254465.
PR 08-MAR-1999; 98US-00254465.
PR 10-MAR-1999; 98US-02005028.
PR 10-MAR-1999; 98US-00265686.
PR 12-MAR-1999; 98US-00267213.
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PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-00311832.
PR 14-MAY-1999; 98US-0134287P.
PR 02-JUN-1999; 98US-0010733.
PR 16-JUN-1999; 98US-0012252.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0142680P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.

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PR 02-DEC-1999; 99US-0028551.
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PR 16-DEC-1999; 99US-00300095.
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PR 05-JAN-2000; 2000US-00000219.
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PR 06-JAN-2000; 2000US-0000377.
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PR 30-MAY-2000; 2000US-00014941.
PR 02-JUN-2000; 2000US-00015264.
PR 28-JUL-2000; 2000US-00020710.
PR 24-AUG-2000; 2000US-00023328.
PR 08-NOV-2000; 2000US-00070238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-00032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-00809552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00871092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00871800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCATCCAGCCAAATGCAATTTCTATCTTTGGCAATCTTACGGGGCTG 60
Db 134 ATGAACACCATCCAGCCAAATGCAATTTCTATCTTTGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTCTTCAAGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 120
Db 194 GCTGCTCTGTCTCTTCCAGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGACAAAGTACGCTCCGCGAGGGGAGAGCGCCACCTTCAGGTGCAATTATGAC 180
Db 254 GCTATGACAAAGTACGCTCCGCGAGGGGAGAGCGCCACCTTCAGGTGCAATTATGAC 313
QY 181 AACCGGCTCACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATCTGCGGAATGAC 240
Db 314 AACCGGCTCACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATCTGCGGAATGAC 373

(GETH ) GENENTECH INC.
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241 AAGTGGTGCCTGGATCCTCGGTGGTCTCTTCTGAGCAACACCCAAACGACGATCAGCATC 300
Db |||||
374 AAGTGGTGCCTGGATCCTCGGTGGTCTCTTCTGAGCAACACCCAAACGACGATCAGCATC 433
Qy GAGATCCAGAACGTTGATGTTATGACGAGGCGCTTTACACCTGCTCGGTGACAGACAGAC 360
Db GAGATCCAGAACGTTGATGTTATGACGAGGCGCTTTACACCTGCTCGGTGACAGACAGAC 493
Qy AACCAACCCAAAGACCTCTAGGTTCCACCTCATTTGTGCAAGTATCTCCAAATTTAGAG 420
Db |||||
494 AACCAACCCAAAGACCTCTAGGTTCCACCTCATTTGTGCAAGTATCTCCAAATTTAGAG 553
Qy ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATAGCTCTACCTCATAGCAACT 480
Db |||||
554 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATAGCTCTACCTCATAGCAACT 613
Qy GTTAGACAGAGCTACGGTTACTTTGAGAGACATCTCTCCAAAGCGGTTGGCTTTGTG 540
Db |||||
614 GTTAGACAGAGCTACGGTTACTTTGAGAGACATCTCTCCAAAGCGGTTGGCTTTGTG 673
Qy AGTGAAGACCAATACCTTGGAAATTCAGGSCATCACCGGAGCAGTCAAGGACCTAGGAG 600
Db |||||
674 AGTGAAGACCAATACCTTGGAAATTCAGGSCATCACCGGAGCAGTCAAGGACCTAGGAG 733
Qy TGCAGTGCCTCCAAATGACGTTGGCGCGCGCGCTGTGAGAGAGTAAAGGTCAACCGTGAAC 660
Db |||||
734 TGCAGTGCCTCCAAATGACGTTGGCGCGCGCGCTGTGAGAGAGTAAAGGTCAACCGTGAAC 793
Qy TATCCACCAATATTCAGAGACCAAGGTTACAGGTGTCCCTGGGACAAAGGGGACA 720
Db |||||
794 TATCCACCAATATTCAGAGACCAAGGTTACAGGTGTCCCTGGGACAAAGGGGACA 853
Qy CTGACGTGGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAGGATGACAAA 780
Db |||||
854 CTGACGTGGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAGGATGACAAA 913
Qy AGACTGATTTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 840
Db |||||
914 AGACTGATTTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
Qy ATCTTCTCAATGCTCTGACATGATGCTATTTGGTCCAGGCGCTCAGCAGGATGAGC 900
Db |||||
974 ATCTTCTCAATGCTCTGACATGATGCTATTTGGTCCAGGCGCTCAGCAGGATGAGC 1033
Qy CTGGGCGCACCAATGCCAGCATGCTATTTGGTCCAGGCGCTCAGCAGGATGAGC 960
Db |||||
1034 CTGGGCGCACCAATGCCAGCATGCTATTTGGTCCAGGCGCTCAGCAGGATGAGC 1093
Qy AACGGCAGCTCGAGAGGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db |||||
1094 AACGGCAGCTCGAGAGGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
Qy CTCTCAAAATTTGA 1035
Db |||||
1154 CTCTCAAAATTTGA 1168

RESULT 12

ACD68655
ID ACD68655 standard; cDNA; 1679 BP.

XX AC ACD68655;

XX AC ACD68655;

DT 17-SEP-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

DE Human; secreted and transmembrane protein; PRO; cytostatic;

XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;

XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;

XX pharmacological; diagnostic; biosensor; bioreactor; tumour; lung tumour;

XX colon tumour; breast tumour; prostate tumour; rectal tumour;

XX liver tumour; bone disorder; cartilage disorder; sports injury;

arthrititis; wound; gene; ss.

XX Homo sapiens.

XX US2003045687-A1.

XX 06-MAR-2003.

XX 12-AUG-2002; 2002US-00218631.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-512315/48.

XX P-PSDB; AB033767.

XX New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or wounds in a mammal.

PS Claim 2; Fig 125; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any of these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTGGCAATCTTCACGGGGCTG 60

Db 134 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTGGCAATCTTCACGGGGCTG 193

Qy 61 GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy 121 GCTATGGACACGTCAGGTCGGCCGCGAGGAGCGCCACCTTCAGTGCACCTATTGAC 180

Db 254 GCTATGGACACGTCAGGTCGGCCGCGAGGAGCGCCACCTTCAGTGCACCTATTGAC 313

07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022291.
 PR 29-OCT-1998; 98WO-US022292.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030399.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2003-352836/33.
 DR P-PSDB; ABU81057.
 XX
 PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
 PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
 PT heart attack.
 XX
 PS Claim 2; Fig 375; 643pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the treatment of diabetes, bone and/or cartilage disorders
 CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
 CC hyper- or hypo-insulinemia, hearing loss, and coagulation disorders
 CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
 CC assays for PRO, by detecting its expression in specific cells, tissues or
 CC serum, and for affinity purification of PRO from recombinant cell culture
 CC or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
 CC the human PRO polypeptides of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from the USPTO web
 CC site at seqdata.uspto.gov/pslpsDIDEntry.html
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.le-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCAAAATGCAATTTCTATCTCTTGGCAATCTTTCAGGGGGCTG 60
 DB 134 ATGAAACCATCCAGCAAAATGCAATTTCTATCTCTTGGCAATCTTTCAGGGGGCTG 193
 QY 61 GTGTCTCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 120
 DB 194 GTGTCTCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 253
 QY 121 GCTATGGAACAAGTGAAGCTCCGGCAGGGGAGAGGCCACCTCAGGTGCATATTGAC 180
 DB 254 GCTATGGAACAAGTGAAGCTCCGGCAGGGGAGAGGCCACCTCAGGTGCATATTGAC 313
 QY 181 AACCGGCTCACCGGGTGGCTGGCTAAACCGCAGCACCATTCTTATCTCTGGGAATGAC 240
 DB 314 AACCGGCTCACCGGGTGGCTGGCTAAACCGCAGCACCATTCTTATCTCTGGGAATGAC 373
 QY 241 AAGTGTGCTGTGATCCTCGGTGCTCTTCTGAGCAACCCCAAACGCGATCAGCATC 300
 DB 374 AAGTGTGCTGTGATCCTCGGTGCTCTTCTGAGCAACCCCAAACGCGATCAGCATC 433
 QY 301 GAGATCCAGAAGCTGGATGCTGATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
 DB 434 GAGATCCAGAAGCTGGATGCTGATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
 QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCAITGTGCAAGTATCTCCCAAAATTTGAGAG 420
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCAITGTGCAAGTATCTCCCAAAATTTGAGAG 553
 QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCACCCTGCAATAGCACT 480
 DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCACCCTGCAATAGCACT 613
 QY 481 GGTAGACACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTTGTG 540
 DB 614 GGTAGACACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTTGTG 673
 QY 541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACCTACGAG 600
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACCTACGAG 733
 QY 601 TGCAGTGCCTCCATGACGTGGCGCGCGCTGGTACGGAGAGATAAGCTCAGCTGGAAC 660
 DB 734 TGCAGTGCCTCCATGACGTGGCGCGCGCTGGTACGGAGAGATAAGCTCAGCTGGAAC 793
 QY 661 TATCCACCATACATTTTCAAGGCCAAGGTTACAGGTGTCCTCCGTTGGGACAAAGGGGACA 720
 DB 794 TATCCACCATACATTTTCAAGGCCAAGGTTACAGGTGTCCTCCGTTGGGACAAAGGGGACA 853
 QY 721 CTGCACTGTGAAGCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGTGTAAGGATGACAA 780
 DB 854 CTGCACTGTGAAGCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGTGTAAGGATGACAA 913
 QY 781 AGACTCATTTGAAGGAAGGAGGTTGAAGTGGAAACAGACCTTTCTCTCAAACTC 840
 DB 914 AGACTCATTTGAAGGAAGGAGGTTGAAGTGGAAACAGACCTTTCTCTCAAACTC 973
 QY 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGCGCTCCCAACAG 900
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGCGCTCCCAACAG 1033
 QY 901 CTGGGCGCACCAATGCCAGCATCATGTATTGTGTCAGGGCGCTCAGCAGGTGAGC 960
 DB 1034 CTGGGCGCACCAATGCCAGCATCATGTATTGTGTCAGGGCGCTCAGCAGGTGAGC 1093
 QY 961 AACGGCACCTCCAGGAGGCGCAGCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 DB 1094 AACGGCACCTCCAGGAGGCGCAGCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153

QY 1021 CTTCTCAAAATTTGA 1035
 Db 1154 CTTCTCAAAATTTGA 1168

RESULT 14
 ID ACA63892
 AC ACA63892; standard; cDNA; 1679 BP.
 DT 16-JUN-2003 (first entry)
 DE Novel human secreted and transmembrane protein PR0337 cDNA.
 KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; inflammatory disease; organ failure;
 KW atherosclerosis; cardiac injury; infertility; birth defect;
 KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
 KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
 KW tissue typing; gene; ss.
 OS Homo sapiens.
 XX US2002192706-A1.
 PN 19-DEC-2002.
 PD 24-OCT-2001; 2001US-00999832.
 PF 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081819P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.

PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082796P.
 PR 07-OCT-1998; 98WO-US021141.
 PR 20-NOV-1998; 98WO-US024855.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032578.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001WO-US009552.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019892.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-328860/31.
 DR P-FSDB; ABU72281.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX
 PS Claim 2; Fig 221; 453pp; English.
 XX
 CC The invention describes an isolated nucleic acid (I) comprising, or which
 CC is at least 80 % sequence identity to, or the full-length coding sequence
 CC of any of 118 300-2100 nucleotide sequences, which encodes its
 CC corresponding PRO polypeptide selected from 118 100-700 amino acid
 CC polypeptides, all given in the specification. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS, cancer, or diabetic complications. The nucleic

CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCATCCAGCCAAATATGCAATTCATCTCTTGGCAATCTTCAGGGGCTG 60
DB 134 ATGAACACCATCCAGCCAAATATGCAATTCATCTCTTGGCAATCTTCAGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGAGTGCCTGTCGCGAGGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCTGTCGCGAGGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACACAGTGCCTGTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 254 GCTATGACACAGTGCCTGTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
QY 181 AACCGGCTCAACCGGGTGGCTGCTAAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
DB 314 AACCGGCTCAACCGGGTGGCTGCTAAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAG 373
QY 241 AAGTGTGCTGATCTCTCGTGGTCTCTTCTGAGCAACACCCAAACGCGATGACATC 300
DB 374 AAGTGTGCTGATCTCTCGTGGTCTCTTCTGAGCAACACCCAAACGCGATGACATC 433
QY 301 GAGATCCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 434 GAGATCCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
QY 361 AACACCCAAAGACCTCTAGGTCCTCACTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACACCCAAAGACCTCTAGGTCCTCACTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCATTAAATGAAGGAAACAATATTAGCTCACTGCTAGCAACT 480
DB 554 ATTCTTTCAGATATCTCATTAAATGAAGGAAACAATATTAGCTCACTGCTAGCAACT 613
QY 481 GGTAGACACGAGCTAGGTTACTTGAGACACATCTCTCCCAAGGGTGGCTTTTGG 540
DB 614 GGTAGACACGAGCTAGGTTACTTGAGACACATCTCTCCCAAGGGTGGCTTTTGG 673
QY 541 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCAATGACGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 734 TGCAGTGCCTCAATGACGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 793
QY 661 TATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTCAGTGTGAACCTCAGCAGTCCCTCAGCAGAAATTCAGGTGGTACAGGATGACAA 780
DB 854 CTCAGTGTGAACCTCAGCAGTCCCTCAGCAGAAATTCAGGTGGTACAGGATGACAA 913
QY 781 AGACTGATTCAGAAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
DB 914 AGACTGATTCAGAAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
QY 841 ATCTTCTTCAATGCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCCAACAG 900
DB 974 ATCTTCTTCAATGCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCCAACAG 1033
QY 901 CTGGGCGACACCAATGCCAGCATCATCTATTTGGTCCAGGCGCGTCCAGCGAGGTGAGC 960

DB 1034 CTGGGCGACACCAATGCCAGCATCATCTATTTGGTCCAGGCGCGTCCAGCGGTGAGC 1093
QY 961 AACGGCACGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 1094 AACGGCACGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
QY 1021 CTCTCAAAATTTGA 1035
DB 1154 CTCTCAAAATTTGA 1168

RESULT 15
ACA03790
ID ACA03790 standard; cDNA; 1679 BP.
XX
AC ACA03790;
AC AC
DT 23-MAY-2003 (first entry)
XX
cDNA encoding human PRO polypeptide #188.
DE Human; PRO polypeptide; secreted and transmembrane protein;
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN US2033036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 17-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98WO-US019437.
PR 29-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.

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PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004414.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806889.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski FU, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31.
DR P-PSDB; ABU66757.
DR New secreted and transmembrane PRO nucleic acids, useful for gene
XX therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT
```

PT typing, and in chromosome identification.

XX Claim 2; Fig 375; 660pp; English.

XX The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The PRO polypeptides are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipspIDEntry.html

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCAGCCAAATAATGCAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 60
Db 134 ATGAAACCATCAGCCAAATAATGCAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 193
Qy 61 GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCGAGCGGAGTGCACCTTCCCAAA 120
Db 194 GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCGAGCGGAGTGCACCTTCCCAAA 253
Qy 121 GCTATGACAACTGACGGTCCGCGAGCGGAGCGCCACCTTCAGTGCATATTGAC 180
Db 254 GCTATGACAACTGACGGTCCGCGAGCGGAGCGCCACCTTCAGTGCATATTGAC 313
Qy 181 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCACCTCTTATGTGGGAATGAC 240
Db 314 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCACCTCTTATGTGGGAATGAC 373
Qy 241 AAGTGGTGCCTGGATCCTCGCTGCTTCTTGAGCAACCCCAACCGCAGTACAGCATC 300
Db 374 AAGTGGTGCCTGGATCCTCGCTGCTTCTTGAGCAACCCCAACCGCAGTACAGCATC 433
Qy 301 GAGATCCAGAACGTTGATGTATGAGAGGGCCCTTTACACCTGCTCGGTGCACAGAC 360
Db 434 GAGATCCAGAACGTTGATGTATGAGAGGGCCCTTTACACCTGCTCGGTGCACAGAC 493
Qy 361 AACCAACCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAATTGTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAATTGTAGAG 553
Qy 421 ATTTCTTCAGATATCTCCATTATGAAGGAAACAATATTAGCTCCTCCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTATGAAGGAAACAATATTAGCTCCTCCTGCATAGCAACT 613
Qy 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGTTGGCTTTGTG 540
Db 614 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGTTGGCTTTGTG 673
Qy 541 AGTGAAGACGAATCTTGAAATTCAGGGGATCACCAGGAGCAGTACAGGGACTACAGAG 600
Db 674 AGTGAAGACGAATCTTGAAATTCAGGGGATCACCAGGAGCAGTACAGGGACTACAGAG 733
Qy 601 TGCAGTGCCTCCANTGACGTGGCGCCCGTGTGTGAGGAGTAAAGGTCAACCGTGAAC 660
Db 734 TGCAGTGCCTCCANTGACGTGGCGCCCGTGTGTGAGGAGTAAAGGTCAACCGTGAAC 793

PS Claim 2; Fig 51; 255pp; English.

XX The invention describes an isolated, secreted and transmembrane

CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting

CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,

CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth

CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for

CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a

CC cell expressing the polypeptides. The bioactive molecule causes cell

CC death. (II) is useful as hybridisation probes, in chromosome and gene

CC mapping, in generation of antisense RNA and DNA, in the preparation of

CC PRO polypeptide, for generating transgenic animals or knockout animals

CC which in turn are useful in the development and screening of

CC therapeutically useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chromosome

CC identification. (I) or Ab is useful for the preparation of medicament for

CC treating conditions which are responsive to the PRO polypeptide or anti-

CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes

CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for

CC inhibiting tumour growth, enhances vascular permeability and immune

CC response, for inducing regeneration of auditory hair cells and for

CC treating hearing loss in mammals, and for treating bone and/or cartilage

CC disorders such as sports injuries and arthritis. This sequence encodes a

CC novel human secreted and transmembrane polypeptide associated

CC oligonucleotide

XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTTGGCAATCTTACGGGGCTG 60

DB 134 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTTGGCAATCTTACGGGGCTG 193

QY 61 GCTGCTCTGTCTCTTCCAAAGAGTGGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 120

DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 253

QY 121 GCTATGGCAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGTGCACTATTGAC 180

DB 254 GCTATGGCAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGTGCACTATTGAC 313

QY 181 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTTATGCTGGGATGAC 240

DB 314 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTTATGCTGGGATGAC 373

QY 241 AAGTGGTGGCTGGATCTCTCGGTGGTCTTCTGAGCAACACCAACGAGTACGATC 300

DB 374 AAGTGGTGGCTGGATCTCTCGGTGGTCTTCTGAGCAACACCAACGAGTACGATC 433

QY 301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360

DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493

QY 361 AACCAACCAAGACCTCTAGGGTCCACCTTGTGCAAGTATCTCCCAAAATTTGAGAG 420

DB 494 AACCAACCAAGACCTCTAGGGTCCACCTTGTGCAAGTATCTCCCAAAATTTGAGAG 553

QY 421 ATTCTCTCAGATATCTCCAAATTAAGAGGGAACAATATTAGCCTCACTGCAATAGCACT 480

DB 554 ATTCTCTCAGATATCTCCAAATTAAGAGGGAACAATATTAGCCTCACTGCAATAGCACT 613

QY 481 GGTAGACACGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540

DB 614 GGTAGACACGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673

QY 541 AGTGAAGACGAATATCTTGAATTTAGGGCATCACCGGGAGCAGTTCAGGGGACTACGAG 600

DB 674 AGTGAAGACGAATATCTTGAATTTAGGGCATCACCGGGAGCAGTTCAGGGGACTACGAG 733

QY 601 TGCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGGTGAC 660

DB 734 TGCAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCACCGGTGAC 793

QY 661 TATCCACCATACATTTCAAGAGCCAAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 720

DB 794 TATCCACCATACATTTCAAGAGCCAAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 853

QY 721 CTGCAAGTGTGAAGCTTCAGCAGTCCCTCCACAGCAGNAATCCAGTGTGTACAAGGTCACAA 780

DB 854 CTGCAAGTGTGAAGCTTCAGCAGTCCCTCCACAGCAGNAATCCAGTGTGTACAAGGTCACAA 913

QY 781 AGACTGATTGAAGGAAAGAAAGAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 840

DB 914 AGACTGATTGAAGGAAAGAAAGAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 973

QY 841 ATCTTCTTCAATGTCTCTGAACATGACTATATGGGAACATACACTTGGTGGCTCTCAACAG 900

DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATATGGGAACATACACTTGGTGGCTCTCAACAG 1033

QY 901 CTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 960

DB 1034 CTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 1093

QY 961 AACGCGACGTCGAGGAGGCGAGGCTGCTGCTGGTGTGCTCTTCTGGTCTTGACCTG 1020

DB 1094 AACGCGACGTCGAGGAGGCGAGGCTGCTGCTGGTGTGCTCTTCTGGTCTTGACCTG 1153

QY 1021 CTCTCAAAATTTGA 1035

DB 1154 CTCTCAAAATTTGA 1168

RESULT 17

ACAT72056

ID ACA72056 standard; cDNA; 1679 BP.

XX AC ACA72056;

XX AC ACA72056;

DT 11-AUG-2003 (first entry)

XX

DE Human secreted and transmembrane PRO polypeptide #37 cDNA.

XX Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;

KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;

KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;

KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;

KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;

KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;

KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;

KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;

KW inflammatory bowel disease; reproductive disorder; premature labour.

XX Homo sapiens.

OS

XX US2002177553-A1.

PN

XX 28-NOV-2002.

PD

XX 15-OCT-2001; 2001US-00978192.

PF

XX 17-OCT-1997; 97US-0062250P.

PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 13-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00040220.

PR 20-MAR-1998; 98US-0078866P.

PR 20-MAR-1998; 98US-0078910P.


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PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079234P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079669P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265886.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 10-FEB-2000; 2000WO-US003365.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001WO-US016920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR XX (GETH ) GENENTECH INC.
PR XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
PR XX WPI; 2003-328499/31.
PR DR P-PSDB; ABUS4961.
PR XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
PR XX Claim 2; SEQ ID NO 522; 55pp; English.
PR XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC pre-eclampsia; carcinogenesis. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPIO at
CC seqdata.uspto.gov/sequence.html?DocID=20020177553
PR XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAACCATCCAGCCAAAATGCAAAATCTATCTCTGGGCAATCTTCACGGGGCTG 60
DB 134 ATGAAAACCATCCAGCCAAAATGCAAAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
QY 61 GCTGCTCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACAACTGACGCTGCGCAGCGGAGGAGCCACCTCAGGTGCATTATTGAC 180
DB 254 GCTATGACAACTGACGCTGCGCAGCGGAGGAGCCACCTCAGGTGCATTATTGAC 313
QY 181 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCAGCACCATCCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCAGCACCATCCTCTATGCTGGGAATGAC 373
QY 241 AAGTGTGCTTGGATCCTGCGTGTGCTCTTCTGAGCAACACCCAAACGAGTACAGATC 300
DB 374 AAGTGTGCTTGGATCCTGCGTGTGCTCTTCTGAGCAACACCCAAACGAGTACAGATC 433
QY 301 GAGATCCAGAACGTTGATGATGACGAGGGGCGCTTACCTGCTCGGTGCGAGCAGAC 360
DB 434 GAGATCCAGAACGTTGATGATGACGAGGGGCGCTTACCTGCTCGGTGCGAGCAGAC 493
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QY 361 AACACCCAGAGACCTCTAGGCTCCACCTCATTTGTGGAAGTATCTCCCAAAATTGTAGAG 420
Db 494 AACACCCAGAGACCTCTAGGCTCCACCTCATTTGTGGAAGTATCTCCCAAAATTGTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATGACCACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATGACCACT 613
QY 481 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
Db 614 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
QY 541 AGTGAAGACGAAATCTTGAAATTCAGGCGCATCACCCGGGAGCAGCTCAGGGGACTTACGAG 600
Db 674 AGTGAAGACGAAATCTTGAAATTCAGGCGCATCACCCGGGAGCAGCTCAGGGGACTTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCCGCGCCGCTGAGGAGTAAAGGTCAACCGTGAAC 660
Db 734 TGCAGTGCCTCCAAATGACGTGGCCGCGCCGCTGAGGAGTAAAGGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTTTCAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAGGATGACAAA 780
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAGGATGACAAA 913
QY 781 AGACTGATGAAGGAAAGAAAGGGGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 914 AGACTGATGAAGGAAAGAAAGGGGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 973
QY 841 ATCTCTTCAATGTCTCTGACATGATGGAATGGAATGGAATGGAATGGAATGGAATGGA 900
Db 974 ATCTCTTCAATGTCTCTGACATGATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1033
QY 901 CTGGGCCACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 960
Db 1034 CTGGGCCACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGTCAGAGAGGCGAGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTG 1020
Db 1094 AACGGCAGTCAGAGAGGCGAGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 18
ID ABX89328 standard; cDNA; 1679 BP.
XX AC ABX89328;
XX DT 13-MAY-2003 (first entry)
XX DE DNA encoding novel secreted and transmembrane protein PRO337.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
OS Homo sapiens.
XX

PN XX US2003017563-A1.
PD XX 23-JAN-2003.
XX PF 07-MAY-2002; 2002US-00140808.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 08-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
DR P-PSDB; ABUS9838.
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX Claim 2; Fig 375; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO826, PRO826, PRO1068 or PRO132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's

CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCCAAAATGCAATTTCTTCTTGGGCAATCTTACGGGGCTG 60
DB 134 ATGAAACCATCCAGCCCAAAATGCAATTTCTTCTTGGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTGTCCTTCCAGGAGTGCCGTCGCGAGGAGATGCCACCTTCCCAAAA 120
DB 194 GCTGCTCTGTGTCCTTCCAGGAGTGCCGTCGCGAGGAGATGCCACCTTCCCAAAA 253
QY 121 GCTATGGACAACGTCGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGGACAACGTCGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCACCCGGGTGGCTGGCTAAACCCGAGACCATCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCACCCGGGTGGCTGGCTAAACCCGAGACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGCTGGATCCTCGCTGGTCTTCTGAGCAACACCCAAACCGAGTACAGCATC 300
DB 374 AAGTGGTGCTGGATCCTCGCTGGTCTTCTGAGCAACACCCAAACCGAGTACAGCATC 433
QY 301 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACCCACCAAGACCTCTAGGGTCACTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCCACCAAGACCTCTAGGGTCACTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTCTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCACCCTGATAGCAACT 480
DB 554 ATTCTCTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCACCCTGATAGCAACT 613
QY 481 GGTAGACCAAGACCTTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTTGTG 540
DB 614 GGTAGACCAAGACCTTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTTGTG 673
QY 541 AGTGAAGACGAATATTGGAAATTCAGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGACGAATATTGGAAATTCAGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCCCAATGACCTGGCGCGCGCTGGTACGGAGAGTAAAGTCAACCGTGAAC 660
DB 734 TGCAGTGCCTCCCAATGACCTGGCGCGCGCTGGTACGGAGAGTAAAGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAAGACCAAGGTCACAGGTGTCCTCCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTTTCAAGACCAAGGTCACAGGTGTCCTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTCACAGGATGACAA 780
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTCACAGGATGACAA 913
QY 781 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGAACAGACACTTCTCTCAAAACTC 840
DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGAACAGACACTTCTCTCAAAACTC 973
QY 841 ATCTTCTTCAATGTCCTGAACATGACTATGGGAATCACTTGTGCGTGGCTCCCAACAG 900
DB 974 ATCTTCTTCAATGTCCTGAACATGACTATGGGAATCACTTGTGCGTGGCTCCCAACAG 1033
QY 901 CTGGGCGACACCAATGCCAGCATCTGCTATTGTTGGTCCAGGCGCCCTCAGCGAGGTGAGC 960

PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806899.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.

PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
(GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Garritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-466355/44.
DR P-PSDB; ABO25028.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
XX PRO4978, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.
XX Claim 2; Fig 375; 659pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 80%
XX sequence identity to a PRO (secreted and transmembrane protein) cDNA
XX comprising a nucleic acid (a) encoding a PRO polypeptide, or its
XX extracellular domain (with or without its associated signal peptide),
XX which comprises any of the 275 120-850 residue amino acid sequences,
XX given in the specification; (b) comprising any of the 275 300-3500
XX nucleotide sequences, given in the specification; or (c) comprising the
XX full-length coding sequence of the nucleotide sequences given in the
XX specification, or of the DNA deposited under any of the American Type
XX Culture Collection (ATCC) Accession Numbers listed in the specification.
XX Also included are a vector comprising the novel nucleic acid, a host cell
XX comprising the vector, producing a PRO polypeptide, the isolated PRO
XX polypeptides detailed above, a chimeric molecule comprising the PRO
XX polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
XX antibody, detecting a PRO polypeptide in a sample suspected of containing
XX the PRO polypeptide, linking a bioactive molecule to a cell expressing a
XX PRO polypeptide, modulating at least one biological activity of a cell
XX expressing a PRO polypeptide, stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
XX cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
XX modulating the uptake of glucose or FFA by skeletal muscle cells or
XX adipocyte cells, stimulating the proliferation or differentiation of
XX chondrocyte cells (or proliferation of or gene expression in pericyte
XX cells), stimulating the proliferation of inner ear utricular supporting
XX cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
XX binding of A-peptide to factor VIIA, or differentiation of adipocyte
XX cells, detecting the presence of a tumour in a mammal and an
XX oligonucleotide probe derived from any of the nucleotide sequences given
XX in the specification. The polynucleotide is useful in molecular biology,
XX including uses as hybridisation probes, in chromosome and gene mapping,
XX in generating antisense RNA and DNA, and in gene therapy. The
XX recombinant techniques, and in generating either transgenic animals or
XX knock-out animals which, in turn, are useful in the development and
XX screening of therapeutically useful reagents. The PRO polypeptide or the
XX antibody is used in preparing a medicament for treating a condition
XX responsive to the polypeptide or antibody, such as tumours, and in
XX various diagnostic assays. The present sequence encodes a PRO polypeptide
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCAAAATGCACAAATCTATCTCTTGGGCAATCTTCACGGGCTG 60
DB 134 ATGAAACCATCCAGCCAAAATGCACAAATCTATCTCTTGGGCAATCTTCACGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAGGAGTGCCTGTGGCAGCGGAGATGCCACCTTCCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAGGAGTGCCTGTGGCAGCGGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGGACACCTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCTATTGAC 180

Db 254 GCTATGTGACACGCTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTACCCGGGTGGCTGGCTTAACCCGAGCAGCACCATCTCTATGCTGGGAATGAC 240
Db 314 AACCGGGTACCCGGGTGGCTGGCTTAACCCGAGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGTGCTCGATCCTCGCGTGGTCTCTTCTGAGCAACACCCCAACGAGCATACAGCATC 300
Db 374 AAGTGTGCTCGATCCTCGCGTGGTCTCTTCTGAGCAACACCCCAACGAGCATACAGCATC 433
QY 301 GAGATCCAGAACGCTGGATGATGAGAGGGCCCTTACACTGCTCGGTGCGAGACAGAC 360
Db 434 GAGATCCAGAACGCTGGATGATGAGAGGGCCCTTACACTGCTCGGTGCGAGACAGAC 493
QY 361 AACACCCCAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
Db 494 AACACCCCAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 481 GGTAGACAGAGCTTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTG 540
Db 614 GGTAGACAGAGCTTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAAGGGGACTACGAG 600
Db 674 AGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAAGGGGACTACGAG 733
QY 601 TGCAGTGCCTTCAATGACGTGGCGCGCCGCTGGTACGGAGAGTAAAGTCAACCGTGAAC 660
Db 734 TGCAGTGCCTTCAATGACGTGGCGCGCCGCTGGTACGGAGAGTAAAGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTCAGAGCCAGGGTACAGGTGTCCTCGTGGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTCAGAGCCAGGGTACAGGTGTCCTCGTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAA 780
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAA 913
QY 781 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAACAGAGCTTTCTCTCAAAACTC 840
Db 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAACAGAGCTTTCTCTCAAAACTC 973
QY 841 ATCTTCTTCAATGCTCTGAACATGACTATGGGAACATACACTTGGCGGCTCCAAAG 900
Db 974 ATCTTCTTCAATGCTCTGAACATGACTATGGGAACATACACTTGGCGGCTCCAAAG 1033
QY 901 CTGGGCCACCAATGCCAGCATCATCTATTGGTCCAGGCGCGGTACGAGGTGAGC 960
Db 1034 CTGGGCCACCAATGCCAGCATCATCTATTGGTCCAGGCGCGGTACGAGGTGAGC 1093
QY 961 AACGGCAGCTCGAGGGGAGGCTGCTGCTGGCTGCTCTTCTGCTTGTGCTTGCACCTG 1020
Db 1094 AACGGCAGCTCGAGGGGAGGCTGCTGCTGGCTGCTCTTCTGCTTGTGCTTGCACCTG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 21

ACA60526

ID ACA60526 standard; cDNA; 1679 BP.

XX ACA60526;

AC ACA60526;

XX 11-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

DE

XX Human; secreted and transmembrane polypeptide; PRO;
KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW FGFR-2; PRO004; PRO4350; PRO2630; PRO265; PRO951; bioactive molecule;
KW toxin; radiolabel; antibody; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tissue typing; gene; ss.
XX Homo sapiens.
XX US2002177165-A1.
XX 28-NOV-2002.
XX 01-FEB-2002; 2002US-00066500.
XX 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 27-OCT-1997; 97US-0063082P.
PR 29-OCT-1997; 97US-0063329P.
PR 21-NOV-1997; 97US-0063733P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 01-MAR-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.

PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM;
 PI Wood WL, Zhang Z;
 XX
 DR WPI; 2003-328482/31.
 DR P-PSDB; ABU72061.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, for identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 2; Fig 51; 254pp; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
 CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,
 CC PRO10036, PRO346, PRO307, PRO6003, fibroblast growth factor receptor
 CC (FGFR)-3, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
 CC PRO951 polypeptide, and for linking a bioactive molecule to a cell
 CC expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction. The
 CC polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the PRO
 CC and for the genetic analysis of individuals with genetic disorders, in
 CC gene therapy, for chromosome identification and as a chromosome marker.
 CC (I) and (II) are useful for tissue typing. This sequence encodes a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGAAACACCATCCAGCAAAATGCAATTTCTATCTTGGCAATCTTACGGGGGTG 60
 134 ATGAAACACCATCCAGCAAAATGCAATTTCTATCTTGGCAATCTTACGGGGGTG 193
 61 GCTGCTCTGTGCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
 194 GCTGCTCTGTGCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 253
 121 GCTATGGCAACGTGACCGTCCGGCAGGGGAGAGGCCACCTCAGTGGCACTATTGAC 180
 254 GCTATGGCAACGTGACCGTCCGGCAGGGGAGAGGCCACCTCAGTGGCACTATTGAC 313

QY 181 AACCGGTGTCACCGGTGGCTGGCTAAACCGGAGCACCATTCTCTATGCTGGGAATGAC 240
 DB 314 AACCGGTGTCACCGGTGGCTGGCTAAACCGGAGCACCATTCTCTATGCTGGGAATGAC 373
 QY 241 AAGTGGTGCCTGGATCCTTCGCGTGGTCTCTTCGAGCAACACCCAAACGCACTACAGCATC 300
 DB 374 AAGTGGTGCCTGGATCCTTCGCGTGGTCTCTTCGAGCAACACCCAAACGCACTACAGCATC 433
 QY 301 GAGATCCAGAAACGTTGATGTATGACGAGGGCCCTTATACCTGCTCGGTGGAGACAGAC 360
 DB 434 GAGATCCAGAAACGTTGATGTATGACGAGGGCCCTTATACCTGCTCGGTGGAGACAGAC 493
 QY 361 AACCAACCCAAAGACCTCTAGGGTCCACCTCAATGTCGAAGTATCTCCCAAAATTTGTAGAC 420
 DB 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCAATGTCGAAGTATCTCCCAAAATTTGTAGAC 553
 QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACTGCTGATAGCAACT 480
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACTGCTGATAGCAACT 613
 QY 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
 DB 614 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
 QY 541 AGTGAAGACGAATATCTTGAAATTTCAAGGCATCACCCGGGAGCAGTCAAGGGGACTTACCGAG 600
 DB 674 AGTGAAGACGAATATCTTGAAATTTCAAGGCATCACCCGGGAGCAGTCAAGGGGACTTACCGAG 733
 QY 601 TGCAGTGCCTCCAATGACGTGGCGCGCCCTGCTGCTGAGAGTAAAGGTCAACGTTGAAC 660
 DB 734 TGCAGTGCCTCCAATGACGTGGCGCGCCCTGCTGCTGAGAGTAAAGGTCAACGTTGAAC 793
 QY 661 TATCCACCATACATTTCAAGAGCCAAAGGTTACAGGTGTCCCGGTGGGACAAAGGGGACA 720
 DB 794 TATCCACCATACATTTCAAGAGCCAAAGGTTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
 QY 721 CTGCACTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAGGATGACAAA 780
 DB 854 CTGCACTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAGGATGACAAA 913
 QY 781 AGACTGATGAAGGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAAATC 840
 DB 914 AGACTGATGAAGGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAAATC 973
 QY 841 ATCTTCTCATGTCTCTGACATGACTATGGAACACTACCTTGGTGGCTTCCAAACAG 900
 DB 974 ATCTTCTCATGTCTCTGGAACACTGACTATGGAACACTACCTTGGTGGCTTCCAAACAG 1033
 QY 901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGTGAGCGAGTGAGC 960
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGTGAGCGAGTGAGC 1093
 QY 961 AACGGCAGTGGAGAGGCGAGGCTGGTCTGGCTGCTGCTCTTCTGCTTGGTACCTG 1020
 DB 1094 AACGGCAGTGGAGAGGCGAGGCTGGTCTGGCTGCTGCTCTTCTGCTTGGTACCTG 1153
 QY 1021 CTCTCAAAATTTGA 1035
 DB 1154 CTCTCAAAATTTGA 1168
 RESULT 22
 ID ACA04516 standard; cDNA; 1679 BP.
 XX
 AC ACA04516;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO337 DNA.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;

```
KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW obesity; diabetes; insulinemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003032062-A1.
XX
XX 13-FEB-2003.
XX
XX 01-FEB-2002; 2002US-00066273.
XX
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063329P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0066364P.
XX 25-NOV-1997; 97US-0066840P.
XX 16-DEC-1997; 97US-0069694P.
XX 09-FEB-1998; 98US-0074086P.
XX 08-FEB-1998; 98US-0074092P.
XX 25-MAR-1998; 98US-0079294P.
XX 08-APR-1998; 98US-0081049P.
XX 14-JUL-1998; 98WO-US014552.
XX 10-AUG-1998; 98US-0095998P.
XX 18-AUG-1998; 98US-0097000P.
XX 09-SEP-1998; 98US-0099601P.
XX 10-SEP-1998; 98US-0099803P.
XX 10-SEP-1998; 98US-0099811P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98US-0100858P.
XX 17-SEP-1998; 98WO-US019437.
XX 24-SEP-1998; 98US-0101922P.
XX 28-OCT-1998; 98US-0106032P.
XX 20-NOV-1998; 98US-0109304P.
XX 20-NOV-1998; 98WO-US024855.
XX 25-NOV-1998; 98WO-US025190.
XX 01-DEC-1998; 98WO-US025108.
XX 08-MAR-1999; 98WO-US005028.
XX 23-MAR-1999; 98US-0125778P.
XX 02-JUN-1999; 98WO-US012525.
XX 15-JUN-1999; 98US-0139695P.
XX 20-JUL-1999; 98US-0145070P.
XX 26-JUL-1999; 98US-0145698P.
XX 17-AUG-1999; 98US-0149396P.
XX 01-SEP-1999; 98WO-US020111.
XX 08-SEP-1999; 98WO-US020594.
XX 15-SEP-1999; 98WO-US021090.
XX 15-SEP-1999; 98WO-US021547.
XX 30-NOV-1999; 98WO-US028313.
XX 01-DEC-1999; 98WO-US028301.
XX 02-DEC-1999; 98WO-US028565.
XX 07-DEC-1999; 98US-0169495P.
XX 20-DEC-1999; 98WO-US030999.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005641.

PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
XX Wood WI, Zhang Z;
XX
XX WPI; 2003-341963/32.
XX P-PSDB; ABU67162.
XX
XX New secreted and transmembrane polypeptide for modulating biological
XX activity of a cell expressing the polypeptide, identifying agonists or
XX antagonists of the polypeptide, and as molecular weight markers.
XX
XX Claim 2; Fig 51; 254pp; English.
XX
XX The invention describes an isolated, secreted and transmembrane
XX polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
XX PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
XX PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
XX factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
XX linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
XX cell expressing the polypeptides. The bioactive molecule causes cell
XX death. (II) Is useful as hybridisation probes, in chromosome and gene
XX mapping, in generation of antisense RNA and DNA, in the preparation of
XX PRO polypeptide, for generating transgenic animals or knockout animals
XX which in turn are useful in the development and screening of
XX therapeutically useful reagents, and for the genetic analysis of
XX individuals with genetic disorders, in gene therapy, and for chromosome
XX identification. (I) Or Ab is useful for the preparation of medicament for
XX treating conditions which are responsive to the PRO polypeptide or anti-
XX PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
XX or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
XX inhibiting tumour growth, enhances vascular permeability and immune
XX response, for inducing regeneration of auditory hair cells and for
XX treating hearing loss in mammals, and for treating bone and/or cartilage
XX disorders such as sports injuries and arthritis. This sequence encodes a
XX novel human secreted and transmembrane polypeptide
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAACCATCCAGCCAAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG 60
Db 134 ATGAAAACCATCCAGCCAAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG 193
QY 61 GCTGCTCTGTGTCTCTTCCAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 120
Db 194 GCTGCTCTGTGTCTCTTCCAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 253
```

121 GCTATGGAACGTCGCGTCCGCGAGGCGGAGCGCCACCTCAGGTGCACTATTGAC 180
254 GCTATGGAACGTCGCGTCCGCGAGGCGGAGCGCCACCTCAGGTGCACTATTGAC 313
181 AACCGGGTACCGGGTGGCTGCTAAACCGCAGCAGCACTCTCTATGCTGGGAATGAC 240
314 AACCGGGTACCGGGTGGCTGCTAAACCGCAGCAGCACTCTCTATGCTGGGAATGAC 373
241 AAGTGGTCCCTGGATCTCTGCGTGGTCTCTGAGCAACCCAAACGCGAGTACAGATC 300
374 AAGTGGTCCCTGGATCTCTGCGTGGTCTCTGAGCAACCCAAACGCGAGTACAGATC 433
301 GAGATCCAGACGCTGGATGCTATGACGAGGCGCTTACCTCTGCTGTCAGACAGAC 360
434 GAGATCCAGACGCTGGATGCTATGACGAGGCGCTTACCTCTGCTGTCAGACAGAC 493
361 AACCAACCAAGACCTCTAGGCTCCACCTCAATGTCGAAGTATCTCCAAAATTTGAG 420
494 AACCAACCAAGACCTCTAGGCTCCACCTCAATGTCGAAGTATCTCCAAAATTTGAG 553
421 ATTCTTCAGATATCTCAATTAATGAAGGAACTATTAAGCTCCTGCTGATGCAACT 480
554 ATTCTTCAGATATCTCAATTAATGAAGGAACTATTAAGCTCCTGCTGATGCAACT 613
481 GGTAGACCAAGCCTTACCGTCTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
614 GGTAGACCAAGCCTTACCGTCTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
541 AGTGAAGACGAATCTCTGGAATTCAGGGCATCAACCGGGAGCAGTCAAGGAGCTACGAG 600
674 AGTGAAGACGAATCTCTGGAATTCAGGGCATCAACCGGGAGCAGTCAAGGAGCTACGAG 733
601 TGCAGTGCCTCAATGACGTGCGCGCGCGCTGCTGTCGAGAGTAAAGGTCAACGTGAAAC 660
734 TGCAGTGCCTCAATGACGTGCGCGCGCGCTGCTGTCGAGAGTAAAGGTCAACGTGAAAC 793
661 TATCCACCATATCTCTAGAGCCCAAGGCTACAGGTGTCCTCGGGGACAAAGGGGACA 720
794 TATCCACCATATCTCTAGAGCCCAAGGCTACAGGTGTCCTCGGGGACAAAGGGGACA 853
721 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAAA 780
854 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAAA 913
781 AGACTGATGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAATC 840
914 AGACTGATGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAATC 973
841 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGTGGCTTCCCAACAG 900
974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGTGGCTTCCCAACAG 1033
901 CTGGGCGACACCAATGCGCAGATCATGCTATTTGGTCCAGGCGCGTCAAGAGGTGAGC 960
1034 CTGGGCGACACCAATGCGCAGATCATGCTATTTGGTCCAGGCGCGTCAAGAGGTGAGC 1093
961 AACGGACCTCCAGGAGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
1094 AACGGACCTCCAGGAGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
1021 CTCTCAAAATTTGA 1035
1154 CTCTCAAAATTTGA 1168

RESULT 23

ACA66437

ID ACA66437 standard; cDNA; 1679 BP.

XX ACA66437;

AC ACA66437;

XX 24-JUN-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO337.
DE Human; ss; gene; secreted protein; transmembrane protein; PRO;
XX malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW leukemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW infertility; premature aging; psoriasis; inflammatory disease;
KW renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW hepatitis; multiple sclerosis; gene therapy.
XX Homo sapiens.
OS US2003004102-A1.
XX 02-JAN-2003.
PD 15-OCT-2001; 2001US-009781B9.
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265886.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 30-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US0003565.

18-FEB-2000; 2000WO-US004341.
 24-FEB-2000; 2000WO-US005004.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000WO-US006319.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000US-00703238.
 10-NOV-2000; 2000WO-US030873.
 27-NOV-2000; 2000US-00723749.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US008520.
 22-MAR-2001; 2001US-00816744.
 22-MAR-2001; 2001US-00816920.
 22-MAR-2001; 2001WO-US009552.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00854280.
 23-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001WO-US017800.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001WO-US019692.
 23-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 30-JUL-2001; 2001US-00918585.
 (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 WPI: 2003-341189/32.
 P-FSDB; ABU80426.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Claim 2; Fig 221; 460pp: English.

The invention relates to a new isolated nucleic acid molecule comprises a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,

CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, CC necrosis, atherosclerosis, infertility, premature aging, psoriasis, CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia, CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The CC PRO polypeptides are useful in drug screening, particularly as targets CC for therapeutic intervention in these diseases, and in the diagnostic CC determination of the presence of these diseases. The PRO polypeptides are CC also useful as molecular weight markers, or for chromosome CC identification. The PRO genes are useful as hybridisation probes, or for CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may CC also be used in gene therapy, particularly for replacing a defective CC gene. The present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07; Indels 0; Gaps 0;
 Matches 1035; Conservative 0; Mismatches 0;

QY 1 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTTGGGCAATCTTACGGGGCTG 60
 DB 134 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTTGGGCAATCTTACGGGGCTG 193
 QY 61 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGGTGGCAGCGGAGATGCCACTTCCCAAA 120
 DB 194 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGGTGGCAGCGGAGATGCCACTTCCCAAA 253
 QY 121 GCTATGGACAAGTGAAGCTCCGGCAGGGGAGAGCCACCTCAGTGGCACTATTGAC 180
 DB 254 GCTATGGACAAGTGAAGCTCCGGCAGGGGAGAGCCACCTCAGTGGCACTATTGAC 313
 QY 181 AACCGGCTCACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTCTATCTGGGAATGAC 240
 DB 314 AACCGGCTCACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTCTATCTGGGAATGAC 373
 QY 241 AAGTGTGCTGTGATCTCTCGGTGGTCTTCTGTAGCAACACCAACGAGTACAGATC 300
 DB 374 AAGTGTGCTGTGATCTCTCGGTGGTCTTCTGTAGCAACACCAACGAGTACAGATC 433
 QY 301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGTCTGGTGCAGACAGAC 360
 DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGTCTGGTGCAGACAGAC 493
 QY 361 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
 DB 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 421 ATTTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCTCCTACCTGCATAGCACT 480
 DB 554 ATTTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCTCCTACCTGCATAGCACT 613
 QY 481 GGTAGACCAAGCCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
 DB 614 GGTAGACCAAGCCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 541 AGTGAAGACCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTCCGGGACTAGAG 600
 DB 674 AGTGAAGACCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTCCGGGACTAGAG 733
 QY 601 TGCAGTGCCTCCATGACGTGGCGCGCGCTGTAGCGAGAGTAAAGGTCCCGTGAAC 660
 DB 734 TGCAGTGCCTCCATGACGTGGCGCGCGCTGTAGCGAGAGTAAAGGTCCCGTGAAC 793
 QY 661 TATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCTCCCGTGGGACAAAAGGGGACA 720
 DB 794 TATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCTCCCGTGGGACAAAAGGGGACA 853
 QY 721 CTCAGTGTGAGCCTCAGCAGTCCCTCAGCAGAGATTCAGTGTGTACAGGATGACAAA 780
 DB 854 CTCAGTGTGAGCCTCAGCAGTCCCTCAGCAGAGATTCAGTGTGTACAGGATGACAAA 913
 QY 781 AGCTGATTGAGGAAGAAAGGGGTCAAGTGTGAAACAGACCTTCTCTCAAACTC 840

Db 914 AGACTGATTGAAGGAAGAAGGGGTGAAGTGAAGGAAACAGACCTTCTCTCAAACTC 973
Qy 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTCGCTGGCTCCAAAG 900
Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTCGCTGGCTCCAAAG 1033
Qy 901 CTGGGCCACACATGCCAGCATCATCTATTGGTCCAGGCGCGTCAAGGAGTGAGC 960
Db 1034 CTGGGCCACACATGCCAGCATCATCTATTGGTCCAGGCGCGTCAAGGAGTGAGC 1093
Qy 961 AACGSCAGTCTGAGGAGGCGAGCTGCTCTGGCTGCTGCTCTTCTGGTCTTGACCTG 1020
Db 1094 AACGSCAGTCTGAGGAGGCGAGCTGCTCTGGCTGCTGCTCTTCTGGTCTTGACCTG 1153
Qy 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 24
ACA68559
ID ACA68559 standard; cDNA; 1679 BP.
XX
AC ACA68559;
XX
DT 25-JUN-2003 (first entry)
DE
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN US2003088063-A1.
XX
PD 08-MAY-2003.
XX
XX 12-AUG-2002; 2002US-00219003.
PF
PF 25-JUL-2000; 2000US-0220664P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI
XX WPI; 2003-393229/37.
DR P-PSDB; ABU82110.
DR
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 2; Fig 125; 314pp; English.
PS
XX The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,

CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This sequence encodes a novel
CC human secreted and transmembrane PRO polypeptide
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAACCATCCAGCCAAAATGCAAAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 60
Db 134 ATGAAAACCATCCAGCCAAAATGCAAAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 193
Qy 61 GCTGCTCTGTGCTCTCTTCCAAAGAGTGCCTGGCGAGCGGAGATGCCACCTTCCCCAAA 120
Db 194 GCTGCTCTGTGCTCTCTTCCAAAGAGTGCCTGGCGAGCGGAGATGCCACCTTCCCCAAA 253
Qy 121 GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATATTGAC 180
Db 254 GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATATTGAC 313
Qy 181 AACCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
Db 314 AACCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
Qy 241 AAGTGGTCCCTGGATCTCGGGTGGTCTTCTTGAGCAACACCCAAACGACGTACAGCATC 300
Db 374 AAGTGGTCCCTGGATCTCGGGTGGTCTTCTTGAGCAACACCCAAACGACGTACAGCATC 433
Qy 301 GAGATCCAGAACGTGGATGTGTATGACGAGGCGCTTACACCTGTCTCGGTGAGACAGAC 360
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGCGCTTACACCTGTCTCGGTGAGACAGAC 493
Qy 361 AACCAACCAAGACCTCTAGGGTCCACCTCAATTGTGCAAGTATCTCCAAAATTGTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCAATTGTGCAAGTATCTCCAAAATTGTAGAG 553
Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTAGCTCACCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTAGCTCACCTGCATAGCAACT 613
Qy 481 GTGAGACAGAGCTTACCGTTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540
Db 614 GGTAGACAGAGCTTACCGTTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
Qy 541 AGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGAGCAGTCAAGGGGACTACGAG 600
Db 674 AGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGAGCAGTCAAGGGGACTACGAG 733
Qy 601 TGCAGTGCCTCAATGACGTGGCCCGCCGCTGGTACGGAGAGTAAGGTCAACCGTGAC 660
Db 734 TGCAGTGCCTCAATGACGTGGCCCGCCGCTGGTACGGAGAGTAAGGTCAACCGTGAC 793
Qy 661 TATCCACCATCATATTTTCAAGACCAAGGTCACAGTGTCCCGTGGGACAAAAGGGGACA 720
Db 794 TATCCACCATCATATTTTCAAGACCAAGGTCACAGTGTCCCGTGGGACAAAAGGGGACA 853
Qy 721 CTGCAAGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGAAATTCAGAGATACAAA 780
Db 854 CTGCAAGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGAAATTCAGAGATACAAA 913
Qy 781 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAACTC 840
Db 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAACTC 973
Qy 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTTCGCTGGCTCCCAAG 900
Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTTCGCTGGCTCCCAAG 1033
Qy 901 CTGGGCCACACCAATGCCAGCATCATCTATTGGTCCAGGCGCGTCAAGGAGTGAGC 960

PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 2; Fig 375; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
CC extracellular domains and mature sequences, methods of detecting PRO
CC proteins, methods for stimulating the release of TNF-alpha (tumour
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of chondrocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release of proteoglycans from
CC cartilage, proliferation of inner ear utricular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of
CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. The present sequence encodes a PRO protein
CC of the invention
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCAGCCAAATGCAATCTATCTCTGGCAATCTTCAGGGGCTG 60
DB 134 ATGAAACCATCAGCCAAATGCAATCTATCTCTGGCAATCTTCAGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGAGTGGCCGTGGCAGGGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGGCCGTGGCAGGGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACAACTGACGGTCCGGCAGGGGAGAGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGACAACTGACGGTCCGGCAGGGGAGAGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGGCTGGATCCTCGCTGGTCTCTTCTGAGCAACACCCAAACGCAATCAGCATC 300
DB 374 AAGTGGTGGCTGGATCCTCGCTGGTCTCTTCTGAGCAACACCCAAACGCAATCAGCATC 433
QY 301 GAGATCCAGAACGTTGATGATGACGAGGGCCCTTACCTGCTCGGTGCGACAGAC 360
DB 434 GAGATCCAGAACGTTGATGATGACGAGGGCCCTTACCTGCTCGGTGCGACAGAC 493
QY 361 AACCAACCAAGACCTTAGGGTCCACTATGTCAGATCTCTCCCAAAATGTAGAG 420
DB 494 AACCAACCAAGACCTTAGGGTCCACTATGTCAGATCTCTCCCAAAATGTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCCTCAGCTGATGCAACT 480

DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCCTCAGCTGATGCAACT 613
QY 481 GGTAGACCAAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540
DB 614 GGTAGACCAAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 541 AGTGAACACCAATATTTGGAATTCAGGCAATCACCCGGGAGCAGTCCAGGGGACTACGAG 600
DB 674 AGTGAACACCAATATTTGGAATTCAGGCAATCACCCGGGAGCAGTCCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCCGCCCGTGGTACGAGAGTAAAGGTACCGTGAAC 660
DB 734 TGCAGTGCCTCCAAATGACGTGGCCGCCCGTGGTACGAGAGTAAAGGTACCGTGAAC 793
QY 661 TATCCACATACATTTCAAGACCAAGGCTACAGGTGTCCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACATACATTTCAAGACCAAGGCTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGAGTGGTACAAAGATGACAAA 780
DB 854 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGAGTGGTACAAAGATGACAAA 913
QY 781 AGACTGATGAAGAAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAACTC 840
DB 914 AGACTGATGAAGAAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAACTC 973
QY 841 ATCTTCTCAATGTCTCTGAACATGACTATGCGGAACATACACTTGGTGGCTCCCAACAAG 900
DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGCGGAACATACACTTGGTGGCTCCCAACAAG 1033
QY 901 CTGGGCCACACCAATGCGCAGCATCATGCTATTTGGTCCAGCGCGCGTCCAGGAGGTGAGC 960
DB 1034 CTGGGCCACACCAATGCGCAGCATCATGCTATTTGGTCCAGCGCGCGTCCAGGAGGTGAGC 1093
QY 961 AACGCGACGTCCAGAGGCGGAGGCTGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1020
DB 1094 AACGCGACGTCCAGAGGCGGAGGCTGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
QY 1021 CTCTCTCAAAATTTGA 1035
DB 1154 CTCTCTCAAAATTTGA 1168
RESULT 26
AC65657
ID ACA65657 standard; cDNA; 1679 BP.
XX
AC 65657;
AC AC
XX AC
DT 19-JUN-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO337.
XX
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
XX Genetic disorder; gene therapy.
OS Homo sapiens.
XX
XX US2003032057-A1.
FN
XX
PD 13-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00002796.
PF
XX 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.

QY	301	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACTGTCTGGTGCAGACAGAC	360
Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACTGTCTGGTGCAGACAGAC	493
QY	361	AACACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG	420
Db	494	AACACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG	553
QY	421	ATTTCCTTCAGATATCTCAATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT	480
Db	554	ATTTCCTTCAGATATCTCAATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT	613
QY	481	GGTAGACCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAACGGTTGGCTTTGTG	540
Db	614	GGTAGACCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAACGGTTGGCTTTGTG	673
QY	541	AGTGAAGACGATATCTTGGAAATTCAGGGCATCACCCGGGACAGTCAGGGGACTACGAG	600
Db	674	AGTGAAGACGATATCTTGGAAATTCAGGGCATCACCCGGGACAGTCAGGGGACTACGAG	733
QY	601	TGCAGTGCCTCCAATGATCGTGGCCCGCCGCTGTGTACGGAGAGTAAAGGTCACCGTGAAC	660
Db	734	TGCAGTGCCTCCAATGATCGTGGCCCGCCGCTGTGTACGGAGAGTAAAGGTCACCGTGAAC	793
QY	661	TATCCACCATACATTTTCAGAAAGCCAAAGGTCACAGGTGTCCCGTGGGACAAAGGGGACA	720
Db	794	TATCCACCATACATTTTCAGAAAGCCAAAGGTCACAGGTGTCCCGTGGGACAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTACAAAGGATGACAAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTACAAAGGATGACAAA	913
QY	781	AGACTGATTGAAGGAAGAAAGAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAACCTC	840
Db	914	AGACTGATTGAAGGAAGAAAGAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAACCTC	973
QY	841	ATCTTCTTCAATGTCTCTGAAATGACATATGGGAACTACATTCGGTGGCTCCAAACAG	900
Db	974	ATCTTCTTCAATGTCTCTGAAATGACATATGGGAACTACATTCGGTGGCTCCAAACAG	1033
QY	901	CTGGGCCACACCAATGCCAGACATCATGTATTTGGTCCAGGCGCCTCAGCGAGTGCAGC	960
Db	1034	CTGGGCCACACCAATGCCAGACATCATGTATTTGGTCCAGGCGCCTCAGCGAGTGCAGC	1093
QY	961	AACGGCAGCTCAGAGAGGCGAGGCTCGCTCTGGTGTGCTCTTCTGGTCTTCACCTG	1020
Db	1094	AACGGCAGCTCAGAGAGGCGAGGCTCGCTCTGGTGTGCTCTTCTGGTCTTCACCTG	1153
QY	1021	CTTCTCAAATTTTGA 1035	
Db	1154	CTTCTCAAATTTTGA 1168	
RESULT 27			
ADA45894			
ID	ADA45894 standard; cDNA; 1679 BP.		
XX			
AC	ADA45894;		
XX			
DT	20-NOV-2003 (first entry)		
XX			
DE	Novel human secreted and transmembrane protein PRO337 cDNA.		
XX			
KW	Human; secreted and transmembrane protein; PRO; gene; ss;		
KW	tumour necrosis factor alpha release; TNF-alpha release;		
KW	glucose uptake modulator; FFA uptake modulator;		
KW	cell proliferation stimulator; cell differentiation stimulator;		
KW	cell differentiation inhibitor; cytokine release stimulator; tumour;		
KW	lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;		
KW	cervical tumour; liver tumour; chromosome mapping; gene mapping;		
KW	gene therapy; chromosome identification; chromosome marker.		
XX			
OS	Homo sapiens.		

CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources (I) and (II) are useful for tissue typing. This sequence encodes
CC a novel human secreted and transmembrane PRO polypeptide.

XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCAGCCAAATGCAATTTCTTCTTCTTGGCAATCTTCAGGGGCTG 60
DB 134 ATGAAACCATCAGCCAAATGCAATTTCTTCTTGGCAATCTTCAGGGGCTG 193
QY 61 GCTGCTCTGCTCTTCCAAAGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGCTCTTCCAAAGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGGAACAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGGAACAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGTCACCCGGTGGCTGGCTAAACCGCAGCACCCTCCTCTATCTGCGGAATGAC 240
DB 314 AACCGGTCACCCGGTGGCTGGCTAAACCGCAGCACCCTCCTCTATCTGCGGAATGAC 373
QY 241 AAGTGTGCTCGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
DB 374 AAGTGTGCTCGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACTGGATGATGAGCAGAGGGCCCTTACCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAACTGGATGATGAGCAGAGGGCCCTTACCTGCTCGGTGAGACAGAC 493
QY 361 AACACCCCAAGACCTCAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACACCCCAAGACCTCAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCCTCAGTCCATAGCAACT 480
DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCCTCAGTCCATAGCAACT 613
QY 481 GGTAAGCAGAGCTACCGTTTCTTGAGAGACATCTCTCCAAAGGGTGGCTTTGTG 540
DB 614 GGTAAGCAGAGCTACCGTTTCTTGAGAGACATCTCTCCAAAGGGTGGCTTTGTG 673
QY 541 AGTGAAGCAGATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGCAGATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCAGTGGCTCCAAATGAGTGGCGCCCGCGTGTGTAAGGAGTAAGAGTCCCGTGAAC 660
DB 734 TGCAGTGGCTCCAAATGAGTGGCGCCCGCGTGTGTAAGGAGTAAGAGTCCCGTGAAC 793
QY 661 TATCCACATACATTTGAGAGCCAAAGGTACAGGTGTCCTCCGTCGAGCAAAAGGGGACA 720
DB 794 TATCCACATACATTTGAGAGCCAAAGGTACAGGTGTCCTCCGTCGAGCAAAAGGGGACA 853
QY 721 CTGCAAGTGAAGCTCAGCAGTCCCTTCAGCAGAAATTCAGGTGTACAGAGTACAGAA 780
DB 854 CTGCAAGTGAAGCTCAGCAGTCCCTTCAGCAGAAATTCAGGTGTACAGAGTACAGAA 913
QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACTC 840
DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACTC 973
QY 841 ATCTTCTTCAATGCTCTGAACATGACTATGGGACTACCTTGGTGGCTCCCAACAG 900
DB 974 ATCTTCTTCAATGCTCTGAACATGACTATGGGACTACCTTGGTGGCTCCCAACAG 1033
QY 901 CTGGCCACACCAATATGCGCAGCATCATGTTATTTGTCAGGCGCGCTCAGCGAGGTGAGC 960

PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021666.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-0028072.
PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-584997/55.
DR P-PSDB; ADA45895.

XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 375; 659pp; English.

XX The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PBMC cells, for inhibiting the binding of
CC A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (II) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.

361 AACACCCAAAAGACCTCTAGGGTCCACCTCATTTGTGAAGTATCTCCCAAATTTAGAG 420
494 AACACCCAAAAGACCTCTAGGGTCCACCTCATTTGTGAAGTATCTCCCAAATTTAGAG 553
421 ATTTCTTCAGATATCTCATTAATGAAGGAAACATATAGCTTACCTGCAATACCAACT 480
554 ATTTCTTCAGATATCTCATTAATGAAGGAAACATATAGCTTACCTGCAATACCAACT 613
481 GTAGACACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAAGCGTTGGCTTTGTG 540
614 GTAGACACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAAGCGTTGGCTTTGTG 673
541 AGTGAAGACCAATATCTTGGAAATTCAGGGCATACCCCGGAGCAGTCAAGGAGTACGAG 600
674 AGTGAAGACCAATATCTTGGAAATTCAGGGCATACCCCGGAGCAGTCAAGGAGTACGAG 733
601 TCGAGTGCCTCAATGAAGTGGCCCGCCCGTGGTACGGAGAGTAAAGTCAACCTGTAAC 660
734 TCGAGTGCCTCAATGAAGTGGCCCGCCCGTGGTACGGAGAGTAAAGTCAACCTGTAAC 793
661 TATCCACCATATATTTTCAAGAGCCCAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 720
794 TATCCACCATATATTTTCAAGAGCCCAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 853
721 CTGAGTGTGAAGCCTTACAGTGTCCCTCAGCAGATTCAGTGTGTAAGGATGACAAA 780
854 CTGAGTGTGAAGCCTTACAGTGTCCCTCAGCAGATTCAGTGTGTAAGGATGACAAA 913
781 AGACTGATTAAGGAAAGGAGGTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
914 AGACTGATTAAGGAAAGGAGGTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973
841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCTCCCAACAG 900
974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCTCCCAACAG 1033
901 CTGGGACACACCAATGCGAGCATCTGCTATTTGGTTCAGGCGCCCTCAGGAGGTGAGC 960
1034 CTGGGACACACCAATGCGAGCATCTGCTATTTGGTTCAGGCGCCCTCAGGAGGTGAGC 1093
961 AAGGACAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
1094 AAGGACAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
1021 CTCTCTCAAAATTTTGA 1035
1154 CTCTCTCAAAATTTTGA 1168
RESULT 29
ABT44288
ID ABT44288 standard; cDNA; 1679 BP.
XX
AC ABT44288;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO337 cDNA.
XX
KW PRO: proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; ss;
KW differentiation; dermal fibroblast; tumour; gene therapy; gene;
XX
OS Homo sapiens.
XX
FN US2003050448-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230414.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.

DR MPI; 2003-687639/65.
DR P-PSDB; ADA76326.
XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; Fig 375; 659pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCAAATGACAAATTTCTATCTTGGGCAATCTTCCAGGGGCTG 60
DB 134 ATGAAACCATCCAGCCAAATGACAAATTTCTATCTTGGGCAATCTTCCAGGGGCTG 193
QY 61 GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 194 GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253
QY 121 GCTATGGAACGTCAGCGTCCGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 254 GCTATGGAACGTCAGCGTCCGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
QY 181 AACCAGGTCACCGGGTGCCTGGTGAACCCAGCAGCACCATCTCTATGCTGGGAAATGAC 240
DB 314 AACCAGGTCACCGGGTGCCTGGTGAACCCAGCAGCACCATCTCTATGCTGGGAAATGAC 373
QY 241 AAGTGTGTGCTGGATCTCTCGCTGTGCTCTTGTAGCAACCCAAACGAGTACAGATC 300
DB 374 AAGTGTGTGCTGGATCTCTCGCTGTGCTCTTGTAGCAACCCAAACGAGTACAGATC 433
QY 301 GAGATCCAGAAAGTGTGATGTAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 434 GAGATCCAGAAAGTGTGATGTAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493

PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
PA Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PU;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WJ;
PI WPI; 2003-521818/49.
XX P-PSDB; ABJ72290.
XX
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.
XX
XX Claim 2; Fig 125; 315pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, the stimulation of human dermal fibroblast cell
CC proliferation and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
CC cDNA of the invention
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAAACCATCCAGCCAAATGCAATCTCTCTTGGGCAATCTTCCAGGGGCTG 60
134 ATGAAACCATCCAGCCAAATGCAATCTCTCTTGGGCAATCTTCCAGGGGCTG 193
61 GCTGCTCTGTGCTCTTCCAGGAGTGCCGCGCAGCGGAGATGCCACCTTCCCAA 120
194 GCTGCTCTGTGCTCTTCCAGGAGTGCCGCGCAGCGGAGATGCCACCTTCCCAA 253
121 GCTATGGACAACTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCTATTGAC 180
254 GCTATGGACAACTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCTATTGAC 313
181 AACCGGCTCACCGGGTGGCTGGCTAAACCGCAGCACCACCTCTATGCTGGGAATGAC 240
314 AACCGGCTCACCGGGTGGCTGGCTAAACCGCAGCACCACCTCTATGCTGGGAATGAC 373
241 AAGTGGTGCCTGGATCTCGGCTGGCTCTTCTGAGCNAACCCAAACGGAGTACAGATC 300
374 AAGTGGTGCCTGGATCTCGGCTGGCTCTTCTGAGCNAACCCAAACGGAGTACAGATC 433
301 GAGATCCAGAACGTTGATGATGAGAGGGGCTTACACCTGCTCGGTCAGACAGAC 360
434 GAGATCCAGAACGTTGATGATGAGAGGGGCTTACACCTGCTCGGTCAGACAGAC 493
361 AACCAACCAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAG 420
494 AACCAACCAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAG 553
421 ATTTCTTTCAGATATCTCCATTAATGAAGGGGAAACAATATTAGCTCCTCAGTACAGCACT 480
554 ATTTCTTTCAGATATCTCCATTAATGAAGGGGAAACAATATTAGCTCCTCAGTACAGCACT 613
481 GGTAGACAGAGCCCTAGCTTACTTGGGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
614 GGTAGACAGAGCCCTAGCTTACTTGGGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
541 AGTCAAGACGAATACTTTGGAATTCAGGGCATCCCGGAGCAGTCCAGGGGACTACGAG 600

574 AGTGAAGACGATATCTTTGGAATTCAGGGCATCACCGGGAGCAGTCCAGGGGACTAGAG 733
501 TGCAGTGCCTCCCAATGACGTGGCGCGCGCTGATAGGAGTAAAGGTCAACGCTGAAC 660
734 TGCAGTGCCTCCCAATGACGTGGCGCGCGCTGATAGGAGTAAAGGTCAACGCTGAAC 793
661 TATCCACCATACATATTTTCAAGGCAAGGGTACAGGTGTCTCCCGTGGGACAAAAGGGGACA 720
794 TATCCACCATACATATTTTCAAGGCAAGGGTACAGGTGTCTCCCGTGGGACAAAAGGGGACA 853
721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGAGGTACACAAA 780
854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGAGGTACACAAA 913
781 AGACTGATTGAAGGAAAGGAGGTTGAAAGTGGAAACAGACCTTTCTCTCAAAATC 840
914 AGACTGATTGAAGGAAAGGAGGTTGAAAGTGGAAACAGACCTTTCTCTCAAAATC 973
841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACATCTGCTGGGCTCTCAACAG 900
974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACATCTGCTGGGCTCTCAACAG 1033
901 CTGGGCGACACCAATGCGAGCATCATGCTATTTGCTCAGGCGCGCTCAGGAGGTGAGC 960
1034 CTGGGCGACACCAATGCGAGCATCATGCTATTTGCTCAGGCGCGCTCAGGAGGTGAGC 1093
961 AACGCGCAGTCTGAGGAGGCGAGGCTGCTGCTGCTGCTGCTCTTCTGCTTTCACCTG 1020
1094 AACGCGCAGTCTGAGGAGGCGAGGCTGCTGCTGCTGCTGCTCTTCTGCTTTCACCTG 1153
1021 CTCTCTCAAAATTTGA 1035
1154 CTCTCTCAAAATTTGA 1168
RESULT 30
ADA18975
ID ADA18975 standard; cDNA; 1679 BP.
XX ADA18975;
AC ADA18975;
XX 20-NOV-2003 (first entry)
XX Human PRO polynucleotide #188.
DE Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
XX tumour; breast; prostate; rectum; cervix; liver; tumour; cancer;
XX glucose uptake; PFA; adipocyte cell; pericyte cell; proteoglycan;
XX cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
XX factor VIIA; endothelial cell.
XX Homo sapiens.
XX US2003054517-A1.
XX 20-MAR-2003.
XX 08-MAY-2002; 2002US-00141755.
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 29-OCT-1998; 98WO-US022992.

PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US000502.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US021547.
PR 15-SEP-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00736498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-521854/49.
DR P-PSDB; ADA18976.
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
XX Claim 2; Fig 375; 660pp; English.
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC cells, for stimulating the proliferation of or gene expression in
CC pericyte cells, for stimulating the release of proteoglycans from
CC cartilage, for stimulating the proliferation of inner ear utricular
CC supporting cells, for stimulating the release of cytokines from PBMC
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for
CC inhibiting the differentiation of adipocyte cells and for stimulating the
CC proliferation of endothelial cells. This sequence represents a human PRO
CC polynucleotide of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATTCAGCCAAATGCAATTTCTATCTCTTGGCAATCTTTCACGGGGCTG 60
Db 134 ATGAAACCATTCAGCCAAATGCAATTTCTATCTCTTGGCAATCTTTCACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGAGATGCCACCTTCCCCAAA 120
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGGACAACTGACCGGTCCGGCAGGGGAGAGCGCCACCTCAGTGTGACTTATGAC 180
Db 254 GCTATGGACAACTGACCGGTCCGGCAGGGGAGAGCGCCACCTCAGTGTGACTTATGAC 313

Tue Jun 1 09:37:50 2004

QY 181 AACGGGTCAACCGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
 Db |
 QY 314 AACGGGTCAACCGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
 Db |
 QY 241 AAGTGGTCCCTGGATCCCTGGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 300
 Db |
 QY 374 AAGTGGTCCCTGGATCCCTGGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 433
 Db |
 QY 301 GAGATCCAGAACGCTGGATGTGTATCAGCAGGCGCCCTTACACCTGCTCGGTGCAGACAGAC 360
 Db |
 QY 434 GAGATCCAGAACGCTGGATGTGTATCAGCAGGCGCCCTTACACCTGCTCGGTGCAGACAGAC 493
 Db |
 QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTTAGAG 420
 Db |
 QY 494 AACCAACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTTAGAG 553
 Db |
 QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
 Db |
 QY 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
 Db |
 QY 481 GGTAGACCAAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
 Db |
 QY 614 GGTAGACCAAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
 Db |
 QY 541 AGTGAAGACGAATACCTTGAATTCAGGGCATCAACCGGGAGCAGTACGGGAGCTACGAG 600
 Db |
 QY 674 AGTGAAGACGAATACCTTGAATTCAGGGCATCAACCGGGAGCAGTACGGGAGCTACGAG 733
 Db |
 QY 601 TGCAGTGGCTCCCAATGACGTGGCGCGCGGTGACGAGAGTAAAGGTCAACCGTGAAC 660
 Db |
 QY 734 TGCAGTGGCTCCCAATGACGTGGCGCGCGGTGACGAGAGTAAAGGTCAACCGTGAAC 793
 Db |
 QY 661 TATCCACCATACATTTCAAGACCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
 Db |
 QY 794 TATCCACCATACATTTCAAGACCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 Db |
 QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 780
 Db |
 QY 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
 Db |
 QY 781 AGACTGATTTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATC 840
 Db |
 QY 914 AGACTGATTTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATC 973
 Db |
 QY 841 ATCTTCTTCAATGTCTGAAACATGACTATGGAACTACACTTGGGTGGCTCCAAACAG 900
 Db |
 QY 974 ATCTTCTTCAATGTCTGAAACATGACTATGGAACTACACTTGGGTGGCTCCAAACAG 1033
 Db |
 QY 901 CTGGGCGACACCAATGCCAGCATCTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 960
 Db |
 QY 1034 CTGGGCGACACCAATGCCAGCATCTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 1093
 Db |
 QY 961 AACGGCACGTCGAGGAGGCGAGGCTGGCTCTGGCTGCTGCTCTTCTGGTCTTGCACCTG 1020
 Db |
 QY 1094 AACGGCACGTCGAGGAGGCGAGGCTGGCTCTGGCTGCTGCTCTTCTGGTCTTGCACCTG 1153
 Db |
 QY 1021 CTTCTCAAAATTTGA 1035
 Db |
 QY 1154 CTTCTCAAAATTTGA 1168
 Db |

Search completed: May 28, 2004, 15:50:40
 Job time : 463.39 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:29:05 ; Search time 89.2373 Seconds

(without alignments)
6436.482 Million cell updates/sec

Title: US-10-017-084A-522_COPY_134_1168

Perfect score: 1035

Sequence: 1 atgaaccaccacccagccaaa.....acctgcttcctcaatttga 1035

Scoring table: IDENTITY_NUC

Gapop 1.0 , Gapext 0.1

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1035	100.0	1693	4	US-09-700-397-2
2	1032	99.7	1032	4	US-09-700-397-1
3	939	90.7	939	4	US-09-700-397-5
4	489.9	47.3	1238	2	US-08-414-657D-3
5	489.9	47.3	1238	4	US-09-135-080-3
6	482.5	46.6	1014	2	US-08-414-657D-5
7	482.5	46.6	1014	4	US-09-135-080-7
8	477	46.1	1195	4	US-09-976-594-403
9	463.9	44.8	977	2	US-08-414-657D-1
10	463.9	44.8	977	4	US-09-135-080-1
11	453.7	43.8	945	2	US-08-414-657D-8
12	445.6	43.0	11673	4	US-09-334-220-3
13	445.5	43.0	6942	2	US-08-460-309-3
14	445.5	43.0	6942	4	US-08-125-077-3
15	445.5	43.0	9419	4	US-09-562-702A-7
16	445.5	43.0	9420	4	US-09-562-702A-3
17	445.5	43.0	9534	4	US-09-562-702A-5
18	445.5	43.0	9534	4	US-09-561-709B-8
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21	444.6	43.0	10348	3	US-08-556-419-13
22	444.6	43.0	10348	3	US-09-041-882A-5
23	444.6	43.0	10366	1	US-08-246-982A-5
24	444.6	43.0	10366	1	US-08-453-265-5
25	444.5	42.9	924	2	US-08-414-657D-7
26	443.9	42.9	3002	4	US-09-369-364A-1
27	443.7	42.9	2603	1	US-08-179-481-1

28	443.5	42.9	2232	1	US-08-179-481-97	Sequence 97, Appl
29	443.4	42.8	4768	1	US-07-596-467-1	Sequence 1, Appl
30	443.4	42.8	4768	1	US-07-934-374-1	Sequence 1, Appl
31	443.4	42.8	4768	1	US-07-783-861C-3	Sequence 3, Appl
32	443	42.8	5329	4	US-09-562-702A-19	Sequence 19, Appl
33	443	42.8	5329	4	US-09-561-818A-19	Sequence 19, Appl
34	443	42.8	5689	4	US-09-562-702A-17	Sequence 17, Appl
35	443	42.8	5689	4	US-09-561-818A-17	Sequence 17, Appl
36	442.5	42.8	7672	4	US-09-220-132-24	Sequence 24, Appl
37	441.7	42.7	6153	2	US-08-347-594A-1	Sequence 1, Appl
38	441.7	42.6	5117	4	US-09-060-299-40	Sequence 40, Appl
39	441.3	42.6	5117	4	US-09-402-923A-40	Sequence 40, Appl
40	441.3	42.6	6153	3	US-08-463-682-2	Sequence 2, Appl
41	441.2	42.6	4880	3	US-09-031-563-1	Sequence 1, Appl
42	441.2	42.6	4880	4	US-09-392-777-1	Sequence 1, Appl
43	441.2	42.6	4880	4	US-09-258-000-1	Sequence 15, Appl
44	441.1	42.6	5433	4	US-09-562-702A-15	Sequence 15, Appl
45	441.1	42.6	5433	4	US-09-561-818A-15	Sequence 13, Appl
46	441.1	42.6	5613	4	US-09-562-702A-13	Sequence 13, Appl
47	441.1	42.6	5613	4	US-09-561-818A-13	Sequence 10, Appl
48	441.1	42.6	5613	4	US-09-561-709B-10	Sequence 148, Appl
49	440.8	42.6	12127	4	US-08-961-527-148	Sequence 1, Appl
50	440.7	42.6	4039	1	US-08-363-300-1	Sequence 2, Appl
51	440.5	42.6	4430	2	US-08-918-914-2	Sequence 1, Appl
52	440.5	42.6	5141	1	US-08-337-690A-1	Sequence 1, Appl
53	440.5	42.6	5141	3	US-09-048-887-3	Sequence 3, Appl
54	440.5	42.6	70000	4	US-09-851-896-3	Sequence 1, Appl
55	440.4	42.6	2218	4	US-03-350-457A-1	Sequence 1, Appl
56	440.4	42.6	8598	4	US-08-305-790B-1	Sequence 20, Appl
57	440.3	42.5	3783	4	US-08-506-296B-20	Sequence 5, Appl
58	440.2	42.5	3069	4	US-09-514-907A-5	Sequence 5, Appl
59	440.2	42.5	3069	4	US-09-896-994-5	Sequence 1, Appl
60	440.1	42.5	4149	2	US-08-737-715-1	Sequence 1, Appl
61	440.1	42.5	4723	4	US-09-023-655-1137	Sequence 1137, Appl
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63	440.1	42.5	4843	4	US-09-402-923A-41	Sequence 41, Appl
64	440.1	42.5	7541	4	US-09-637-048C-4	Sequence 4, Appl
65	439.9	42.5	7286	4	US-08-793-273C-1	Sequence 1, Appl
66	439.9	42.5	7286	5	PCT-US95-11684-1	Sequence 1, Appl
67	439.7	42.5	8078	4	US-09-702-251-3	Sequence 3, Appl
68	439.6	42.5	22671	4	US-08-976-259-14	Sequence 14, Appl
69	439.4	42.5	4360	1	US-08-470-350B-1	Sequence 1, Appl
70	439.4	42.5	7577	4	US-09-637-048C-3	Sequence 3, Appl
71	439.4	42.5	7621	4	US-09-637-048C-6	Sequence 6, Appl
72	439.3	42.4	8575	4	US-09-381-261A-2	Sequence 2, Appl
73	439.2	42.4	3105	3	US-08-542-635-1	Sequence 1, Appl
74	439.2	42.4	3319	4	US-08-976-259-85	Sequence 85, Appl
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76	439.1	42.4	5125	3	US-09-392-277-4	Sequence 4, Appl
77	439.1	42.4	5125	4	US-09-258-000-4	Sequence 4, Appl
78	439.1	42.4	5421	1	US-08-118-441-28	Sequence 28, Appl
79	439.1	42.4	5421	3	US-08-338-579A-28	Sequence 28, Appl
80	439.1	42.4	5421	5	PCT-US94-09851-28	Sequence 28, Appl
81	438.9	42.4	3811	4	US-09-620-312D-538	Sequence 538, Appl
82	438.9	42.4	4601	1	US-08-470-058-3	Sequence 3, Appl
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84	438.9	42.4	4601	3	US-09-285-310-3	Sequence 3, Appl
85	438.6	42.4	5095	4	US-08-092-817-3	Sequence 3, Appl
86	438.6	42.4	5095	4	US-08-485-128-3	Sequence 3, Appl
87	438.6	42.4	11517	1	US-07-920-281C-1	Sequence 1, Appl
88	438.6	42.4	11517	3	US-08-466-277-1	Sequence 1, Appl
89	438.6	42.4	13930	4	US-09-976-594-1011	Sequence 1011, Appl
90	438.5	42.4	2361	3	US-08-705-771-7	Sequence 7, Appl
91	438.5	42.4	2361	4	US-09-417-540-7	Sequence 7, Appl
92	438.4	42.4	5056	2	US-08-793-126-2	Sequence 2, Appl
93	438.4	42.4	5056	3	US-09-132-271-2	Sequence 2, Appl
94	438.4	42.4	5067	3	US-09-142-334-23	Sequence 23, Appl
95	438.4	42.4	8035	4	US-09-215-694-29	Sequence 29, Appl
96	438.4	42.4	11560	4	US-09-334-220-4	Sequence 19, Appl
97	438.4	42.4	31328	4	US-09-215-694-19	Sequence 19, Appl
98	438.2	42.3	3703	4	US-09-023-655-1293	Sequence 1293, Appl
99	438.2	42.3	3716	4	US-09-620-312D-537	Sequence 537, Appl
100	438.2	42.3	4950	4	US-09-023-655-1284	Sequence 1284, Appl

ALIGNMENTS

RESULT 1
US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
; LOCATION: (130)..(1161)
; NAME/KEY: sig_peptide
; LOCATION: (130)..(213)
; NAME/KEY: mat_peptide
; LOCATION: (214)..()
US-09-700-397-2
Query Match 100.0%; Score 1035; DB 4; Length 1693;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCAAATGACAAATCTATCTTGGCAATCTTTCAGGGGCTG 60
Db 130 ATGAAACCATCCAGCCAAATGACAAATCTATCTTGGCAATCTTTCAGGGGCTG 189
QY 61 GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCAGGAGATGCCACCTTCCCAA 120
Db 190 GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCAGGAGATGCCACCTTCCCAA 249
QY 121 GCTATGGCAAGCTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGACAT 180
Db 250 GCTATGGCAAGCTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGACAT 309
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QY 241 AAGTGGTGGCTGGATCTCTCGGTGCTCTTCTGAGCAACACCAACCGAGTACGATC 300
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QY 301 GAGATCCAGAACGTGGATGTATGACGAGGCGCTTACACCTGCTCGGTGACAGAC 360
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QY 361 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 420
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Db 550 ATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTAGCTCACCTGCAATGCAACT 609
QY 481 GGTAGACGAGCTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTG 540

Db 610 GGTAGACGAGCTTACGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 669
QY 541 AGTGAAGACGAATACTTGGAAATTCAGGGGATCACCOCGGAGCAGTCAAGGGGACTTACGAG 600
Db 670 AGTGAAGACGAATACTTGGAAATTCAGGGGATCACCOCGGAGCAGTCAAGGGGACTTACGAG 729
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QY 961 AACGCGACGTCGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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Db 1150 CTCTCAAAATTTGA 1164
RESULT 2
US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-1
Query Match 99.7%; Score 1032; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCAAATGACAAATCTATCTTGGCAATCTTTCAGGGGCTG 60
Db 1 ATGAAACCATCCAGCCAAATGACAAATCTATCTTGGCAATCTTTCAGGGGCTG 60
QY 61 GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCAGGAGATGCCACCTTCCCAA 120
Db 61 GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCAGGAGATGCCACCTTCCCAA 120

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121 GCTATGACAAACGTCACGGTCCGCGCAGGGGAGAGCGCCACCTCTCAGGTGCACTATTGAC 180
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181 AACCGGCTCACCGGGTGGCTGGCTAAACCGCAGCACCACTCTCTATGCTGGGAATGAC 240
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241 AAGTGTGCTCGATCTCTCGGTGGTCTCTTGAGCAACACCCAAACGCGAGTACAGCATC 300
301 GAGATCCAGAACGTCGTATGATGACGAGGGCCCTTACACCTCTCGGTGCGACAGAC 360
301 GAGATCCAGAACGTCGTATGATGACGAGGGCCCTTACACCTCTCGGTGCGACAGAC 360
361 AACCAACCAAGACCTCTAGGCTCCACCTCATTTGTCAAGTATCTCCCAAAATTTGTAG 420
361 AACCAACCAAGACCTCTAGGCTCCACCTCATTTGTCAAGTATCTCCCAAAATTTGTAG 420
421 ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCTCACTGCAATGCAACT 480
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481 GGTAGACAGAGCCTTACGGTCTCTTGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
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661 TATCCACCATACATTTCAAGACCAAGGTTACAGGTGTCCTGCTGGGCAAAAGGGGACA 720
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RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of

FILE REFERENCE: Q61459
CURRENT APPLICATION NUMBER: US/09/700,397
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: JP 10-131815
PRIOR FILING DATE: 1998-05-14
PRIOR APPLICATION NUMBER: PCT/JP99/02485
PRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 939
TYPE: cDNA
ORGANISM: Homo sapiens
US-09-700-397-5

Query Match 90.7%; Score 939; DB 4; Length 939;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 CGCAGCGAGATGCCACCTTCCCAAGCTATGACAAACGTCGCTCCGCGAGGGGAG 153
DB 1 CGCAGCGAGATGCCACCTTCCCAAGCTATGACAAACGTCGCTCCGCGAGGGGAG 60
QY 154 AGCCCAACCTCAGGTGCACTATTGACAAACGCGGTCAACCGGTGGCTGGCTAAACCGC 213
DB 61 AGCCCAACCTCAGGTGCACTATTGACAAACGCGGTCAACCGGTGGCTGGCTAAACCGC 120
QY 214 AGCACCATCTCTATGCTGGGAATGACAAAGTGGCTGCTGATCTCTCGGTGGTCTTCTG 273
DB 121 AGCACCATCTCTATGCTGGGAATGACAAAGTGGCTGCTGATCTCTCGGTGGTCTTCTG 180
QY 274 AGCAACACCCAAACGCGAGTACAGCATCGAGATCCAGAACGTCGATGTGTATGACAGGGC 333
DB 181 AGCAACACCCAAACGCGAGTACAGCATCGAGATCCAGAACGTCGATGTGTATGACAGGGC 240
QY 334 CTTTACACCTGCTCGGTGCGACAGACAAACCCCAAGACCTTAGGGTCCACTCATT 393
DB 241 CTTTACACCTGCTCGGTGCGACAGACAAACCCCAAGACCTTAGGGTCCACTCATT 300
QY 394 GTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAAC 453
DB 301 GTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAAC 360
QY 454 AATATTAGCCTCACCTGATAGCAACTGCTAGACAGAGCTACGTTTCTTGGAGACAC 513
DB 361 AATATTAGCCTCACCTGATAGCAACTGCTAGACAGAGCTACGTTTCTTGGAGACAC 420
QY 514 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAAATCTTGGAAATTCAGGGCATC 573
DB 421 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAAATCTTGGAAATTCAGGGCATC 480
QY 574 ACCCGGAGCAGTCAAGGGGACTACGAGTGCAGTGCCTCCAATGACGTCGCGCGCCCGTG 633
DB 481 ACCCGGAGCAGTCAAGGGGACTACGAGTGCAGTGCCTCCAATGACGTCGCGCGCCCGTG 540
QY 634 GTACGAGAGTAAAGGTCAACCGTGAACCTATCCACATATTTTGAAGACCCAGGGTACA 693
DB 541 GTACGAGAGTAAAGGTCAACCGTGAACCTATCCACATATTTTGAAGACCCAGGGTACA 600
QY 694 GGTGTCCCGTGGGCAAAAGGGGACCTGAGTGTGAAGCCTCAGCAGTCCCTCAGCA 753
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QY 754 GAATTCAGTGTGTACAAAGGATGACAAAGACCTGATTTGAAGGAAAGAGGGGTGAAAGTG 813
DB 661 GAATTCAGTGTGTACAAAGGATGACAAAGACCTGATTTGAAGGAAAGAGGGGTGAAAGTG 720
QY 814 GAAAAACAGACCTTTCTCTCAAAATCTCATCTTTTCAATGTCTCTGAACATGACTATGGG 873
DB 721 GAAAAACAGACCTTTCTCTCAAAATCTCATCTTTTCAATGTCTCTGAACATGACTATGGG 780
QY 874 AACTACACTGCTGCTGCTCCCAAGCTGCGGCAACCAATGCCAGCATCTGCTATTTT 933

Db 781 AACTACACTTGGCTGCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATT 840

Qy 934 GTTCCAGGCGCGTCAAGCGAGTGAGCAACGCGACGTCGAGAGGCGAGCTGCGTCTGG 993

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Qy 994 CTGCTGCCTCTTCTGCTTCTTGCACTGCTTCTCAAAATTT 1032

Db 901 CTGCTGCCTCTTCTGCTTCTTGCACTGCTTCTCAAAATTT 939

RESULT 4

US-08-414-657D-3
Sequence 3, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1238 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 56...1069
OTHER INFORMATION:

US-08-414-657D-3

Query Match 47.3%; Score 489.9; DB 2; Length 1238;
Best Local Similarity 61.6%; Pred. No. 2.9;
Matches 724; Conservative 0; Mismatches 178; Indels 273; Gaps 101;

Qy 2 TGAACAACA-T-CC-AGCCAAAATG-C---ACAATTCTATCTCTTGGCAATC--T 49

Db 34 TG---ACCACTGCGCGAGGCCACCATGTCGGGAGAGTTCAACTGATCGG-AAACAGT 89

Qy 50 T--CACGGG----GCTG-G-CTGCTCTGTGTCTTT-CCA-AGGAGTCCCGTGGCAGC 99

Db 90 TGCCACTGGTCTACTGAGACTGCTCTGCT-TCITCCACAGGACTGCCCGTTCGCAGC 148

Qy 100 GGAGATGCCACTTCCCAAAAGCTATGGAACAAGTGAAGTCCGGCAGGGGAGAGCGCC 159

Db 149 GTGGAT-----TTTAAACGAGGC-ACGGAACAACATCACCGTGAGCAGGGGACACGCGC 202

Qy 160 ACCCTCAGTGCACCTAT--T-----GACAAACGGGTCAACCG--GGTGGCCTTGGCTAAACC 211

Db 203 ATCCCTCAGGTG---TGTGTAGAACAA-----G-ACTCGAAAGTGGCTGTTGAACC 254

Qy 212 GC---AGCACCATCTCTATGCTGGGAATGACAAGTGTGTGATCTCTCGCTGGTCC 268

Db 255 GCTCTGGCATCATCTTC---GCTGGACACGACAAGTGGTCTCTGGACCTCG---GGT-- 306

Qy 269 TTCTGAGC-----AACACCCAAACGC-----AGTACAGCAT-CCAGATCCAGAACTGG 316

Db 307 ---TGAGCTGGAGAAACGCC---ATGCTCTGGAATACAGCTCCCGA-ATCCAGAACTGG 359

Qy 317 ATGTGTATGACGAGG--CCCTTACACCTGTCTGGTGCAGACAGACAACCA-----CCCAA 370

Db 360 ATGTCTATGATGAAGATCC--TACACATGCTCAGTTCAGAC--AC-AGCATGAGGCC-A 413

Qy 371 AGACCTCT--AGGTCCACCTCATTTGCAAGTATCTCCAAA-AT-TGTAGAGATTTCT 426

Db 414 AGACCTCTCAA--GTTTACTTGAATTGTAACAAGT-TCCACCAAAGATCTCCA-ACATCTCC 469

Qy 427 TCAGATATCTCCATTAATGAAGGAAACATATTAGCTTCACTGCATAGCAACTGTAGA 486

Db 470 TCGGATGTCACTGTGAATGAGGCGAGCAATGTAACTTGTCTGTATGCCATGGCGC 529

Qy 487 CCAGAGCCTTACCGTT---ACTTGGAGACACATCTCTC-CCAAAGCGTTTG--CMT 536

Db 530 CTTGAACTT---GTTATCACTGGAGACAC--CTTACACCA---C--TTGGAAGAGAA 579

Qy 537 TG--TGAGTGAAGACGAATCTTGGAAATTCAGGCAATCACCCGGGAGCAGTCNGGGAC 594

Db 580 TGAAGGA--GAAGAAGAATATCTGGAGATCTTAGGCATCACCAGGAAACAGTCAGGCAA 637

Qy 595 TAGGAGTGCAGTGCCTCCCAATGACGTGGCGCGCGCTGTGTACGGA-G-----AGTAA 646

Db 638 TATGAGTGAAGGTGCCA---ACGAGGTCTCTCTCG---CGGATGTCAAAAGATCA 689

Qy 647 AGGTCAACCGTGAATAT---CCACAT-ACA---TTT-----CA--GAAGCA-----AG 687

Db 690 AGGTCACTGTGAATATCCACCACCATCACAGAGTCAAGAGCAATGAAGCCACCACAG 749

Qy 688 G-GTACAGGTGTCCTCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCC 746

Db 750 GACGCAAGCTTCCC--T-----CAAA-----TGTGAAGCCTCAGCGGTGCC 789

Qy 747 CTCAGCAGAAATTCAGTGTGTACAAAGGATGACAAAAGACTGATTGAAGGAAAG---AAAG 803

Db 790 TGCACTGACTTTGAGTGTGTACCGGATGACACAG--GAT-AA--ACAGTGCAAAACG 842

Qy 804 G--GTGAAGTGAA-A--ACAGA---CCTTCTCTCAAAACTCA--T--CTTCTTCA 850

Db 843 GCCTTGAGATT--AAGAGCACTGAGGCGCAGTCTC-C-----CTGACGGTGAC-----CA 890

Qy 851 ATGTCTCT--GAACATGACTATGGGAATCTACACTTGTGGTGGCTCCAAACAGCTGGCC 907

Db 891 ACGTCACTGAGAAC---ACTACGGCACTATACCTGTGTGGTGTCCACACAGCTCGCG 947

Qy 908 ACACCAATGCCAGCATCATCTATTGTTCCAGGCGCC--GTGACGAGGTGAG-----959

Db 948 TCACCAATGCCAGCTAGTCTT-TTT---CAGAC-CCGGGTC-----GGTGAGAGAAAT 996

Qy 960 CAACGGCACTGAGGAGGCGAGCTG--CGT-----C--TGGCTGCT-----GCCTCTTCT 1007

Db 997 CAACGG-A--TCCA-----TCAGTCTGGCGGTACCACTGTGTGCTGGCAGCGTC-CCT 1047

Qy 1008 GGTCTTCGACCTGCTTCT---CAAAATTT-----GA 1035

Db 1048 GTTC-TGC-----CTTCTCAGCAAAATGTTAATAGA 1076

RESULT 5
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56..1069
; OTHER INFORMATION:
; US-09-135-080-3
Query Match 47.3%; Score 489.9; DB 4; Length 1238;
Best Local Similarity 61.6%; Pred. No. 2.9;
Matches 724; Conservative 0; Mismatches 178; Indels 273; Gaps 101;
Qy 2 TGAATAACA-T-CC-AGCCAAAATG-C--ACAAATTCATCTCTTGGCAATC-T 49
Db 34 TG--ACCAACTCCGAGGCCACATGGTCGGGAGAGTTCAACCTGATCGG-AAACAGT 89
Qy 50 T-CACGGG---GCTG-G-CTGCTCTGTCTCTTT-CCA-AGGAGTGCCTGCGCAGC 99
Db 90 TGCCTAGTGTCTACTGAGACTGTCTGCTT-TCTTCCACAGGACTGCCCTTTCGCGC 148
Qy 100 GGAGATGCCACTTCCCAAGCTATGGACAACTGACGGTCCGCGCAGGGGGAGCGCC 159
Db 149 GTGGAT-----TTTAACCGAGGC-ACGACAAACATCACCGTACGAGCGAGGGGACACGCGCC 202
Qy 160 ACCCTCAGTGCACAT-T-T-----GACAAACGGGTACCGG--GGTGGCTGGCTAAACC 211
Db 203 ATCTCAGGTG---TGTGGTAGAGACAA-----G-ACTCGAAAGTGGCTGTGTAACC 254
Qy 212 GC---AGCACCATCTCTATGCTGGGAATGACAACTGGTGTGCTGATCTCTCGCGTGGTCC 268

Db 255 GCTCTGGCATCATCTTC---GCTGGACACGAAAGTGGTCTCTGGACCCCTCG---GGT--- 306
Qy 269 TTCTGAGC-----AACACCCAAACGC-----AGTACAGCAT-CGAGATCCAGAACGTGG 316
Db 307 ---TCAGCTGGAGAAACGCC---ATGCTCTGGAATACAGCCTCCGA-ATCCAGAAAGTGG 359
Qy 317 ATGTGTATGACGAGG--CCCTTACACCTGCTCGGTGCAGACAGACACCA-----CCCAA 370
Db 360 ATGTCTATGATGAAGATCC--TACACATGCTCAGTTTCAGAC--AC-AGCATGAGCCCA-A 413
Qy 371 AGACCTCT--AGGGTCCACCTCATTTGTGCAAGTATCTCCAAA-AT-TGTAGAGATTTCT 426
Db 414 AGACCTCTCAA--GTTTACTTGAITGTACAAAGT-TCCACCAAGATCTTCCA-ACATCTCC 469
Qy 427 TCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCTCCTGTCATGCAACTGTTAGA 486
Db 470 TCGGATGTCTGTAATGAGGGGAGCAATGTAACCTCTGCTGTGATGCCAATGGGCGC 529
Qy 487 CCAGAGCCTACGGTT---ACTTTGAGACACATCTCTC-CCAAAGCGGTTGG-----CTT 536
Db 530 CCTGAACCT---GTTATCACCTGGAGACAC--CTTACACCA---C--TTGGAAGAGAAT 579
Qy 537 TG--TGAGTGAAGACGAATATCTTGGAAATTCAGGSCATCACCCGGGAGCAGTCAGGGGAC 594
Db 580 TGAAGCA--GAAGAAGAATATCTGAGATCTCTAGGCATCACCGGGAACAGTCAGGCAAA 637
Qy 595 TACGAGTGCAGTGCCTCCAAATGACGTGCGCGCGCTGGTACCGA-G-----AGTAA 646
Db 638 TATGAGTGCAGGCTGCCA---ACAGGTCTCTCTCG-----CGATGTCAACAAAGTCA 689
Qy 647 AGTCAACCGTGAACATAT---CCACCAT-ACA---TTT-----CA-GAAGCA---AG 687
Db 690 AGTCACTGTGAACATATCCACCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAG 749
Qy 688 G-GTACAGGTGCTCCCGTGGGCAAAAGGGGACACTGCACTGTGAAGCTTGAAGCTCAGCAGTCC 746
Db 750 GACGACAAAGCTTCCC--T-----CAAA-----TGTGAAGCTCTAGCGGTGCC 789
Qy 747 CTCAGCAGAAATCCAGTGTGTACAAAGGATGCAAAAGACTGATTTGAAGGAAAG---AAAG 803
Db 790 TGCACTGACTTTGAGTGGTACCGGATGACACCAG---GAT--AA--ACAGTGAACAG 842
Qy 804 G--GTGAAAGTGA--A--ACAGA---CCTTTCTCTCAAACTCA---T--CTTCTTCA 850
Db 843 GCCTTGAGATT--AAGAGCACTGAGGCGCAGTCTC-C---CTGACGGTGAC-----CA 890
Qy 851 ATGTCTCT---GAAATGACTATGGAACTACACTTGGCTGGCTCCCAAGCTGGGCC 907
Db 891 ACGTCACTGAGAAC---ACTACGGCAACTATACCTGTGTGGCTGCCAACAGCTGGCG 947
Qy 908 ACACCAATGCCAGCATCATGCTATTGTTGCTCCAGCGGCC---GTGAGCGAGGTGAG----- 959
Db 948 TCACCAATGCCAGCTAGTCTCT-TTT-----CAGAC-CCGGGTC-----GGTGAAGAGAT 996
Qy 960 CAACGGCACTGAGGAGGCGCAGGTG--CGT-----C--TGGCTGCT---GCCTCTTCT 1007
Db 997 CAACGG-A--TCCA-----TCAGTCTGGCGGTACCACTGTGGTGTGCTGGCAGCGTC-CCT 1047
Qy 1008 GGTCTTGCACCTGCTCTCT---CAAAATTTT-----GA 1035
Db 1048 GTTC-TGC-----CTTCTCAGCAATGTTAATAGA 1076

RESULT 6
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
; US-08-414-657D-5
;
; Query Match 46.6%; Score 482.5; DB 2; Length 1014;
; Best Local Similarity 62.3%; Pred. No. 2.8;
; Matches 711; Conservative 0; Mismatches 173; Indels 257; Gaps 100;
;
; QY 22 ATG--C--ACAATCTATCTCTGGGCAATC--TT--CACGG--GCTG-G-CTGCT 66
; DB 1 ATGGTCGGGAGAGTTCAACCTGATCGG-AAACAGTTGCCACTGGTCTTACTAGAGACTGCT 59
;
; QY 67 CTGTGCTCTT--CCA-AGAGTGCCCGTCGCGAGCGGAGATGCCACCTTCCCAAGCTA 124
; DB 60 CTGCGCT-TCTTCCACAGACTGCGCGTTCGACAGGTGAT-----TTTAAACGAGGC-A 112
;
; QY 125 TGACAAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGACTAT--T-----G 178
; DB 113 CGGACAAATCATCCGTCGAGCGAGGGGACACGCCATCTCAGGTG--TGTGGTAGAG 169
;
; QY 179 ACACCGGGTCACCG--GGTGGCTGGCTTAACCGC--AGCACCTCTCTATGCTGG 233
; DB 170 ACAA-----G-AACTCGAAAGTGGCTGGTGTGAACCGCTCTGGCATCATCTTC--GCTGG 221
;
; QY 234 GAATGACAGTGTGCTGTGATCTCGCGTGGTCTTCTTGAGC-----AACACCCCAAC 287
; DB 222 ACAGCAAGTGTCTCTGAGCCCTCG--GGT-----TGAGCTGGAGAAACGCC--AT 270
;
; QY 288 GC-----AGTACAGCAT--CGAGATCCAGAACGTGGATGTGTATGACAGGG--CCCTTAC 339
; DB 271 GCTCTGGAATACAGCTCCGA-ATCCAGAGGTGGATGTCTATGATGAAGGATCC--TAC 327
;
; QY 340 ACCTGCTCGGTGACAGACAGACACCA-----CCCAAGACCTCT--AGGCTCCACCTCAT 393
; DB 328 ACATGCTCAGTTCAGAG--AC-AGCATGAGCCCC-AAGACCTCTCAA--GTTTACTTGATT 381

394 GTGCAAGTATCTCCCAA-AT-TGTAGAGATTCTTTCAGATATCTCCATTAATGAGGGA 451
DB GTACAGGT-TCCACCAAGATCTCA-ACATCTCTCGGATCTCACTGTGAATGAGGGA 439
QY ACAATATTAGCCTCACCTGATAGCAACTGGTAGACCCAGAGCCTACGGTT-----ACTTGA 508
DB GCAATGTAACTTGGTCTGATGGCAATGGCGGCTGAACCT--GTTATCACTCTGA 496
QY GACACATCTCTC-CCAAAGCGGTTGG-----CTTTGTGA--GTGAAGACGAATATCTCG 559
DB GACAC-CTTACACCA--C--TTGAAGAGAAAT--TGAGAGAGAGAAATATCTGG 547
QY AAATTCAGGGCATCACCGGAGCAGTCAGGGGACTACAGTGCAGTGCCTCCAAATGAG 619
DB AGATCTTAGGCATCACCGGAGACAGTCAGGCAAAATATGAGTGCAGAGGCTGCCA--ACG 604
QY TGGCCCGGCGCGGTGGTACGGA-G-----AGTAAAGGTCCACGTAACCTAT-----CCAC 667
DB AGGTCTCTCTCG-----CGGATGTCAAACAAGTCAAGGTCACTGTGAACCTATCCACCCAC 659
QY CAT-ACA-----TTTCAGAGCCAGGCTACAGGTGTCC-CGCTGGGACAAAAGGG--GACA 720
DB CATCAGAGTCTAAG-AG-CAATG--A-AG-----CCACC-----ACA-----GGACGACA 701
QY --CTGC-----AGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTAAGGA 773
DB AGCTTCCCTCAATGTGAAGCCTCAGCGGTGCTGCACTGACTTTGAGTGTGACCGGGA 761
QY TGACAAAAGACTGATTAAGGAAG--AAAGG--GTGAAAGTGGAA-A--ACAGA-- 822
DB TGACACGAG--GAT--AA--ACAGTGAACAAAGCGCTTGAGATT--AAGAGCACTGAGGG 812
QY CCTTTCTCTCAAAACTCA--T--CTTCTTCAATGTCTCT--GAACATGACTATGGA 874
DB CCAGTCTCTC-----CTGACGGTGCAC-----CAACGTCACTGAGGAAC--ACTACGGA 859
QY ACTACACTTGGTGGCTCCAAAGCTGGGCGCACCAATGCGCAGATCCAGCATCATGCTATTG 934
DB ACTATAGCTGTGTGGCTGCGCAACAAAGCTCGCGCTCACCAATGCGCAGCTAGTCTCT-TTT- 917
QY GTCACAGGCGC--GTCAGCAGGTGAG-----CAACGGCAGCTCGAGGAGGCGGCTG 986
DB ---CAGAC-CGGGTC-----GGTGAGAGAAATCAACGG-A--TCCA-----TCAGTCTG 960
QY --CGT-----C--TGCTGCT-----GCCTCTTCTGCTGTGCACTGCTCT--CAAAAT 1031
DB GCCGTACCACTGTGGCTGCTGGCAGCGTC-CCTGTTC-TGC-----CTTCTCAGCAATG 1013
QY 1032 T 1032
DB 1014 T 1014

RESULT 7
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
;
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1014
OTHER INFORMATION:
US-09-135-080-7

Query Match 46.6%; Score 482.5; DB 4; Length 1014;
Best Local Similarity 62.3%; Pred. No. 2.8;
Matches 711; Conservative 0; Mismatches 173; Indels 257; Gaps 100;

QY 22 ATG-C---ACAACTCTATCTTGGGCAATC-TT-CACGGG---GCTG-G-GTGT 66
DB 1 ATGGTGGGAGAGTTCAACCTGATCG-AAAAGTTGCCACTGGTCTACTGAGACTGCT 59
QY 67 CTGTGTCTCTT-CCA-AGAGTGGCCGTGCGGAGGGGAGAGCGCCACCTCAGTGCATAT-T-----G 178
DB 60 CTGGCT-TCTTCCACAGAGCTGCCGTTCGAGCGTGGAT-----TTTAAACGAGGC-A 112
QY 125 TGGACAACTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCATAT-T-----G 178
DB 113 CGGACAAATCATCCGTGAGCGAGGGGAGAGCGCCATCTCTCAGGTG---TGTGGTAGAG 169
QY 179 ACNACGGGTACCCG-GTGGCCCTGGCTTAACCGC---AGCACATCTCTATCTGCTGG 233
DB 170 ACNAC---G-ACTCGAAAGTGGCTGGTGAACCGCTCTGGCATCATCTTC---GCTGG 221
QY 234 GAATGACAACTGCTGGATCTCGCGTGGTCTCTTCTGAGC-----AACACCCAAAC 287
DB 222 ACAGCAAGTGTCTCTGACCCCTCG---GGT-----TGAGCTGGAGAAACGCC---AT 270
QY 288 GC-----AGTACAGCAT-CCAGATCCAGAACGTGGATGTGTATGACAGGG---CCCTTAC 339
DB 271 GCTCTGGAATACAGCTCCGA-ATCCAGAGGTGGATGTCTATGATGAAGGATCC---TAC 327
QY 340 ACTGTCTGGTGGAGACAGACACCA---CCAAAGACCTCT---AGGGTCCACCTCAT 393
DB 328 ACATGCTCAGTTACAGC-AC-AGCATGAGGCC-AAGACCTCTCA--GTTTACTTGATT 381
QY 394 GTGCAAGTATCTCCCAA-AT-TGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGA 451
DB 382 GTACAGT-TCCACCAAGATCTCCA-ACATCTCTCGGATGTCACTGTGAATGAGGGCA 439
QY 452 ACAATATTAGCTTCACTGCAATAGCAACTGTGACAGAGCCCTACCGTT---ACTTGA 508
DB 440 GCAATGTAACCTTGTCTGCATGCGCAATGGCGCCCTGACCT---GTTATCACCTGGA 496
QY 509 GACATCTCTC-CCAAAGCGGTTGG-----CTTTGTGA-GTGAAGACGAATCTGG 559

Db 497 GACAC-CTTACACCA---C---TTGGAAGAGAATT-TGAAGGAGAAGAATAATCTGG 547
QY 560 AAATTGAGGATATCACCCGGGAGCAGTACGGGACTACGAGTGCAGTGCCTTCAATCAGC 619
DB 548 AGATCTTAGCATATCACCCAGGAAACAGTCAAGGCAATATGATGCAAGCTGCGCA---ACG 604
QY 520 TGGCGGCGCCGTTGATACGA-G-----AGTAAAGGTCAACGTTGAACATAT---CCAC 667
DB 605 AGGTCTCTCTCG-----CGATGTCAAAAGTCAAGTCAAGTCACTGTGAATATCCACCCAC 659
QY 668 CAT-ACA---TTTCAGAAAGCCAGGTTACAGGTGTC-CCGTGGGCAAAAGGG---GACA 720
DB 660 CATCACAGAGTCTAAG-AG-CAATG--A-AG-----CCACC-----ACA-----GGACGACA 701
QY 721 ---CTGC-----AGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGGTACAAGGA 773
DB 702 AGCTTCTCTCAAAATGTAAGCTTCCAGCGGTGCTGACCTGACTTTGAGTGGGTACCGGA 761
QY 774 TGACAAAAGACTGATTGAAGGAAAG---AAAGGG--GTGAAAGTGA--A-ACAGA---822
DB 762 TGACACAG---GAT--AA-ACAGTGCMAACGCTTGAGATT--AAGAGCACTGAGGG 812
QY 823 CCTTCTCTCAAAACTCA---T---CTTCTCAATGTCTCT---GAACATGACTATGGA 874
DB 813 CCAGTCTCTC---CTGACCGTGCAC-----CAACGTCACTGAGGAAC---ACTACGGCA 859
QY 875 ACTACACTTGGTGGCTCCCAACAGCTGGGCCACCAATGCCAGCATCATGCTATTG 934
DB 860 ACTATACCTGTGTGGCTGCCCAACAGCTCGCGCTCCACCATGCCAGCTAGTCTCT-TTT- 917
QY 935 GTCCAGGCGCC--GTCAGCGAGGTGAG-----CAACGGCAGCTGAGAGGGGAGGCTG 986
DB 918 ---CAGAC-CGGGCTC-----GGTGAGAGGAATCAACGG-A--TCCA-----TCAGTCTG 960
QY 987 ---CGT-----C---TGCTCTCT---GCCTCTCTGCTGTGCACTGCTTCT---CAAAAT 1031
DB 961 GCGGTACCACTGTGGCTCTGCGCAGCGTC-CCTGTTCT-TGC-----CTTCTCAGCAATG 1013
QY 1032 T 1032
DB -014 T 1014

RESULT 8
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CE1
US-09-976-594-403

Query Match 46.1%; Score 477; DB 4; Length 1195;
Best Local Similarity 61.0%; Pred. No. 4.9;
Matches 706; Conservative 0; Mismatches 171; Indels 281; Gaps 100;
QY 22 ATG-C---ACAAATCTATC---TCTTGGGCAATC---TT---CAGGG---GCTG-G-CT 63

Db	1	ATGTCGGGAGAGTTCAACCGATC---GG-AAACAGTTGCCACTGGTCTCTACAGATT	56
Qy	64	GCTCTGTGTCTCTTT-CCA-AGGAGTGCCTCGCGCAGCGAGATGCCACCTTCCCCAAAG	121
Db	57	GCTCTGTGCT-TCTTCCACACAGGACTGCTCTTCCGACGCTGGAT-----TTTAACCGAGG	110
Qy	122	CTATGGCAACGCTGACGGTCCGGAGGGGAGAGCGCACCCCTCAGGTGC--ACTA-TTG	178
Db	111	C-ACGGACAACATCACCGTGAAGCGAGCGGAGACAGCCATCCTCAGGTGCTTGAAG	169
Qy	179	ACACCGGG--TCACCGGCTGCTGCTGCTAAACCG--CAGCACCATCTCTATGCTGG	233
Db	170	ACAA-----GAACTCA--AAGTGGCCCTGGTTGAACCGTTCTG--GCATCATTTTGTGCG	221
Qy	234	GAATGACAAAGTGTGCTGATCTCGCGTGGTCTCTTCTGAGC-----AACAC-CCAAAC	287
Db	222	ACATGACAAAGTGTCTCTGGACCCACG---GGT-----TGAGCTGGAGAA-ACGCCATTC	272
Qy	288	GC-----AGTACAGAT-CGAGATCCAGAACGTTGGATGTGTATGACGAGG--CCCTTACAC	341
Db	273	TCTGGAATACAGCTCCGGA-ATCCAGAAAGTGGATGCTATGATGAGGGTTCC--TACAC	329
Qy	342	CTGCTCGGTGACAGACAGACCA--CCCAAGACCTCTAGGGTCC-----ACCTCA	391
Db	330	TGCTCAGTTCAGAC--AC-AGCATGAGCCC-AGACCTC-----CCAAAGTTTACTTGA	379
Qy	392	TTGTGCAAGTATCTCCCA--AAATGTAGAGATTCTTTCAGATATCTCC-----AT-----	440
Db	380	TGTTACAAAG-----TCCCAACCA--AGA--TCTCCA-ATATCTCTCGGATGTGAC	425
Qy	441	--T-AATGAAGGACAAATATAGCTCAC-----CTGCATAGCAACTGTTAGACAGA	491
Db	426	TGTGAATGAGGCGACAA-----CGTGACTCTGGTCTGCAITGGCCATGCGGCTCTGA	479
Qy	492	GCCTACGGTT---ACTTGGAGACATCT--CTCCCA-----AAGCGTTGGCTTTTGA-	541
Db	480	ACCT---GTATCACCCTGGAGACAC--CTTACACCAACTGGAAG-----GGAATT-TGAA	528
Qy	542	-GTGAAGACGAATATTGGAATTCAGGGCATCACCGGAGCAGTCAAGGGACTACAG	600
Db	529	GGAGAAGAAGATATCTGAGATCTCTTGGCATCACAGGAGCAGTCAAGGCAAAATATAG	588
Qy	601	TGAGTGCTCCAAAGAGTGCCTGCGCGCGCTGGT---ACGAGAGTAAAGGTCAACCTG	657
Db	589	TGCAAGCTGCCAAGAGTCTCTCGCGGATGTCAAC--A-AGTCAAGTCACTGTG	645
Qy	658	AACTATCC-ACCA-TA-CATTTTCAAGGCCAAGGTTACA--GGTGTCCCGTGGGACAAA	712
Db	646	AACTATCTCTCCACTATCA--CAGATCCAAAG--CAATGAAGCCACC-----ACA--	693
Qy	713	AGGG--GACA--CTGC-----AGTGTGAAGCTCAGCATGCCCTCCAGCAATTCAGT	763
Db	694	--GGACGACAAGCTTCACTCAATGTGAGGCTCGGCAGTCTGCACCTGACTTTGAGT	751
Qy	764	GTACAGAGATGACA-----AAAGACTG--A-----TTGAAGA--AAGA--AAGGG	804
Db	752	GGTACCGGATGACACTAGATTAATAGTGCCAAATGGCCCTTGA--GATTAAGACACGG-	808
Qy	805	GTGAAGTGGAAACACAGACTTCTCTCTCAAAAC--TCATCTTCTTCAATGTCTTGAAC	862
Db	809	-----AG-GG-----CCAGTC--TTCC-CT---GACGGTGA-----C--CAACGTCACTGAGG	847
Qy	863	ATGACTATGGAACTACTTGGTGGCTTCCAAACAGCTGGGCCACACCAATGCCAGCA	922
Db	848	AGCACTACGGCAACTACACTGTGTGGTGGCCAAACAGCTGGGGGTCAACATGCCAGCC	907
Qy	923	TCATGTATTGTGTCCAGGCGCGCTCAGCGAGGTGAG-----CAACGGCAGCTCGAGGA	976
Db	908	TAGTCTTTTCAGACTGG-----GTC-----GGTGAGAGGAATAATGG-A--TCCA---	952
Qy	977	GGGACAGCTG--CGT-----C--TGGGTGCT-----GCCTCTTCTGTGCTTGCACCTGCTTC	1024

Db	953	--TCAGTCTGGCGCTACCACTGTGTGCTGTGGCAGCATC-TCTGTCTC-TGC-----CTTC	1003
Qy	1025	T---CAAAATTT---GA	1035
Db	1004	TCAGCAATGTTAATAGA	1021
RESULT 9			
US-08-414-657D-1			
; Sequence 1, Application US/08414657D			
; Patent No. 5861283			
; GENERAL INFORMATION:			
; APPLICANT: Levitt, Pat			
; APPLICANT: Pimenta, Aurea			
; APPLICANT: Fischer, Itzhak			
; APPLICANT: Zhukareva, Victoria			
; TITLE OF INVENTION: Limbic System-Associated Membrane			
; TITLE OF INVENTION: Protein and DNA			
; NUMBER OF SEQUENCES: 60			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Dechert Price & Rhoads			
; STREET: 997 Lenox Drive, Building 3, Suite 210			
; CITY: Lawrenceville			
; STATE: NJ			
; COUNTRY: USA			
; ZIP: 08543			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq For Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/414,657D			
; FILING DATE: 31-MAR-1995			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER:			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bloom, Allen			
; REGISTRATION NUMBER: 29,135			
; REFERENCE/DOCKET NUMBER: 317743-102			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 609-520-3214			
; TELEFAX: 609-520-3259			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 977 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; FEATURE:			
; NAME/KEY: Coding Sequence			
; LOCATION: 2...976			
; OTHER INFORMATION:			
US-08-414-657D-1			
Query Match			
Best Local Similarity			
Matches			
Score			
DB 2;			
Length			
977;			
Pred. No.			
6.1;			
Mismatches			
0;			
Indels			
248;			
Gaps			
94;			
Qy	22	ATGC-----ACAATT-CTATCTTTGGGCAATCTTTCACGGGCTGGCTCTGTCTCT	76
Db	3	AT-CGGAACACAGTTGC---CACT--GG---TCCT-ACTGAGAT---TGCTCTGCT-TCT	48
Qy	77	T-CCA-AGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAGCTATGACAAAGT	134
Db	49	TCCACAGAGCTGCTGTTTCGAGGTGGAT-----TTTAACCGAGGC-ACGACAACT	102
Qy	135	GACGCTCGGCAAGGGGAGAGCGCCACCTCTCAGGTGC--ACTA-TTGACAAACCGGG--T	188
Db	103	CACCGTGAGGAGGGGACACAGCCATCTCTCAGGTGCTTCTAGAAGACAA-----GAAC	158

189 CACCCGGTGGCTGGCTAAACCG--CAGCAACATCTCTATGCTGGATGACAACTGG 246
159 CA--AAGGTGGCTGGTGAACCGTTCTG--GCATCATTTTGTGTCGACATGACAACTGG 214
247 TGCCTGGATCTCGCGTGGCTCTTCTGAGC-----AACAC--CCAAAC-----GCAGTACAGC 297
215 TCTCTGGACCCAGC--GGT-----TGAGCTGGAGAA--ACGCCATTTCTTGGATACAGC 265
298 AT--CGAGATCCAGAACGTTGGATGTGTATGACAGGG--CCCTTACACCTGCTCGGTGAG 354
266 CTCGGA--ATCCAGAGGTGGATGTCTATGATGAGGGTTCC--TACACTTGTCTCAGTTTCAG 322
355 ACAGACACCA-----CCCAAGACCT--CTAGGTCCACCTCATTTGCAAGTATCTCCC 408
323 AC--AC--AGCATGAGCC--AAAGCCTCCAA--GTTTACTGATCGTACAG--TCCC 372
409 A--AAATTGTAGAGATTTCTTTCAGATATCTCC-----AT-----T--AATGAAGGGAACA 454
373 ACCAA-----AGA--TCTCCA--ATACTCTCTCGATGTCACTGTGAATGAGGCGACGA 422
455 ATATTAGCTC--ACCTGCATAGCAACTGGTAGACAGAGCTACGGTT-----ACTTGAG 509
423 ACGT--GACTCTGGTCTGCAATGCGCAATGCGCTCTGAACT--GTTATCACCTGGAG 477
510 ACACATCT--CTCCCA-----RAGCGTGGCTTTCTGGA--GTGAAGACGAATCTTGGAA 561
478 ACAC--CTTACACCACTGGAG--GGAATT--TGAGGAGAGAGAAATATCTGGAG 529
562 ATTACAGGGCATCACCGGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTTCCCAATGACGTG 621
530 ATCTTGGCATCACAGGGAGCAGTCAAGCAATATGATGCAAAAGCTGCCAACAGGTC 589
622 GCGCGCGCTGGT--ACGGAGAGTAAGTCAAGTCAAGTCACTATCC--ACCA--TA--CAT 675
590 TCCTCGCGGATGTCAAAC--A--AGTCAAGTCACTGTGAATATCTCTCCCACTATCA-- 644
676 TCAGAGCCCAAGGGTACA--GGTGTCCCGTGGGCAAAAGGG--GACA--CTGC----- 724
645 -CAGAAATCCAGAG--CAATGAAGCCACC-----ACA-----GGACGACAGTTTCACTCA 692
725 AGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGAGGATGACA----- 778
693 AATGTGAGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGATGACACTAGGA 752
779 -AAGACTG--A-----TTGAGGA--AAGA--AAGGGTGAAGTGGAAACAGACCT 825
753 TAAATAGTCCCAATGGCCTTGA--GATTGAAGACAGC-----AG--GG-----CCAGTC-- 798
826 TTCCTCTCAAAAC--TCATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTT 883
799 TTCC--CT--GACGGTGA-----C--CAAGCTCACTGAGGAGCACTACGCGCACTACACT 848
884 GCGTGGCCTCCAAAGCTGGGCCACCAATGCCAGCATCATGTATTTGGTCCAGGCG 943
849 GTGTGGCTGCAACAAGCTGGGGGTCAACCAATGCCAGCCTAGTCTCTTTTTCAGACCTGG-- 906
944 CCGTACGAGGTGAG-----CAAGCGACGTGAGGAGGCGAGGCTG--CGT-----C-- 990
907 --GTC-----GGTGAGAGGAATAAATGG--A--TCCA-----TCAGTCTGGCCGTACCACT 951
991 -TGCGTGTCT--GCTCTTCTGTGTCT 1012
952 GTGGCTGTGGCAGCATC--TCTGTCT 977

RESULT 10

US-09-135-080-1

; Sequence 1, Application US/09135080
; Patent No. 6423627
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 2...976
OTHER INFORMATION:
US-09-135-080-1

Query Match 44.8%; Score 463.9; DB 4; Length 977;
Best Local Similarity 61.9%; Pred. No. 6.1;
Matches 685; Conservative 0; Mismatches 174; Indels 248; Gaps 94;
QY 22 ATGC-----ACAAAT--CTATCTCTTGGGCAATCTTCAAGGGCTGGCTGTCTCTCT 76
Db 3 AT--CGAAACAGTTGC-----CACT--GG-----TCCT--ACTGAGAT--TGCTCTGCCT--TCT 48
QY 77 T--CCA--AGGAGTCCGCTGCGCAGCGGAGATGCCACCTTCCCAAGCTATGGAACAACGT 134
Db 49 TCCCAGAGACTGCTCTTGTTCGAGGGTGGAT-----TTTAACCGAGGC--ACGGAACAAT 102
QY 135 GACGGTCCGCGCAGGGGAGGAGCCACCTCAGGTGC--ACTA--TTGACAAACGGG--T 188
Db 103 CACCGTGAGCGAGGGGACACAGCCATCTCAGGTGGGTTCTAGAAGACAA-----GAACT 158
QY 189 CACCGGGTGGCTGGCTAAACCG--CAGCAACATCTCTATGCTGGGATGACAGTGG 246
Db 159 CA--AAGGTGGCTGGTTGAACCGTTCTG--GCATCATTTTGGTGGACATGACAAGTGG 214
QY 247 TGCCTGGATCTCGGTGGTCTCTTGAGC-----AACAC--CCAAAC-----GCAGTACAGC 297
Db 215 TCTCTGGACCCAGC--GGT-----TGAGCTGGAGAA--ACGCCATTTCTTGGATACAGC 265
QY 298 AT--CGAGATCCAGAACGTTGGATGTGTATGACAGGG--CCCTTACACCTGCTCGGTGAG 354
Db 266 CTCGGA--ATCCAGAGGTGGATGTCTATGATGAGGGTTCC--TACACTTGTCTCAGTTTCAG 322
QY 355 ACAGACAAACA-----CCCAAGACCT--CTAGGTCCACCTCATTTGTGCAAGTATCTCCC 408

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323 AC--AC-AGCATGAGCC--AAGACCTCCAA--GTTACTTGATCGTCAAG-----TCCC 372
409 A--AAATTGTAGATTTCTTCAGATATCTCC-----AT-----T-AATGAAGGAACA 454
373 ACCAA-----AGA--TCTCCA-ATATCTCTCGGATGTCACTGTGAATGAGGCGACA 422
455 ATATTAGCTC--ACCTGATAGCACTGGTGTAGACAGAGCCCTACGGTT--ACTTGGAG 509
423 ACCT--GACTCTGGTCTGATGCCAATGCCCTCTCTGAACCT--GTTATCACCTGGAG 477
510 ACACATCT--CTCCCA-----AAGCGTGTGGCTTTGTA--GTGAACGAATACTTTGGA 561
478 ACAT--CTTACACCACTGGAAG-----GGAAT--TGAAGGAGGAAGAAATATCTGGAG 529
562 ATTCAAGGATCATCCCGGAGCAGTCAAGGAGCTACGAGTGCAGTGCCTCCCAATGACGTG 621
530 ATCTTTGGCATCACCGGAGCAGTCAAGGCAATATAGTGCAGAACTGCCAACGAGGTG 589
622 GCGGCGCCGTGGT--ACGGAGGTAAAGGTCACTGTAAGTCACTATCG-ACCA-TA-CATT 675
590 TCCTCGCGGATGTCAAC--A-AGTCAAGGTCACTGTGAACCTATCTCTCCACTATCA-- 644
576 TCAGAGCCAGGCTACA--GGTGTCCCGTGGGACAAAGGG--GACA--CTGC----- 724
645 -CAGATCCAGAG--CAATGAAGCCACC-----ACA-----GGACGACAGCTTCACTCA 692
725 AGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACA----- 778
693 AATGTGAGGCTCGGAGTGCCTGCACTGACTTTGAGTGGTACCGGATGACACTAGGA 752
779 -AAGACTG--A-----TTGAGGA--AAGA--AAGGGTGAAGTGAAGGAAACAGACCT 825
753 TAAATAGTGCATGAGCTTGA--GATTGAAGACACG-----AG-GG--CGAGTC-- 798
826 TTCTCTCAAAAC--TCATCTTTCTCAATGCTCTGAACATGACTATGGGAACCTACACTT 883
799 TTCC-CT--GACGGTGA-----C--CAACGTCACTGAGGAGCACTACGGCACTACACT 848
884 GCGTGGCTCCAAAGCTGGGCGACACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 943
849 GTGTGGCTGCAACAAAGCTGGGGGTCAACAAATGCGAGCTAGTCTTTTCAGACCTGG-- 906
944 CCGTACGCGAGGTGAG-----CAACGCGAGTGGAGGAGGAGGAGGAGGAGGAGGAGG 990
907 --GTC-----GGTGAAGGAAATAATGG-A--TCCA-----TCAGTCTGGCGGACCACT 951
991 -TGGCTGCT--GCTCTTCTGCTCT 1012
952 GTGGCTGTGGCAGCATC-TCTGCTCT 977

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RESULT 11
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5961283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..945
; OTHER INFORMATION:
; US-08-414-657D-8

Query Match 43.8%; Score 453.7; DB 2; Length 945;
Best Local Similarity 62.8%; Pred. No. 9.2;
Matches 664; Conservative 0; Mismatches 166; Indels 227; Gaps 89;

Qy 22 ATG-C--ACAATTTCTATCTTTGGCAATC--TT--CACGG-----GCTG-G-CTGCT 66
Db 1 ATGTCGGGAGAGTTCAACCTGATCGG-AAACAGTTGCCACTGGTCTCTAGACTGTCT 59
Qy 67 CTGTGCTCTT-CCA-AGGAGTCCCGTGGCAGCGAGATGCCACTTCCCAAGCTA 124
Db 60 CTGCTT-TCCTCCACAGACTGCCCTGTCGAGCGTGGAT-----TTTAACCGAGGC-A 112
Qy 125 TGGACAACGTGAGCTCCGCGAGGGGAGCGCCACCTCTAGGTGACTAT--T-----G 178
Db 113 CGCACAAATCACTCCGTGAGGCGAGGCGACACGGCCATCTCTCAGGTG--TGTTGTAAG 169
Qy 179 ACACCGGGTCACTCG--GGTGGCTGGCTTAACCCG--AGCACCATCTCTATGCTGG 233
Db 170 ACAA-----G-ACTCGAAAGTGGCTGGTTGAACCGCTCTGGCATATCTTC--GCTGG 221
Qy 234 GAATGACAAAGTGGTGCCTGGATCTCGCGTGGTCTTCTGAGC-----AACACCCAAAC 287
Db 222 ACAGCAAGTGGTCTCTGACCCCTCG--GGT-----TGAGCTGGAGAAACGCC--AT 270
Qy 288 GC-----AGTACAGCAT-CCAGATCCAGACGTGGATGTGTATGACGAGG--CCCTTAC 339
Db 271 GCTCTGGAATACAGCCCTCCGA-ATCCAGAAAGTGGATGTCTATGATGAAGATCC--TAC 327
Qy 340 ACCTGCTCGGTGACAGACAAACA-----CCCAAGACCTCT--AGGGTCCACCTCATT 393
Db 328 ACATGCTCAGTTTCAAG--AC-AGCATGAGGCC--AAGACCTCTCAA--GTTTACTTGATT 381
Qy 394 GTCAAGTATCTCCCAAA-AT-TGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGA 451
Db 382 GTCAAGT-TCCACCAAGATCTCCA-ACATCTCTCGGATGTCACTGTGAATGAGGCA 439
Qy 452 ACAATATTAGCTCACTGATAGCACTGTGACAGGAGCTTACCGTT--ACTTGA 508
Db 440 GCAATGTAAACCTGCTGTGATGCGCAATGGCGCCCTCGAACCT--GTTATCACCTGGA 496
Qy 509 GACACATCTCTC-CCAAAGCGTTGG-----CTTTGTGA--GTGAAGACGAATACTTGG 559
Db 497 GACAC--CTTACACCA-----TTGGAAGAGAAAT--TGAAGGAGAGAAATATCTGG 547

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Db 8353 GGCCC-TGTT--GGAAGAAATGCTTTTGAATGTTCTTAGACACAAACTTCAGTGAAT 8409
Qy 660 -----CTATCC-----ACCATAC-----ATT-----T-----CAGA--- 680
Db 8410 GAGAAATGGCTCT-TCCATGATGACTGTACAGTGGAAAGATTCTGTGACTCGCCAGATGG 8468
Qy 681 -----AGCCA-----AGG-GTA--CAGGTG--TC-----CC--- 701
Db 8469 TGTATGCTCTGTGGCAGCCTGATGACGAGAGGTGTATGCA-GTGACTCATGACTGA 8527
Qy 702 CG-----TG-----GGA-CA--A--AAG-----G--GGACACTGC--AGTG--TG 730
Db 8528 CGCCCACTGAGAACTGATCATGCACTGATCAAGATCTCTGTGGA--TGCAAAAGTGGCTG 8584
Qy 731 AA-----GCC-----TCA--GCAGT-----C----- 744
Db 8585 AAAAAATGGCCAGAAATCAAAATCACTGTCAGTCTTTCTACTGACTTTGGCGTGAGCTGGA 8644
Qy 745 -----CCCTCAG-----CA-----GAA-----TTC-CA-- 761
Db 8645 GTTATTAGTCCCTCAGTCTTACCCGCCCAAGGTGTTCTGAGAGGTTTCTCAAC 8704
Qy 762 -----GTGGT-----AC--AAGATGACAAAAG-----A-----CTGA--- 787
Db 8705 CGTCTGTGTTCTTCCCACTGAAGGGTG-GAAAAGGATCACCTACCGCTTCTCTGAAGC 8763
Qy 788 TTGAA--GGNA-----AG-----AAAG-----GGG-- 805
Db 8764 TT-AACGGGAATCCTGTAAGATTTAGTTCTACCAAAAGTACTCAGATGTGAGTGGC 8822
Qy 806 ---TGA-AA-----G--TGGAAAAC-----AGA--- 822
Db 8823 AATTGACAAATTTCTACCTTGCCCTGGATGTTTGGACAACTGTGGAGCCACGAGACTG 8882
Qy 823 CCT-----T-TC-----CT-CTCA-----AACT-CACTTT--CTTC 849
Db 8883 CCTAAGGAACAGTGTATCTGTGACCCAGGCTACTCAGGGCCAAACTGCTACTTAAC-TC 8941
Qy 850 A-----ATGCTC--CTGAA-----CA-----TGACT-- 868
Db 8942 ACAGCTGAAGACTTTCTGAGAGGCGCTTTGACAGTGGAGATCAAGCTGACTTAT 9001
Qy 869 --ATG-----GGAA--C--TA-CACT-----TGCTGG-CCT--CC--AAACA-AG 900
Db 9002 GGATGTCCTTGGAAAGCGGAAGCACTTGTACAGAGTGGGGGTCTCGCGGAGAACTG 9061
Qy 901 C-----TGGG-----CCAC-----AC-CAATGCC--AGCATC--- 924
Db 9062 CACTCTATTTTGGGGATCCACTGTGACAAAGCTATTACTCAA-GACTTAG-ATCTCAG 9119
Qy 925 A--TGC--TATT--TG--GTCCAGGCGCGT-----CAGCGAG-----GTGA--- 959
Db 9120 AGGTGCAAAATTCCTGCAGTACTGGGACGTATCGGCACTGAGAACACATGACTCTTG 9179
Qy 960 -CAAGCGACATC-G-AGGAGGCGAGGCTGGTCTGGCTGTG--C-CTCTTC---TGG 1009
Db 9180 CCATCGGCTGTCTGCGGGAAGAG---GGT---GCTGTGACTTCTCTACGGATGG 9233
Qy 1010 ---T--CTTGACC--TGCTTC-----TC---AA---ATTT---TGA 1035
Db 9234 AGGAATCACTTGGACCTTGGTTCACGAGATGGATTTCAGAAATACATTTCTGTGA 9289

RESULT 13

US-08-460-309-3

; Sequence 3, Application US/08460309

; Patent No. 5837496

; GENERAL INFORMATION:

; APPLICANT: Engvall, Eva

; APPLICANT: Leivo, Ilmo

; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

; TITLE OF INVENTION: Fragments and Uses Thereof

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6942 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-460-309-3

Query Match 43.0%; Score 445.5; DB 2; Length 6942;

Best Local Similarity 38.1%; Pred. No. 4.9e+02;

Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

Qy 1 ATGAAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36

Db 2190 ATGG-AAGCAATTCAGCAGCTGTAGAGTGTGTAGTGTGTCAGTGGCCACCAGGTATCTGGCTCC 2248

Qy 37 TCTTGGCAATCTT-----CAC-GG-----GGC-----TGGC-- 62

Db 2249 TCTTGTG-AATCTTGTGGCTAGGCACAGCGAGTTAACGGCACTATTTTGTGGTCAT 2307

Qy 63 -----TGCT-----CTGT-----GTCTCT-----T- 77

Db 2308 CTGTAGCCATGTCAGTCTTGTGTATGCGAGTCTGTGATGACGTCTACTGGAGATG 2367

Qy 78 CC-----AAGGA-----GT-GCCC-----GTG-----C-- 94

Db 2368 CCTGAATGTAAAGATTCACACAGTGGCCCATATTGTGATAAATGCTTCTCTGTTCTA 2427

Qy 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113

Db 2428 TGGCGAGCTTACTAAAGGAACCTCTGAAGACTGTCAACCTCTGCTGCTCAATAT 2487

Qy 114 CC---CCAA-----AGC-----TA-----TGGA--CAAC-GTGA 136

Db 2488 CCCATCAATAACTTTTAGCCCAACGTGCCATTTAGACCGAGTCTTGATGTCTGTGA 2547

Qy 137 -----CGTCCGG--CAGG-----GGGAGA-----GC----- 158

Db 2548 TGGATGCCCTGTGGGTACACAGGACCACGCTGTGAGAGGTGTGACAGGCTATTTGG 2607

RESULT 14
US-08-125-077-3
Sequence 3, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Fragments a
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6942 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-125-077-3

Query Match 43.0%; Score 445.5; DB 2; Length 6942;
Best Local Similarity 38.1%; Pred. No. 4.9e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;
QY 1 ATGAAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
DB 2190 ATGG-AAGCATTCAGCAGCTGTAGAGTGTGTCAGTGCACACGAGGTATACCTGGCTCC 2248
QY 37 TCTTGGGCAATCTT-----CAC-GG-----GGC-----TGGC-- 62
DB 2249 TCTTGTG-AAATCTTGTGGCCTAGGCACAGCGAGTTAACGGCACTATTTTGTGGCAT 2307
QY 63 -----TGCT-----CTGT-----GTCTCT-----T- 77
DB 2308 CTGTGAGCCATGTCTAGTCTTGTGTCATGCGGAGTCTCTGTGTAGCGTCACTGGAGATG 2367
QY 78 CC-----AAGGA-----GT-GCCC-----GTG-----C-- 94
DB 2368 CTTGAATCTAAGGATATACACAGGTGGCCCATATTGTGATAAATGCTCTTCTGGTTTCTA 2427
QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
DB 2428 TGGCGAGCCTACTAAAGAAACCTCTGAAGACTGTCAACCCCTGTGCTCTCCACTCAATAT 2487
QY 114 CC-----CCAA-----AGC-----TA-----TGA--CAAC-GTGA 136
DB 2488 CCCATCCATAACTTTAGCCCAACGTGCCATTTAGACCGGAGTCTTGGATGATCTGTGA 2547
QY 137 -----CGGTCCGG-----CAGG-----GGAGA-----GC----- 158
DB 2548 TGGATGCCCTGTGCGGTATACAGGACCAACGCTGTGAGAGGTGTGAGAAGGCTATTTTGG 2607
QY 159 -C-ACCCTC-----AGG-----TG-----CA--CTAT-----TGACAACCGGG----- 187

DB 2608 ACAACCTCTCTGTACCTGGAGGATCATGTGAGCAATGCAATGCAATGCAATGCAATGCAAT 2667
QY 188 -T-CA-CCC-GG-----GTG--GC-----CTGGC-----TAAAC--G--C 213
DB 2668 CTCCATCTCTGGCAGCTGTGACAGCTTGTCTGGCTCTGTCTGATATGTAACACAGGTAC 2727
QY 214 AGCA--CC--ATC-----CTCTATGCTG--GGA-AT-----GACA-----AG-TGCTGC-- 249
DB 2728 AACAGGCCGGA-CTGTGAGCTCTGTCTGATGATATTTTGGAGATGAGTTGATGGA 2786
QY 250 -----CTG-GATCC-----TGGC-----GTGG--TCCT--TCTGA-----GCAACACCC 283
DB 2787 AGAATCTGTCAGCCCTGTGCTGTAAATGCGGTGGCTCTTCTCTGAGGTGGCCACAGTC 2846
QY 284 AAAC--G-CAGT-----ACAGCATCGAGATCCAGAACGT-----G-GATGTG--TAT 324
DB 2847 AACTGGACAGTGTGAGTGA--GAG--CC--AACGTTCCAGGCTCAGAGATGTGACAAAT 2900
QY 325 GACGA-----GGGCCCT--TACA-----CTTGC----- 345
DB 2901 G-CAAGGCTGGGACCTTTGGCCTACAATCAGCAAGGGGCTGTGTTCCCTGCAACTGCAAT 2959
QY 346 -----TCG--GTGCAGACA--GACAA-----CCACCC-- 368
DB 2960 TCTTTTGGGTCTAAGTCTGACTGTGAGAGGTGACAAATGTTGGTCCCACTGGA 3019
QY 369 -----AAA--GACCTCTAGGTCCAC--CTCATTTGCAAGTATCTCCCAA-- 410
DB 3020 GTCACAGGGAAGAAATGTGACCGCT--GTGCCACGGCT--ATT-T-CAA-----CTTCCAAG 3071
QY 411 AA-----TTCTAGAGAT--TTCT--TCAG-----ATA--TCT--CCATTAT 444
DB 3072 AAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCATCTGGGTAAATGTTGACCCA--AA- 3126
QY 445 GA-AGGCAACAAT--ATTAGCTCTCACTGC-ATAGCAACTGTGAGACCA--G-CCT- 495
DB 3127 GACTGGG--CGATGCA--TGGC--CACC--CAATA-CCAATTGG-AG--AGAAATGTTCTA 3176
QY 496 ACGGT-----TACTTGGAGACATCTCTCCCAAAGG-GGTT-----GGCTTTGTGAG 542
DB 3177 AATGTGCACCAATATACCTGGGCAAGATTAACA-----CTGTTTGAAGGC--TTGTAAC 3232
QY 543 TGAAG-AC-----CAATACTTGG-----AAATTCAGS-----GCA--T 572
DB 3233 TGACGACAGTGGGATCTTGGATTTCCAAATGCAATGTAATACAGCCCAATGCACTGT 3292
QY 573 CACCC-----GG-----GA--GCAGTC-AGG-----GG-ACTA----- 596
DB 3293 CATCCAAATCTCTGTGCAAAATGTACAGAGTGCAGTGCAGTCACTGGAACCTACCT 3352
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QY 622 GCC-----GGCCCGTGT-----AC--GG-AGAGTA-----AAGGTCACTGT-GA 658
DB 3412 GACTAAATAATGCTCTCTGTAGTATCAAACTGGGAGTGCACCTGTGAAGTGAATGGA 3471
QY 659 A--CTATCCAC-----CA-----T--ACATF-----TCAGAACCAAG----- 687
DB 3472 AGGC-ATCCACTGTGACAGATGCGGCTGCGCAAAATTCGGACTC-GATGCCAAGATCCA 3529
QY 688 --GG-TACAG--G--TG--TC-----CCC-GTG-----GGA-CAAAAGG-- 715
DB 3530 CTTGGCTGCAGAGCTCTATTGCTCGGCACACTACTACCCAGTGTCTGAAGCAAAAGGA 3589
QY 716 -----GGACACTGCACTG-----TGAAGCTCAGCAG-----T-CCCC-- 748
DB 3590 CTGATCCGAC-GTG--GGTGA--CTGAGGCTGAGCAGACCAATCTACCCCTGTGATG 3647
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767 ACAAG-----GATCACAAG-----ACT-----GA-- 787
3708 ACATGGACCTGATGAGAGAGATCTCCATTTTGAACCTTTTATTGGAACCTTCCAGAAC 3767
788 ---TTGAGGAGAGAA-----A--GGGG-----TG-AA-- 809
3768 AATTGAGGAGAGAGATGATGGCTATGGGGCAAACTCAAGTATGCAATCTATTTCG 3827
810 AG--T--GGA--AAACAG-----ACCT--T--TCCTC-----TCA-- 835
3828 AGCTCGGAGAGAGAGAGATTTCTTCTACATATAATCTCTCAAGTGATCATTCGAGGTGGG 3887
836 -A--ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
3888 CACCTACTCATGCTAGAAATTCGTCAGGCATATGGCTCTCTCTGATTCGGCCAAATGA 3947
862 C-----ATGAC-----TATGG----- 872
3948 CAAGGCATGAATTTGAATGACAGAGAGAGATGGAATATTTGCGGATGATCCTCGAG 4007
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4008 TCCATAGACTGTGACCGGAGAGACTT-CTTGGATATATATATATATATCAATTACATT 4066
889 ---GC--CT-----C-CAA-----CA-- 898
4067 CTTATCAAGCTACTTATGGAATTTTCATGCGACAAGAGAGATTTCTGAAATCTCAATG 4126
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4127 GAGGTAGCTGAACAAGAGAGCTGGACACAAATGACTCTCTCCAGCTGACTTGTGATGAAAA 4186
922 ---AT-----CAT--GCTATT-TGG-----TCC-----AGGC-----GGCG-----T 947
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948 C-A--GGC-----AGGT-----GAGCAAC-----GGCAC----- 968
4247 CGACTGCGTTCTCAACAGAGTGGCGGACCCCTGGACCAACCCCTGGGACCTGTGTTCCA 4306
969 -GTGAGG--A--GG-----GCAAGCTGCGT-----CTG----- 992
4307 TGTCAATGTAAGGACAGAGAGCTGTGTGACCTGAAACATGATATGCCAGAAATGCT 4366
993 ---GCTG-----CTG-----C-----CTCTT-----CT--G-----GTC 1011
4367 CAACATCACACTGCTGGTACTTCTGTGAACGATGTGCTCTTGGATPACTATGGAATTGTC 4426
1012 ---TTGC-----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
4427 AAGGGATTGCCAATGACTGTGAGCAATGTGCTGCTGCTCTGATTTCTTCCAGTAACAT 4486
1031 TT 1032
4487 TT 4488

RESULT 15
US-09-562-702A-7
; Sequence 7, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIORITY FILING DATE: 2000-04-28
; PRIOR FILING DATE: 1999-09-24
; PRIOR FILING DATE: 1999-07-12
; PRIOR FILING DATE: 1999-07-12
; PRIOR FILING DATE: 1999-07-12

;; PRIOR FILING DATE: 1999-06-15
;; PRIOR APPLICATION NUMBER: 60/131,720
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 9419
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: CDS
;; LOCATION: (1)..(9264)
US-09-562-702A-7

Query Match 43.0%; Score 445.5; DB 4; Length 9419;
Best Local Similarity 38.1%; Pred. No. 8.4e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

QY 1 ATGAAAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
DB 2075 ATGG-AAGCATTCAGCAGCTGTAGAAGTGTGTCAAGTGTCCACCCAGCGGTATCTGGCTCC 2133
QY 37 TCTTGGGGCAATCTT-----CAC-GG-----GGC-----TGGC-- 62
DB 2134 TCTTGTG-AATCTTGTGGCTAGGCAAGCGGAGTTAAAGCGCACTATTTTGGTGGCT 2192
QY 63 -----TGCT-----CTGT-----GTCTCT-----T- 77
DB 2193 CTGTGAGCCATGTCAGTGCCTTGGTTCATGCGGAGTCTCTGTGATGACGTCCTGGGAATG 2252
QY 78 CC-----AAGGA-----GT-GCCC-----GTG-----C-- 94
DB 2253 CCGTGAACCTGTAAAGGATCACACAGGTGGCCCATATTGTGATAAATGTCTTCTGGTCTCTA 2312
QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
DB 2313 TGGCGAGCTTACTAAAGAACTCTGAAGACTGTCAACCCGTGCTGCTGCTCCACTCAATAT 2372
QY 114 CC-----CCAA-----AGC-----TA-----TGGA--CAAC-GTGA 136
DB 2373 CCCATCCAAATAACTTAAAGCCCAACGTCGCAAGAGTCTTGGATTGATCTGTGA 2432
QY 137 -----CGGTCCGG-----CAGG-----GGAGA-----GC----- 158
DB 2433 TGGATGCCCTGTGCGGTATACAGAGACACGCTGTGAGAGGTGTGCAAGAGCTATTTTGG 2492
QY 159 -C-ACCCTC-----AGG-----TG-----CA-----CTAT-----TGACAACCGGG-- 187
DB 2493 ACAACCCCTCTGTACTGAGGATCAATGTCAGCCATGCCCAGCAATGCAATGCAATGCACTT 2552
QY 188 -T-CA-CCC-GG-----GTG-----GC-----CTGGC-----TAAAC--G--C 213
DB 2553 CTCCTATCCCTGGCAGCTGTGACAGCTTGTCTGGCTCTCTGTGATATGTAACACAGGTAC 2612
QY 214 AGCA--CC--ATC-----CTCTATGCTG--GGA-AT-----GACA-----AG-TGGTGC-- 249
DB 2613 AACAGCCCGGTA-CTGTGAGCTCTGTGCTGATGGATATTTTGGAGATGAGTGTGATGGA 2671
QY 250 -----CTG-GATCC-----TGCC-----GTGG-TCCT--TCTGA-----GCCAACCC 283
DB 2672 AGAATCTGTAGCCCTGTCTGTATATGCGGTGGCTCTTCTCTGAGGTTTGCACAGTC 2731
QY 284 AAAC--G-CAGT--A-CAGCATGAGATCCAGAACGT-----G-GATGTG-----TAT 324
DB 2732 AAACCTGGACAGTGTGAGTGA--GAG--CC--AACGTTCAAGGTGAGAGATGCAAAAT 2785
QY 325 GACGA-----GGGCCCT-----TACA-----CCTGC----- 345
DB 2786 G-CAAGGCTGGGACCTTTGGCCCTTACAAATCAGCAAGGGGTGTGTTCTCTGCAACTGCAAT 2844
QY 346 -----TCG-----GTGCAGACA-----GACAA-----CCACCC-- 368
DB 2845 TCTTTTGGGTCTAAGTCAATTCGACTGTGAAGAGAGTGGCAATGTTGGTGGCACTGGA 2904

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QY 411 AA-----TTGTAGAGAT-TTCT--TCAG-----ATA--TCT--CCATTAAT 444
Db 2957 MAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCATCTGGGTAAATATGTGACCCA-AA- 3011
QY 445 GA-AGGAAACAAT--ATTAGCTTCACTGTG-ATAGCAACTGTGTAGACCA--G-CTT- 495
Db 3012 GACTGGG--CGATGCATTTGCC-CACC--CAATA-CCATTTGG-AG--AGAAATGTTCTA 3061
QY 496 ACGGT-----TACTTGAGACACATCTCTCCCAAGC-GGTT-----GGCTTTGTGTAG 542
Db 3062 AATGTGCACCAATATCTGGGGCCACAGCAATTACCA--CTGGTTGTAGGC-TTGTAC 3117
QY 543 TGAAG-AC-----GAATACTTTGG-----AAATTCAGG-----GCA-----T 572
Db 3118 TGCAGCACAGTGGGATCTTTGGATTTTCCAATGCAATGTAATACAGGCCAATGCAACTGT 3177
QY 573 CACCC-----GG-----GA--GCAGTC-AGG-----GG-ACTA----- 596
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QY 622 GCC-----GGCCCGTGGT-----AC--GG-AGAGTA-----AAGTCAACGCT-GA 658
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Db 3357 AGGC-ATCCACTGTGACAGATGCGCGCTGGCAAAATTCGGACTC-GATGCCAAGATCCA 3414
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Db 3415 CTGGCTGAGCAGCTCTATTGCTTGGCAGTACTACCCAGTCTCTGTAAGCAAAAGGA 3474
QY 716 -----GGACACTGCAGTG-----TGAAGCTCAGCAG-----T-CCCT----- 748
Db 3475 CTGATCCGGAC-GTG-GGTGACTCTGAAGGTGAGCAGACCAATCTACCCCTGTAGATG 3532
QY 749 -----CAGCA--GA-----AT-----TCCAG-----TGCT----- 766
Db 3533 AGGCTCTGCAGCACACGACCAACCAAGGCATTTGTTTCAACATCCAGAGATTTGTGCC 3592
QY 767 ACAAG-----GATGACAAAAG-----A--GGGG-----TG-AA----- 809
Db 3593 ACATGGACCTGATGAGAGAAGATCTCCATTTGGAACCTTTTATTTGGAACCTTCCAGAAC 3652
QY 788 ---TTGAAGAAAGAA-----A-----A-----GGGG-----TG-AA----- 809
Db 3653 AATTTGAAGAAAGAAAGTTGTATGCGCTATGCGGGGCAAACTCAAGTATGCAATCTATTTCG 3712
QY 810 AG--T--GGA-AAAAG-----ACCT-T--TCCTC-----TCA-----A 835
Db 3713 AGGCTCGGGAAGAAACAGGTTTCTCATATATATATCTCAAGTATCATTTGAGGTGGGA 3772
QY 836 A--A--ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
Db 3773 CACTCTCATCTAGATAATTTCTGTCAGGCATATGGCTCTCTGATTTGGCCAATGA 3832
QY 862 C-----ATGAC-----TATGG----- 872
Db 3833 CAAGGCATGAATTAATGACAGAGAAGAAATGGAATATATATTTGGGGATGATCTTCGAG 3892
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Db 3893 TCCATAGAACTGTGACCCGAGAGAACTTT-CTTGGATATATATATGATATTCATTACATT 3951
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QY 889 -----GC-CT-----C-CAA-----CA----- 898
Db 3952 CTTATCAAGCTTACTTATGGAATTTTCATGCGACAAAGCAGGATTTCTGAAATCTCAATG 4011
QY 899 -----AGCTG-----GGCC-----ACACCAATG-----CCAGC----- 921
Db 4012 GAGGTAGCTGAACAAGGACGTGGAAACAATGACTCTCTCCAGCTGACTTGTATTTGAAAAA 4071
QY 922 ---AT---CAT--GCTATT-TGG-----TCC-----AGGC-----GCCG-----T 947
Db 4072 TGTGATTTGCCCTGGCTATTTCTGSCCTGCTCTGTGAGCATGCTTGCCTGGGATTTAT 4131
QY 948 C-A--GCG-----AGGT-----GAGCAAC-----GGCAC----- 968
Db 4132 CGACTGCGTTCTCAACAGGTGGCGGCACCCCTGGACCAACCCCTGGGCACCTGTGTGCCA 4191
QY 969 -GTCAGG--A--GG-----GCAGGCTGGT-----CTG----- 992
Db 4192 TGTCAATGTAATGGACACAGCAGCCTGTGTGACCCCTGAAACATCGATATGCCAGAAATGT 4251
QY 993 -----GCTG-----CTG-----C-----CTCTT-----CT--G-----GTC 1011
Db 4252 CAACATCACTGCTGCTGGTGACTTCTGTGAACGATGCTCTTGGATCTATGGAATGTC 4311
QY 1012 -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
Db 4312 AAGGGATTGCCAAATGACTGTGCAAGATGTGCTGCCCTCTGATTTCTTCCAGTAACAAT 4371
QY 1031 TT 1032
Db 4372 TT 4373
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RESULT 16
US-09-562-702A-3
; Sequence 3, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurhenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 9420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(9267)
US-09-562-702A-3

Query Match 43.0%; Score 445.5; DB 4; Length 9420;
Best local Similarity 38.1%; Pred. No. 8.4e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

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QY 1 ATGAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2075 ATGG-AAGCATTCAGCAGCTGTAGAGTGTGTGCTGTCAGTGCACCAAGGATATCTGGCTCC 2133
QY 37 TCTTGGCAATCTTT-----CAC-GG-----GGC-----TGGC-- 62
Db 2134 TCTTGTG-ATCTTGTGGCTTAGGCACAGCGGAGTTAACGGCACTATTTTGTGTGCAT 2192
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QY 63 -----TGCT-----CTGT-----GTCTCT-----T- 77
Db 2193 CTGTGAGCCATGTCTAGTCTCTTTGGTCTATGCGGAGTCTCTGTGATGACGCTCACTGGAGAATG 2252
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Db 2253 CCTGAACTGTAAAGGATCACACAGGTGGGCCATATTGTGATAAATGTCTTCTGTGTTCTA 2312
QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
Db 2313 TGGGAGCCTACTAAAGGAACCTCTGAAGACTGTCAACCCTGTGCTCTCCACTCAATAT 2372
QY 114 CC-----CCAA-----AGC-----TA-----TGGA--CAAC-GTGA 136
Db 2373 CCCATCCAATAACTTTAGCCCAACGTGCCAATTTAGACCGAGTCTTGGATTGATCTGTGA 2432
QY 137 -----CGGTCCGG-----CAGG-----GGGAGA-----GC-----GC----- 158
Db 2433 TGGATGCCCTGTGCGGTATACAGGACCACGCTGTGAGAGGTGTGCAGAGGCTATTTTGG 2492
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Db 2493 ACAACCCCTGTACCTGGAGGATCATGTGAGCATGTCACCAATGCAATGCAACCTTGACTT 2552
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Db 2732 AAACGTGACAGTGTGATGCA--GAG--CC--AACGTTCAAGGTGAGATGTGACAAAT 2785
QY 325 GACGA-----GGGCCCT--TACA-----CCTGC-----CCTGC----- 345
Db 2786 G-CAAGCTGGGACCTTTGGSCCTACATCAGCAAGGGCTGTGTTCCCTGCAACTGCAAT 2844
QY 346 -----TCG-----GTGCAGACA-----GACAA-----CCACCC----- 368
Db 2845 TCTTTTGGGTCTAAGTCAATTCGACTGTGAAGAGAGTGGCAATGTTGGTGCCCAACTGGA 2904
QY 369 -----AAA-----GACCTCTAGGTCCAC--CTCATTTGCAAGTATCTCCCAA- 410
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QY 411 AA-----TTGTAGAGAT--TTCT--TCAG-----ATA--TCT--CCATTAAAT 444
Db 2957 AAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCATCTGGGTAATAATGTGACCCA--AA- 3011
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Db 3062 AATGTGACCCCAATACCTGGGCCACAGATTACCA--CTGGTTGTAAAGC--TTGTAAAC 3117
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Db 3118 TGCAGCAGTGGGATCTTGGATTTCGAATTCGAATGCAATGTAATAACAGGCCAATGCACTGT 3177
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Db 3297 GACTAAATAATGCTCTCTGTAGTATCAAACTGGGACAGTGCATTTGTAAAGGTGAATGTGA 3356
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QY 688 ---GG-TACAG--G--TG--TC-----CCC-GTG-----GGA-CAAAAGG-- 715
Db 3415 CTGCTGTCAGCAGCTGTCTATTGCTTCGGCACTACTACCCAGTGTCTGTAAGCAAAAGGA 3474
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QY 767 ACAAG-----GATGACAAAAG-----ACT-----GA-- 787
Db 3593 ACATGACCTGATGAGAGAGATCTCCATTTTGAACCTTTTATTGGAAACTTCCAGAAC 3652
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Db 3713 AGGCTCGGGAAGAACAGGTTTCTCATATAATCTCAAGTATCATTCGAGGTGGA 3772
QY 836 -A--ACTCAT-CT-----TCATCA-----ATG-----TC-TCTGA-----A 861
Db 3773 CACCTACTCATCTAGAATTTATCGTCAGGCATATGGCTGCTCTCTGATTGGCCAAATGA 3832
QY 862 C-----ATGAC-----TATGG----- 872
Db 3833 CAAGGCATGAATGAATGACAGAGAAAGATGAATATTTATGGGATGATCTCTCGAG 3892
QY 873 -----GAACT--AC-----ACTTCGCTG----- 888
Db 3893 TCATAGAACTGTGACCCGAGAGACTT-CTTGGATATATATATATATATTCATTACATT 3951
QY 889 -----GC-CT-----C-CAA-----CA-----CA----- 898
Db 3952 CTTATCAAAAGTACTTATGGAATTTTCATGCGACAAAGCAGGATTTCTGAAATCTCAATG 4011
QY 899 -----AGCTG-----GGCC--ACACCAATG-----CCAGC----- 921
Db 4012 GAGGTAGCTGAACAGGACGTGGAAACAAATGATCTCTCCAGCTGACTTGTATTGAAAAA 4071
QY 922 ---AT-----CAT--GCTATT--TGG-----TCC-----AGGC-----GCCG-----T 947
Db 4072 TGTGATTGTCCCTGGGCTATTCTGGCCTGTCTGTGAGGCATGCTTGGCGGATTTAT 4131
QY 948 C-A--GCG-----AGGT-----GAGCAAC-----GGCAC----- 968
Db 4132 CGACTCGTTCACACAGGTCGCGGCACCCCTGGACCAACCCCTGGGCACTGTGTGTCCA 4191
QY 969 -GTCCAGG--A--GG-----GCAGGCTGGCT-----CTG----- 992
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Db 4252 CAACATCACACTGCTGTGACTTCTGTGAACGATGTGCTCTTGGATCTATGGAATGTC 4311
QY 1012 ---TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030

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Db 4312 AAGGATTCGCAAAAGACTGTGAGCAATGTGCTGCCCTGATTTCTTCCAGTACAAAT 4371
QY 1031 TT 1032
Db 4372 TT 4373

RESULT 17
US-09-562-702A-5
; Sequence 5, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(9379)
; NAME/KEY: sig_peptide
; LOCATION: (50)..(115)
US-09-562-702A-5

Query Match 43.0%; Score 445.5; DB 4; Length 9534;
Best Local Similarity 38.1%; Pred. No. 8.6e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

QY 1 ATGAAACCAAT-C-CAGC-CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2190 ATGG-AAGCATTGAGCAGCTGTAGAGTGTGAGTGCAGTGCACCCAGGAGTACTGGCTCC 2248
QY 37 TCTTGGGCAATCTT-----CAC-GG-----GGC-----TGCC-- 62
Db 2249 TCTTGTG-AACTTGTGGCCTAGGCACAGCGGAGTTAAACGGCACTATTTTGTGGCAT 2307
QY 63 -----TGCT-----TGCT-----TGCT-----TGCT-----T- 77
Db 2308 CTGTGAGCAATGTGAGTCTTGTGTCATGCGGAGTCTTGTGATGAGTCACCTGGAGATG 2367
QY 78 CC-----AAGGA-----GT-GCCC-----GTG-----C-- 94
Db 2368 CTTGAACTGTAAAGATCACACAGGTGGGCCAATTTGTGATAAATGTCTTCTGCTGTTCTA 2427
QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
Db 2428 TGGCGAGCCTACTAAAGGAACTCTGAAGACTGTCAACCCCTGTGCTGTCTCAATAT 2487
QY 114 CC-----CCAA-----AGC-----TA-----TGGA--CAAC-GTGA 136
Db 2488 CCATCAATACTTTAGCCCAACAGTGCCATTTAGACCGAGTCTTGGATTGATCTGTGA 2547
QY 137 -----CGGTCCGG-----CAGG-----GGGAGA-----GC----- 158
Db 2548 TGGATCCCTGTGCGGTACACAGGACCGCTGTGAGAGGTGTGCAAGAGGCTATTTTGG 2607
QY 159 -C-ACCCTC-----AGG-----TG-----CA-----CTAT-----TGACAACGGG----- 187
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2608 ACAACCCCTCTGTACCTGGAGGATCATGTAGCCATGCCAATGCAATGACAACTTGAACCTT 2667
188 -T-CA-CCC-GG-----GTG-----GC-----CTGGC-----TAAACC--G--C 213
2668 CTCCATCCCTGGCAGCTGTGACAGCTTGTCTGGCTCCTGTCTGTATATTAACCAAGTAC 2727
214 AGCA--CC-----ATC-----CTCTATGCTG--GGA-AT-----GACA-----AG--TGFTGC-- 249
2728 AACAGCCGGTA-CTGTGAGCTCTGTCTGATGGATATTTTGAGATGCAAGTTGATGCGA 2786
250 ----CTG-GATCC-----TGGC-----GTGG--TCCT--TCTGA-----GCAACACC 283
2787 AGAACTGTGAGCCCTGTCTGCTTAATGCGGTGGCTCTTCTCTGAGGTTTGCACAGTC 2846
284 AAAC--G-CAGT-----ACAGCATGAGATCCAGAACGT-----G-GATGTG-----TAT 324
2847 AAACCTGAGAGTGTGAGTGA--GAG--CC--AACGTTCAAGGTCAGAGATGTGACAAAT 2900
325 GACGA-----GGGCCCT-----TACA-----CCTGC----- 345
2901 G-CAAGGCTGGGACCTTTGGCCCTACAATCAGCAAGGGGCTGTGTTCCCTGCAACTGCAAT 2959
346 -----TGG-----GTGCAGACA--GACAA-----CCACCC----- 368
2960 TCTTTTGGGTCTAAGTCATTTGGACTGTGAAGAGAGTGGACAATGTTGGTCCCACTGGA 3019
369 -----AAA-----GACCTCTAGGGTCCAC--CTCATTTGTGAAGTATCTCCAA-- 410
3020 GTCACAGGAGNAGAAATGTGACCGCT-GTGCCCAAGGCT-ATT-T-CAA-----CTTCCAAG 3071
411 AA-----TTGTAGAGAT-TTCT--TCAG-----ATA--TCT--CCATTAAT 444
3072 AAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCTCATCTGGGTAAATTTGTGACCCA-AA- 3126
445 GA-AGGNAACAAT--ATTAGCCTCACTGC-ATAGCAACTGTGTAGACCAGA--G-CCT- 495
3127 GACTGGG--CGATGCTTTGCC--CACC--CAATTA-CAATTTG-AG--AGAAATGTTCTA 3176
496 ACGGT-----TACTTGGAGACACATCTCTCCAAAGC-GGTT-----GGCTTTGTGAG 542
3177 AATGTGACCCCAATACCTGGGCGCCACAGCATTAACA--CTGGTTGTGAAGC--TTGTAAC 3232
543 TGAAG-AC-----GAATTACTTGG-----AAATTCAG-----GCA--T 572
3233 TGCAGCAGCTGGGATCTTTGGATTTCCAAATGCAATGTAATAACAGGCCAATGCAACTGT 3292
573 CACCC-----GG-----GA--GCAGTC-AGG-----GG-ACCTA----- 596
3293 CATCCAAATTCCTGTGTGCAAAATGTACAGAGTGTGAGTGTGAGTCACTGGAACCTACCT 3352
597 CGAGTGCA-----GTG-----CCTC-----CA-ATG-----AC--GTG----- 621
3353 CG-CTGCAATCTCTGTGACTGTCTTCTCTCCCTGGGACACTGACCAACCTGTGATTCAGA 3411
622 GCC-----GGCCCGCTGT-----AC--GG-AGAGTA-----AAGTTCACCTG-GA 658
3412 GACTAAATAATGCTCTCTGTAGTATCAAACTGGGCACTGCACTTGTAAAGTGTATGGA 3471
659 A--CTATCCAC-----CA-----T--ACATTT-----TCAGAAGCCAAAG----- 687
3472 AGGC-ATCCACTGTGACAGATGCCGGCTGGCAAAATTCGGACTC-GATGCCAAGAAATCCA 3529
688 --GG-FACAG-----G-----TG--TC-----CCC-GTG-----GGA-CHAAAGG- 715
3530 CTTGGCTGCAGCAGCTGTCTATTGCTTCGGCACTACTACCCAGTGTCTGGAAGCAAAAGGA 3589
716 -----GGACACTGCAGTG-----TGAAGCCTCAGCAG-----T-CCCCCT----- 748
3590 CTGATCCGGAC-GTG-GGTGACTCTGAAGGCTGAGAGCAACCAATTTCACTCCCTGGTAGTG 3647
749 -----CAGCA--GA-----AT-----TCCAG-----TGCT----- 766
3648 AGGCTCTGCAGCACAGACCAAGGCAATGTTTTCACATCCAGAGATTTGTGCC 3707
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QY 369 -----AAA-----GACCTCTAGGCTCCAC--CTCATGTGCAAGTATCTCCCAA- 410
Db 3020 GTCACAGGGAAGAAATGTGACCGCT-GTGCCCAAGGCT-ATT-T-CAA-----CTTCCAAAG 3071
QY 411 AA-----TTCTAGAGAT-TTCT--TCAG-----ATA--TCT--CCATTAAT 444
Db 3072 AAGAGGCTGCAAGCTTGT-GA-ATGTTCTCACTGGGTAAATTTGACCCA--AA- 3126
QY 445 GA-AGGGAACAAT--ATTAGCTTCACCTGC-ATAGCAACTGGTAGACCAGA---G-CCT- 495
Db 3127 GACTGGG--CGATGCAATTTGCC-CACC--CAATA-CAATTGG-AG--AGMAATGTTCTA 3176
QY 496 ACGGT-----TACTTGAGACACATCTCTCCCAAGC-GGTT-----GGCTTTGTGAG 542
Db 3177 AATGTGACCCCAATACCTGGGGCCACAGCAATTACCA--CTGGTGTGAAGGC-TTGTAAAC 3232
QY 543 TGAAG-AC--GAATACTTTGG-----AAATTCAGG-----GCA-----T 572
Db 3233 TGACGACAGTGGATCTTGGATTTCCAAATGCAATGTAATACAGGCCCAATGCAACTGT 3292
QY 573 CACCC-----GG-----GA-GCAGTC-AGG-----GG-ACCTA----- 596
Db 3293 CATCCAAATCTCTGTGCAAAATGTACAGAGTGCAGTGCAGGTCACTGGAATACCCCT 3352
QY 597 CGAGTGCA-----GTG-----CCTC-----CA-ATG-----AC-GTG----- 621
Db 3353 CG-CTGCAATCTGTGACTGCTTCTCTCCCTGGACAGATGCCACACCTGTGATTCAGA 3411
QY 622 GCC-----GGCCCGCTGGT-----AC--GG-AGAGTA-----AAGGTCAACGT-GA 658
Db 3412 GACTAAAAATGCTCTGTAGTAGTATCAATCAATGGGAGTGCACCTGTAAAGGTGAATGGA 3471
QY 659 A-CTATCCAC-----CA-----T--ACATT-----TCAGAACCAAG----- 687
Db 3472 AGGC-ATCCACTGTGACAGATGCGCGCTGCGCAAAATTCGGACTC-GATGCCAAGAAATCCA 3529
QY 688 --GG-TACAG--G--TG--TC-----CCC-GTG-----GGA-CAAAAGG- 715
Db 3530 CTGGCTGACAGCTGCTATTGTTTGGCACTACTACCCAGTCTCTGAGCAAAAGGA 3589
QY 716 -----GGACACTGCAGTG-----TGAAGCTCAGCAG-----T-CCCT----- 748
Db 3590 CTGATCCGGAC-GTG-GGTGACTCTGAAGGCTGAGCAGACCATCTCTACCCCTGTAGATG 3647
QY 749 -----CAGCA--GA-----AT-----TCCAG-----TGGT----- 766
Db 3648 AGGCTCTGCAGCACACACACCAAGGCAATGTTTTTCAACATCCAGAGATTTGTGCC 3707
QY 767 ACAAG-----GATGACAAAAG-----A--GGGG-----TG-AA----- 809
Db 3768 AATTTGAAGGAAGAAAGTTGATGGCTATGGGGCAAACTCAAGTATGCAATCTATTTCG 3827
QY 810 AG--T--GGA--AAACAG-----ACCT-T--TCCTC-----TCA-----A 835
Db 3828 AGGCTCGGGAAGAAACAGGTTTCTCATATATATCTCAAGTATCTTCGAGGTGGGA 3887
QY 836 -A--ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
Db 3888 CACTACTCTAGTAAATATCTCGTCAGGCATATGCTGCTCTGATTTGGGCAATTTGA 3947
QY 862 C-----ATGAC-----TATGG----- 872
Db 3948 CAAGCATCAAAATGAAATGACAGAGAAGAAATGGAATATATTGGGGATGATCTCTCGAG 4007
QY 873 -----GAACT--AC-----ACTTGGCTG----- 888
Db 4008 TCCATAGAACTGTGACCCGAGAGACTTT-CTTGGATATATATATGATATTCATTAAT 4066

QY 889 -----GC-CT-----C-CAA-----CA----- 898
Db 4067 CTTATCAAGCTACTTATGGAAATTTTCATGCAAAAGCAGGATTTCTGAATCTCAATG 4126
QY 899 -----AGCTG-----GGCC-----ACACCAATG-----CCAGC----- 921
Db 4127 GAGGTAGCTGAACAAGGAGGTGGAACAACAATGACTCTCTCCAGCTGACTTGTGATTAATAA 4186
QY 922 -----AT-----CAT--GCTATT-TGG-----TCC-----AGGC-----GCGC-----T 947
Db 4187 TGTGATGTCCTCGGCTTATTTCTGCTCTCTCTGTGAGGCAATGCTTGGCGGATTTAT 4246
QY 948 C-A--GCG-----AGGT-----GAGCAAC-----GGCAC----- 968
Db 4247 CGACTGGCTTCTCAACAGGTGGCCGACCCCTGGACCAACCCCTGGCACCTGTGTTC 4306
QY 969 -GTGAGG--A-GG-----GCAGGTGGGT-----CTG----- 992
Db 4307 TGTCAATGTAATGACACACAGCAGCCTGTGTGACCCCTGAAACATCGATATGCCAGAAATGT 4366
QY 993 -----GCTG-----CTG-----C-----CTCTT-----CT--G-----GTC 1011
Db 4367 CAACATCACACTGCTGTGACTTCTGTGAACATGTCTTTGGATATGGAATGTCT 4426
QY 1012 -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
Db 4427 AAGGATTCGCAATGACTGTCAGCAATGTGCTGCTGCTCTGATTTCTTCCAGTAACAAT 4486
QY 1031 TT 1032
Db 4487 TT 4488

RESULT 19

US-09-562-702A-1
; Sequence 1, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(9379)
; NAME/KEY: sig_peptide
; LOCATION: (50)..(115)
US-09-562-702A-1

Query Match 43.0%; Score 445.5; DB 4; Length 9535;
Best Local Similarity 38.1%; Pred. No. 8.6e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

QY 1 ATGAAAACCAAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2190 ATGG-AAGCATTCAGCAGCTGTAGAAGTGTGTCAGTCCCAACAGGATATATGCGCTCC 2248
QY 37 TCTTGGGCAATCTT-----CAC-GG-----GGC-----TGCG-- 62

QY 1012 -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
 Db 4427 AAGGATGCGCAATGACTGTGACAAATGTGCTGCTGCTCTGATGATTTCTTCAGTAAAT 4486
 QY 1031 TT 1032
 Db 4487 TT 4488

RESULT 20

US-08-457-273B-41/c
 ; Sequence 41, Application US/08457273B
 ; Patent No. 5849995
 ; GENERAL INFORMATION:
 ; APPLICANT: Hayden, Michael
 ; APPLICANT: Lin, Biaoyang
 ; APPLICANT: Nasir, Jamal
 ; TITLE OF INVENTION: Mouse Model for Huntington's Disease and
 ; TITLE OF INVENTION: Related DNA Sequences
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Virginia Bennett
 ; STREET: PO Box 37428
 ; CITY: Raleigh
 ; STATE: No. 5849995th Carolina
 ; COUNTRY: US
 ; ZIP: 27627
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/457,273B
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bennett, Virginia C.
 ; REGISTRATION NUMBER: 37,092
 ; REFERENCE/DOCKET NUMBER: 3477-85A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-854-1400
 ; TELEFAX: 919-854-1401
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10348 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; US-08-457-273B-41

Query Match 43.0%; Score 444.6; DB 2; Length 10348;
 Best Local Similarity 39.1%; Pred. No. 1e+03;
 Matches 875; Conservative 0; Mismatches 97; Indels 1264; Gaps 247;
 QY 2 TGAAG-----ACCA-----TCAGCGCAA-----AAATGCAC-----AA- 29
 Db 7715 TCAAACTGAGTACGACTGCTCCAGCTAGTGTGTGATGCGGTAGTGAATCTCTTAAG 7656
 QY 30 --TTCTATCTTTGG-GCAATCTTCAGGGG--CT--G--GCTG-----C 65
 Db 7655 ACTTCCTTTTCTCGAGGAA-CTCCACGGGATCTCAGGGAATGCTGTCACCAAAATCCCC 7597
 QY 66 TC-----T--GTGTC--T-----CTTCCA--AGAGTG-----CCCGTG----- 93
 Db 7596 TCCCGTTTGGTGACCACTCCAGCTTCCACACAGTGGGGGACACGTGTGTAGCTGTT 7537
 QY 94 -C-----GCA-GCG-----GA-GATGCCACCTTCCCAAAAGCTATGGACACGTG 135
 Db 7536 GACAAAGGCGCAGCGGGCCAGGCTGATGATG--ATGTT--CTGAGCAATGG-----CGTG 7485

QY 136 ----ACGTCCGCG-----AGG-----G-----GGAGAG 155
 Db 7484 AGAAAG--CCGCGACGCGCTATTCTTTTATGACCCAGGCAACACCGACTGCGAG 7427
 QY 156 -----C-GCCACC--CT--CAGG-TGC-----ACT-----ATT----- 177
 Db 7426 ACTCCACCATTTCTGCGCACCATCTCACAGGCTGCACTGATATACTTAGGATTTCTGTGTG 7367
 QY 178 ---GA-CAA-----CGGGT-CACC-CG--GGTGGC----- 200
 Db 7366 TTGGATCTACTTCTCTCC--TCCTCTCGTGAATGCTTTTGGGTAATTTGCTCTTTT 7310
 QY 201 CTGG-CTA-AA-----CC--GCAGCAC--CA--TCCTCTATGCTGGGAA-TG-AC 240
 Db 7309 CTGGACTAAGAGCTGCTCTCCAGGCTGCACTGCAACGGCTCCAGAT--GAAGTGAC 7252
 QY 241 A-AGT-----GGTGC--C-TGGATC-----CTCGGTGG-----TC-CTTCTGA 274
 Db 7251 ACAGTAGATGAGGAGCAGCGCTGGGTCAAACTC-TGTGGAGGAGACCAACGCTCCAGA 7193
 QY 275 G--CA--A--CA--CCCA--AAC-GCAGTACA-----GCATCGAGATCCAGA--A 311
 Db 7192 GCCAGGAGCTCAGGGCCAGCAGCAGCAGTCCAGCCCTGCTGGAGATCCAGACTCA 7133
 QY 312 -CGTGGATGTG-----T--AT-----GACGAGGGCC-----C--- 335
 Db 7132 GCG-GGATCTGCTCATGGATCAAAATGCCAGGAC-AGGGCTCAAGGTTGCCACCAAGAA 7075
 QY 336 -TT-ACA-----CTGTCTC-----GGTGCA--GAC-----AGAC 360
 Db 7074 TTTCACAATGTCTCTTCTTTCTCAGGAGGAAGTGCAAATGACTGGCAGCTTTGGAGAC 7015
 QY 361 AACCAACCCAAAG--ACCT--CTAGGCTCC-----A--C--CTCAT--TGTG 396
 Db 7014 CACCAC--AGTA-CTGTGCCGCGGCCCGGCCAGAGTGGCGCAGGACTGATACAGTG 6959
 QY 397 CAAGTATCTCCAAATTTGAGAGATTTTCTTCAGATATCTCAATTA----- 442
 Db 6958 C-AGCATC-CCCAA-----ACAGA--TCATTCACTTGTCTCCAGTAGCCGCGGCTCT 6909
 QY 443 --ATGAAG-----GGAACA-AT-AT--TAGC-----CTCAGCTGCA--TAG--- 475
 Db 6908 GCAGGAGCTCGGGCTGGAAGACATGATGACAGCAGGAGGAGCT--GCTGCAGGT-GCCG 6852
 QY 476 --CA-ACTGTAGACCAAG--CCT-ACGG-----TT-----ACT-----TGG-- 507
 Db 6851 CTCACAGGG-----CCAGAGTCACTCAGGGCTGCTTCAAAGAGGCACTCTTCTGGCC 6796
 QY 508 ---AGACA--CATCTC-TCCC-A-----AAGC--GG--T--TGGCT-----TTG---T 539
 Db 6795 ACCAGAAATTTCA-CTCATCCCTAGGCTTAAGCATGAGCTAGCAGGCTTAGGTTGAAT 6737
 QY 540 -GAG-----TGAAGACA--ATA-CTT-----GGAA-----ATTGAGGCA-----T- 572
 Db 6736 CCAGTTTCATGTAAGGCG-ATTCAATATCTTCAGCAGGAATCCGATTC--CCAGCTCTG 6680
 QY 573 CAC---CCGGGAGCAGT-CAG-----GGGACT--ACGAG-TG-- 602
 Db 6679 CACTTCC--AGCAGTGCAGATCTGACCTGTGTCCACACTGGGATTTTCAAGATGAA 6623
 QY 603 ----CAGT---G-CC-----TCCAATG--ACGTGGCGCGCCCGT----- 632
 Db 6622 CGTACCAGTCTTTGTCTCGGACTCACTGTCTTCCAGTGACACGTGCCCATCCCGCTCAGCG 6563
 QY 633 GGT-----AC-----GGAGAG--TAA----- 646
 Db 6562 GGTGGGAAGACTCGGAGGAGAGGAGTGAATGATGCTTGTGAGGAGAGAGAAACC 6503
 QY 647 -----AGG-----TC-----A--CCG-----TGAA----- 659
 Db 6502 TGTCCAGCAGGAATAGAGCTTTGGTGTCTCTGAGGAGCCCGCTGCTCTGAAGTATT 6443
 QY 660 -----CT---A-----TCCA-----CCA-----TACATTT----- 676

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Db 6442 CTGGAATCTGTGAGTTCTTCCATTGGCAACTGGCCATGCTGCTCTGTAAATTTGCAG 6383
QY 677 CAGAAGC-----CAAGGTAC-AGG-TGTC--CC--CGTG--GGACA 710
Db 6382 CCAGAAGCATTTCTTACCGCGACAAAG-----CAAGGATGTCACCATCGAGCCAGCACA 6327
QY 711 ---AAAGGG---ACA-----CTG-----CAGTGTGAAGC---CTC--A--GC- 740
Db 6326 CGGAAGGGGTGCACAGAAAGCCTGTCCACATACAGCGTG-AGCACAGCTCCCGACTGGCT 6268
QY 741 -AG-----TCCCTC--AGCA--GAA-----TTC--CAG--TGCT- 766
Db 6267 GAGATGGATCCCTCCAGCACTGAAGAGTTTCTTCAGCATGTTGGAGTTGAAGGTT 6208
QY 767 ---ACAA-----GGATGA-----CA-----AAA 781
Db 6207 TTCACACAGAGACTGAATTTGCTGGATGAACAGCGCGCTGGCAGCAGAGTTCCCGATGAAC 6148
QY 782 G-ACTGATTGAAG--GAA--A-----GAAAGG-----G--GT 806
Db 6147 GGCACATGA-TGAAGTCTGTACTGGAGGCTCGTGGAAAGGCTGATCAGATCTTGAATGT 6089
QY 807 GA-----AAGTG-----GAAGT-----GA--AA--AC 819
Db 6088 GATTTACAATGAGCCACAGTTAAGTGTCTCGGAGTCTGAGGAGTTCTGACAGACATAATCAC 6029
QY 820 ACA-----CCT-TTC-----CTCT-----832
Db 6028 AGAAGAGAAATGAGAGCCCTCTTCGTACTTATTTGACATTCACAAAGTTGGGTG 5969
QY 833 -CAA--AA-CTCATCTTCTCA--AT-----GT--CT-----CTGAACA 863
Db 5968 CCAAGTCAAGATCTCTCTTCTCCAGACATCTGGGACTAAGTAACCTTTGCTGGACA 5909
QY 864 TCACTAT-----GGG--AACTACACTTGGTGGCTCCA-----895
Db 5908 -GACTGTGTCTTTTCGGGGTCTGCTGCACTT-C-TGCCACACAGCGGTAGTCGGTGTGGT 5852
QY 896 ---ACAAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACAAGCAGCAGTATCTACACACAGCAGCAGCAGCGCGGTGGGTGATCATCG 5792
QY 916 -----GCCAGCA--TCATGCTATTGGTCCAGG-----CGCC--G--TC 948
Db 5791 AACGAGCCCGCAAGTTCAAGCT-----GTCCAGGGGTAGAAACTGCCCGCCAGCCTATC 5737
QY 949 A-GCG-----AG-----GTGAGCA-----A-----CGGCAC-----G--TCGAGCA 976
Db 5736 ACTGCGGAACAGCCTAGTG-GCAGCTGTCTGTGATTTCTCGGAACATTCAGACAGTTGAAGA 5678
QY 977 -G-GG--CAG-----GC-----TGC-----GT--CTGGC-----TGCTGC- 1000
Db 5677 TGTGGATCAGACACATTAGCAGTGTGCTAGTTCTTGGCAATAGAAAGTATGTTGCTGT 5618
QY 1001 --CT-----CTTCTG--GTCTTGACCC--TG-CTTCTCAA-----TT 1031
Db 5617 CACTCATTTCCACCTTCAGCTGTTTGTAAACATGTTCTTAAAGATGTTCTTAAAGATACCAACAGTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAAACCTTTGA 5542
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RESULT 21

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US-08-556-419-13/c
; Sequence 13, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
```

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; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556.419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 10348
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-556-419-13
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Query Match 43.0%; Score 444.6; DB 3; Length 10348;
Best Local Similarity 39.1%; Pred. No. 1e+03; 97; Indels 1264; Gaps 247;
Matches 875; Conservative 0; Mismatches 0;

QY 2 TGAAG-----ACCA-----TCCAGCCAA-----AAATGCAC-----AA- 29
Db 7715 TCNAAGTCAAGTACGACTGCTCCAGCCTAGTGTGTGATGCGGTAGATGAATCTCTTAAAG 7656
QY 30 ---TTCATCTCTTGG-GCAATCTTCCACGGGG--CT---G---GCTG-----C 65
Db 7655 ACTTCCTTTTCTCTGGAGAA-CTCCACGGGATCTCAGGGAATGCTGTGCCAAATCCCC 7597
QY 66 TC-----T--GTGTC--T-----CTTCCA-AGGAGTG-----CCCGTG----- 93
Db 7596 TCCCGGTTGGTGGTACCATCCAAAGCTTCCACACAGTGGGGGCACACGTGTGTAGTGT 7537
QY 94 --C-----GCA-GCG-----GA-GATGCCACTTCCCAAGCTATGTGACAACTG 135
Db 7536 GACRAAGGGCAGCGGGCGGCGAGCTGATGATG--ATGTT--CCTGAGCAATGG-----CGTG 7485
QY 136 ---ACGTTCCGGC-----AGS-----G---GGAGAG 155
Db 7484 AGAAACG--CGGCAACGCGGCTATTTCTTTATGACCAAGGCCAACACCGACTGCAGAG 7427
QY 156 -----C-GCCACC-CT--CAGG-TGC-----ACT-----ATT----- 177
Db 7426 ACTCCACCATTTCTGCCACCATCTCACAGGCTGCAAGTATATCTTAGGATTTCTGTGT 7367
QY 178 ---GA-CAA-----CGGGT-CACC-GG--GGTGGC-----200
Db 7366 TTGGATCTACTTCTCTCC--TCCTCTCTGCTGATGGCTTTTGGGGTATTTGTCTTCTTT 7310
QY 201 CTGG-CTA-AA-----CC--GCAGAC--CA--TCCTCTATGTGGAA-TG-AC 240
Db 7309 CTGGACTAAGAGCTGCTCTCCAGGCTGCACTGCAACGGCTCCAGGAT--GAAGTGAC 7252
QY 241 A-AGT-----GGTGC--C-TGGATC-----CTCGCTGG--TC-CTTCTGA 274
Db 7251 ACAGTAGATGAGGAGCAGCGGTGGGTCAAACTC-TGTGGAGGAGCAGCGCTCCAGA 7193
QY 275 G--CA--A-----CA--CCCA--AAC-GCAGTACA-----GCATCGAGATCCAGA--A 311
Db 7192 GGCAGGAGCAGTGTGAGGGCCAGGCGCAGCAGCAGTCCAGCCCTGCTGGAGATCCAGACTCA 7133
QY 312 -CGTGGATGTG-----T---AT-----GACGAGGGCC-----C--- 335
Db 7132 GCG-GGATCTGCTCATGGATCAATGCCAGGAC-AGGGGCTCAAGGGTTGCCACCCAGAA 7075
QY 336 -TT-ACA-----CCTGCTC-----GGTGC-A--GAC-----AGAC 360
Db 7074 TTTCATATGCTCTTCTTCTTCTCAGGAGGAGGTGCAATGACTGGGCGAGTTTGGAGAC 7015
QY 361 AACCAACCCAAAG--ACCT--CTAGGGTCC-----A-----C-----CTCAT--TGTG 396
Db 7014 CACCACC---AGGTA-CTGTGCCAGGGCCCGGCCAGAGTGGGGCAGGAGCTGATACAGTG 6959
QY 397 CAAGTATCTCCAAATTTGTAGAGATTTTC-TTCAGATATCTCCATTA-----442
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6958 C-AGCATC-CCAA-----ACAGA--TCATTCACTTGTCTCCAGTAGCGCGCGGTCT 6909
443 --ATGAAG-----GGAACA-AT-AT--TAGC-----CTCAGCTGCA--TAG--- 475
6908 GCAGCAGCTCGGCTGGAAGACATGATGGACAGCAGGAGCT--GCTGCAGGT--GCCG 6852
476 --CA-ACCTGTAGACCCAG--CCT-ACGG-----TT-----ACT---TGG-- 507
6851 CTCACCGG-----CCAGAGTCACTCAGCGCTCTCAAAAGGCGACTCTCTCGCC 6796
508 --AGACA--CATCTC--TCCC-A-----AAGC--GG--T--TGGCT-----TTG--T 539
6795 ACCAGAAATTTCA--CTCATCCCTAGGCTTAAGCATGAGCTAGCAGGCTTAGGTTGA 6737
540 --GAG-----TGAGACGA--ATA-CTT-----GGAA--ATTCAGGGCA--T- 572
6736 CCGAGTTTCATGATGAAGGC-ATTCTATCTTCAGCAGGAATCCGATTTCA--CCAGCTGT 6680
573 CAC-----CCGGAGCAGT--CAG-----GGGACT--ACGAG--TG-- 602
6679 CACCTTCC--AGCAGTCAGAACTGACCTGGTCCACACTGGGATTTGACAAAGATGA 6623
603 -----CAGT--G-CC-----TCAATG--ACGTGGCGCGCCCGT----- 632
6622 CGTACCAGTCTTTGTCCGAGTCACTGTTTCCAGTGACACGTGGCCATCCCGGTCCAG 6563
633 GGT-----AC--GGAGAG--TAA-----TG----- 646
6562 GGTGGAGAGACTGGAGAGGAGGACTAAGTGAAGTCTTGTGATGTTGAGAGACGAAC 6503
647 -----AGG-----TC-----A--CCG-----TGAA----- 659
6502 TGTCCAGCAGGGAATAGAGCCTTTGGTCTCTGAGCGAGCGCGTCTGTAAGGTATT 6443
660 -----CT--A-----TCCA-----CCA-----TACATT----- 676
6442 CTGTGATTTCTGTGATTTCTTCCATVGGCACTGGGCCCATGCTGCTGTGTAATTTG 6383
677 --CAGAAGC-----CAAGGGTAC--AGG-TGTC--CC--CGTG--GGACA 710
6382 CCAGAGCATTTCTACCCGGGACAG--CAAGGATGTGCACCATCGAGCCAGCACA 6327
711 --AAAGGG--ACA-----CTG-----CAGTGTGAAGC-----CTC--A--GC- 740
6326 CGGAAGGGGTGCACAGAGGCTGTCCACATACAGCGTG--AGCAGAGCTCCGAGTGC 6268
741 --AG-----TCCCTC--AGCA--GAA-----TTC--CAG--TGCT----- 766
6267 GAGATGGATCCCTCAGACACTGAAGAGTTTCTTCAAGCTGGTTGAGTTGAAGGTT 6208
767 --ACAA-----GGATGA-----CA-----AAA 781
6207 TTCACACGAGACTGAATTCCTGGATGAACAGCGCGCTGGCAGCAGAGTTCGGATGA 6148
782 G--ACTGATTGAG--GAA-----A-----GAAAG--G-----GT 806
6147 GGCAGTGA--TGAAGTCTGTACTGAGGCTCGTGGGAAAGGCTGTACAGATCTTGAAT 6089
807 GA-----AAGTTG-----GA-----AA--AC 819
6088 GATTTCATGAGCCAGCTTAAGTCTCGAGTCAATGGAGTTCTGACAGACATATAC 6029
820 AGA-----CCT-PTC-----CTCT----- 832
6028 AGAAGAAATGAGAGCCCTCTTCGTACTATTCTCTATTGCACTTCCAAAGTTTGGCTG 5969
833 CAA-----AA--CTCATCTTTTCA--AT-----GT--CT-----CTGAACA 863
5968 CCAAGTCAGAAATCCCTCTCTCTCAGACATCTGGGACTAAGTAATCTTGTGCTGGACA 5909
864 TGACTAT-----GGG--AACTACACTTTCGTTGGGCTTCA----- 895
5908 -GACTGTGTCTTTTCGGGGTCTGTGCACTT-C-TGCCACACCGGCTAGTCGGTGTGGT 5852

QY 896 --ACAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACACGACAGATATCTGACACAGAGCAGCAGGCGCGGTGGTGTGATCATGG 5792
QY 916 -----GCCAGCA--TCATGCTATTTTGTCCAG--CGCC--G--TC 948
Db 5791 AACGAGCCGCAAGTTTCAAGCT-----GTCCAGGTTGTAGAACTGCCGCCACAGCCATC 5737
QY 949 A--GCG-----AG-----GTGAGCA-----A-----CGGCAC--G--TCGAGGA 976
Db 5736 ACTGCGGAACAGCCTAGTG--GCAGCTGCTGTGATTTCTCCGGAACATTTCCAGACTTGAAGA 5678
QY 977 -G-GG--CAG-----GC-----TGC--GT--CTGGC-----TGCTGC- 1000
Db 5677 TGTGGATCAGACATAGCAGTGTGCTAGTTCCTGGCAATAGAAAGTATGTTGCTGCT 5618
QY 1001 --CT-----CTTCTG--GTTTGCACC--TG-CTTCTCAAA-----TT 1031
Db 5617 CACTCAFTTCCACCTTCAGCTGTTTGTAAACATGCTTCTTAAAGAAATACCAACCACTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAAACCTTGA 5542

RESULT 22

US-09-041-886-14/c
; Sequence 14, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 316..9748
; US-09-041-886-14
Query Match 43.08; Score 444.6; DB 3; Length 10348;
Best Local Similarity 39.14; Pred. No. 1e+03;


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QY 660 -----CT-----A-----TCCA-----CCA-----TACATTT----- 676
Db 6442 CCTGGATTCTGTTGAGTCTTCCATATGGCAACTGGGCATCTGCTCTGTAAATTTGAG 6383
QY 677 -CAGAAGC-----CAAGGTAC-AGG-TGTC--CC-----CGTG--GGACA 710
Db 6382 CCAGAAGCATTTCTACCGCGGACAAG-----CAAGGATGTGCAACATGCGAGCCAGCACA 6327
QY 711 ---AAAGGG---ACA-----CTG-----CAGTGTGAAGC-----CTC--A--GC- 740
Db 6326 CGAAAGGGGTGCACAGAAGCCTCTCCACATACAGCGTG-AGCACAGCTCCCGACTGGCT 6268
QY 741 -AG-----TCCCTC--AGCA--GAA-----TTC--CAG--TGCT----- 766
Db 6267 GAGATGATCCCTTCCAGCACTGAGAGATTTCTTTCAGCATGTTGGAGTTGAAGGTT 6208
QY 767 ---ACAA-----GGATGA-----CA-----AAA 781
Db 6207 TTCACACGAGACTGAATTGCTGGATGAACAGGCGCTGGCAGCAGAGTTCCGATGAAC 6148
QY 782 G--ACTGATTAAG--GAA--A-----GAAAG--G-----G--GT 806
Db 6147 GGCACATGA-TGAAGTCTGTACTGGAGCTCTGGGAAAGGCTGATCAGATCTTTGAATGT 6089
QY 807 GA-----AAGTG-----AAGTG-----GA--AA--AC 819
Db 6088 GATTACATGAGCCAGCTTAAGTGTCTGGAGTCAATGAGGTTCTGACAGACATATCAC 6029
QY 820 AGA-----CCT-TTC-----CTCT----- 832
Db 6028 AGAAGAGAATGAGAGCCCTCTTCTGATCTATTTCTATTTGACATTCACAGTTTGGCTG 5969
QY 833 -CAA-----AA-CTCATCTTTCA--AT-----GT--CT-----CTGACA 863
Db 5968 CCAAGTCAAGATCTCTCTCTCCAGACATCTGGGAGCTAAGTAATCTTGTGCTGGACA 5909
QY 864 TCACTAT-----GGG--AACTACACTTCCGTGGCTCCA----- 895
Db 5908 -GACTGTCTTTTCGGGGTCTGCTGCACTT-C-TGCCACACCGGTAGTGGTGGT 5852
QY 896 -ACAAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACAAGCAGCAGTATCTGACACACAGCAGCAGCAGCGCGGTGGTGGTGTGATCATGG 5792
QY 916 -----GCCAGCA--TCATGCTATTGTGCCAGG-----CGCC--G--TC 948
Db 5791 AACGAGCCCGCAAGTTCAAGCT-----GTCCAGGTTGTAGAACTGCGCCGACAGCCATC 5737
QY 949 A--GCG-----AG-----GTGAGCA-----A-----CGGCAC-----G--TCGAGGA 976
Db 5736 ACTGCGGAACAGCTAGTG-GCAGCTGTGTGATTTCTCGGAACATTCAGACTTGAAGA 5678
QY 977 -G-GG--CAG-----GC-----TGC--GT--CTGGC-----TGCTGC- 1000
Db 5677 TGTGATCAGACACATTAAGCAGTGTGCTGATTTCTGGAATAGAAAGTATGTTGCTGCT 5618
QY 1001 --CT-----CTTCTG--GTCTTGACCC--TG-CTTCTCABA--TT 1031
Db 5617 CACTCATTTCCACCTTACGCTGTTTGTAACTGCTTCTTAAGAATAACCAACAGTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAACCTTGA 5542
```

RESULT 24

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US-08-453-265-5/c
; Sequence 5, Application US/08453265
; Patent No. 5693757
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Marcy E.
; APPLICANT: Ambrose, Christine M.
; APPLICANT: Duyao, Mabel P.
```

```
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntington DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-08-453-265-5
```

Query Match

Best Local Similarity 43.0%; Score 444.6; DB 1; Length 10366;
Matches 875; Conservative 0; Mismatches 97; Indels 1264; Gaps 247;

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QY 2 TGAAG-----ACCA-----TCCAGCCAA-----AAATGCAC-----AA- 29
Db 7715 TCAAACTGAGTACGACTGCTGCTCCAGCTAGTGTGTGTTGCGGTAGATGAATCTCTTAAAG 7656
QY 30 --TTCTATCTCTCG-CCATCTTCAGGG--CT--G--GCTG-----C 65
Db 7655 ACTTCTCTTTTCTCGAGGAA-CTCCAGGGGATCTCAGGGGATCTGTGCCAAATCCCC 7597
QY 66 TC-----T-GTGTCT--T-----CTTCCA-AGGAGTG-----CCGCTG----- 93
Db 7596 TCCCGGTTTGGGTGACCATCCAGCTTCCACACCGAGTGGGGGCACAGTGTGTAGCTGTT 7537
QY 94 --C-----GCA-GCG-----GA-GATGCCACCTTCCCAAGCTATGGACAAGTG 135
Db 7536 GACAAGGGGCGAGCGCGGCCAGGCTGATGATG--ATGT--CCTGAGCAATGG-----CGTG 7485
QY 136 ----ACGGTCCGCG-----AGG-----G--GGAGAG 155
Db 7484 AGAAACG--CCGGCAGCGCGCTATTCCTTTATGACCCAGGCCAACACACCGACTGCAGAG 7427
QY 156 -----C-GCCACC--CT--CAGG-TGC-----ACT-----ATT----- 177
Db 7426 ACTCCACCATTTCTGCCACCATCTCAGAGGTGCAAGTATATACTTAGGATCTGTGTGT 7367
QY 178 ---GA-CAA-----CCGGGT-CACC-CG--GGTGGC----- 200
Db 7366 TTGGATCTACTTCTCTCC-----TCCTCTCGCTGATGCTTTTGGGTATTTGCTCTCTTT 7310
QY 201 CTGG-CTA-AA-----CC--GCAGCAC--CA--TCCTCTATGCTGGAA-TG-AC 240
Db 7309 CTGGACTAAGAAAGCTGTCTTCCAGGCTGCACTGCAACCGGCTTCCAGGAT--GAAGTGAC 7252
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Qy	241	A-AGT	-----GGTGC---C-TGATNC-----CTGCGTGG-----TC-CTTCTGA	274
Db	7251	ACAGTAGATGAGGAGCAGCGCTGGGTCA	CAAACTC-TGTGGAGGAGACCA	7193
Qy	275	G--CA--A--CA--CCCA--AAC-CGAGTACA--GCATCGAGATCCAGA--A	311	
Db	7192	GGCCAGGCAGCTGCAGGGCCAGGACAGCAGTCCAGCCCTGCTGGAGATCCAGACTCA	7133	
Qy	312	CGTGGATGTG-----T--AT-----GACGAGGGCC-----C--	335	
Db	7132	GCG--GGATCTGCTCATGGATCAAAATGCCAGAC--AGGGCCCTCAAGGTTGCCACCA	7075	
Qy	336	TT--ACA--CCTGCTC-----GCTGCA--GAC-----AGAC	360	
Db	7074	TTTCACAATGTCTTCTTCTTCTCAGAGGAAGTGCATAATGACTGGCGAGTTTGAGAC	7015	
Qy	361	AACCACCCAAAG--ACCT--CTAGGGTCC-----A-----C-----CTCAT--TGTTG	396	
Db	7014	CACCACC--AGGTA--CTGTGCCAGGGCCGGGCGAGAGTGGCGAGGACTGATACAGTG	6959	
Qy	397	CAAGTATCTCCAAAATGTAGAGATTTC--TTCCAGATATCTCCATTA-----	442	
Db	6958	C-AGATC-CCCAA-----ACAGA--TCATTCAACTTGTCTCAGTAGGCGCGCGCTCT	6909	
Qy	443	--ATGAAG-----GGAACA--AT-AT--TAGC-----CTCACCTGCA--TAG--	475	
Db	6908	GCAGCAGCTCGGGCTGGAGACATGATGCACAGCAGGGAGCT--GCTGCACGGT--GCCG	6852	
Qy	476	--CA--ACTGGTAGACACAGAG--CCT--ACGG--TT-----ACT--TGG--	507	
Db	6851	CTCACACGG-----CCAGAGTCACCTCACGGGGTGTCTCAAAAAGGCACTCTCTGGCC	6796	
Qy	508	---AGACA---CATCTC-TCCC-A-----AAGC--GG--T--TGGCT--TTG--T	539	
Db	6795	ACCAGAAATTCA--CTCATCCTAGGCTTAAGCATGGAGCTAGCAGGCTTAGGTTGA	6737	
Qy	540	--GAG-----TGAAGACGA--ATA-CTT-----GGAA--ATTCAAGGCA--T-	572	
Db	6736	CCGAGTTTCATCATGAAGGC-ATTTCATATCTTCAGCAGGAATCCGATTCA--CCAGCTCTG	6680	
Qy	573	CAC--CCGGAGCAGT-CAG-----GGGACT--ACGAG-TG--	602	
Db	6679	CACCTTC--AGCATGTCAATCTGACCTGCTGCTCAACTGGATTTGACAGATGAA	6623	
Qy	603	---CAGT--G-CC-----TCCATG--ACGTGCCCGCCCGT-----	632	
Db	6622	CGTACCAGTCTTTGTCCGGACTCACTGTTTCCAGTGACACGTGCCCATCCCGTCCAGCG	6563	
Qy	633	GGT-----AC--GGAGG--TAA-----	646	
Db	6562	GGTGGGAAGACTTGGAGAGAGGAGCACTAAGTGA	6503	
Qy	647	---AGG-----TC-----A--CCG-----TGAA-----	659	
Db	6502	TGTCCAGCAGGAATAGAGCCTTTGGTGTCTCTGAGCGAGCCGCTGCTCTGAAGGTATT	6443	
Qy	660	-----CT-----A-----TCCA-----CCA-----TACATTT-----	676	
Db	6442	CCTGGATCTGTGAGTCTTCCATTTGGCAACTGGGCCATGCTGCTCTGTAAATTTGCAG	6383	
Qy	677	-CAGAAGC-----CAAGGGTAC-AGG-TGTC--CC-----CGTG--GGACA	710	
Db	6382	CCAGAGCATTTCTACCGGCGACAG-----CAAGGATGTGACCATTCGAGCGCAGACA	6327	
Qy	711	---AAAGGG---ACA-----CTG-----CAGTGTGAAGC-----CTC--A---GC-	740	
Db	6326	CGGAAAGGGGTGCACAGAAGCCTGTCCACATACACGCTG-AGCACAGCTCCCGACTGGCT	6268	
Qy	741	-AG-----TCCCTTC--AGCA--GAA-----TTC--CAG--TGGT-----	766'	
Db	6267	GAGATGGATCCCTCCAGACACTGAAGAGTTTCTTCAGCATGGTTGGAGTGTGAAGGTT	6208	
Qy	767	---ACAA-----GGATGA-----CA-----AAA	781	

[illegible]

RESULT 25

```

RESOL 23
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;
; GENERAL INFORMATION:
;
; APPLICANT: Levitt, Pat
;
; APPLICANT: Pimenta, Aurea
;
; APPLICANT: Fischer, Itzhak
;
; APPLICANT: Zhukareva, Victoria
;
; TITLE OF INVENTION: Limbic System-Associated Membrane
;
; TITLE OF INVENTION: Protein and DNA
;
; NUMBER OF SEQUENCES: 60
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Dechert Price & Rhoads
;
; STREET: 997 Lenox Drive, Building 3, Suite 210
;
; CITY: Lawrenceville
;
; STATE: NJ
;
; COUNTRY: USA
;
; ZIP: 08543
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
;
; OPERATING SYSTEM: DOS
;
; SOFTWARE: Fastseq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/414.657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 base pairs
TYPE: nucleic acid
STRAINEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...924
OTHER INFORMATION:
US-08-414-657D-7

Query Match 42.9%; Score 444.5; DB 2; Length 924;
Best Local Similarity 61.3%; Pred. No. 13;
Matches 656; Conservative 0; Mismatches 166; Indels 249; Gaps 87;

1 AT--GAAACCAATCCAGCCAAATGACAAATCTATCTCTTGGGCAATCTTACCGGGC 58
2 ATCGGAA-----CAG-----TTGC-CA-----CT---GG-----TCCT-ACTGAGA 33
59 TGGCTGCTGTGTCTTTT-CCA-AGGAGTCCCGTGGCGAGCGGAGATGCCACCTTCCC 116
34 T---TGCTCTGCTCT-TCTTCCACAGGACTGCTGCTTCCGACGCTGGAT-----TTTAAAC 84
117 CAAGCTATGACACACGTCGGTCCGCGAGGGGAGAGCCACCTCAGGTGC--ACT 174
85 CGAGGC-ACGGACAACATCACCGTGGGAGGAGGAGACACGACATCTCAGGTGGTTCT 143
175 A-TTGACAAACCGGG---TCAACCGGGTGGCTGCTAAACCG--CAGCACCATCTCTAT 228
144 AGAAGACAA---GAATCA--AAGGTGCGCTGTTGAACCGTTCTG--GCATCATTTT 195
229 GCTGGAAATGACAGTGGTCTGATCTCTGCTGGTCTCTTCTGAGC-----AACAC-C 282
196 GCTGGACATGACAGTGGTCTCTGACCCACG---GGT-----TGAGCTGGAGAA-AGGC 246
283 CAAC----GCAGTACAGCAT--CGACATCCAGAACTGGATGTATGACGAGGG--CCCT 336
247 CATCTCTGGATACAGCTCTCGA-ATCAGAGAGTGGATGTCTATGATGAGGGTTCC-- 303
337 TACACCTGCTCGGTGACAGACACCA-----CCCAAAGACCT--CTAGGGTCCACCTC 390
304 TACACTTGTCTAGTTCAGAC--AC-AGCATGAGCCC-AAGACCTCCCAA--GTTTACTTG 357
391 ATTGTGCAAGTATCTCCCA--AAATGTGAGATTTCTTCAGATATCTCC-----AT---- 440
358 ATCGTACAA-----TCCCAACAA-----AGA--TCTCCA-ATATCTCTCGGATGCA 403
441 ---T-AATGAGGGAACAAATATTTAGCTC--ACCTGCAATAGCACTGGTAGACAGAGCC 494
404 CTGTGATGAGGCGAGCAACGT--GACTCTGTCTGCAATGGCAATGGCCGCTCTGAACC 461
495 TACGGTT---ACTTGGAGACATCTCTC-CCAA-----AGCGTTGGCTTTGTGA--GT 543
462 T---GTTATCACTCGAGACAC--CTTACACCAACTGGGAAG-----GGAAATT-TGAAGA 510
544 GAAGAGCAATATCTGGAATTCAGGGCATCACCGGAGCAGTACAGGAGCTACAGATGC 603
511 GAAGAAGAATATCTGGAGATCTTGGCATCACAGGAGGAGCAGTACAGGCAAAATATGATGC 570

QY 604 AGTGCCTCCATGAGTGGCGCGCCCGTGT---ACGGAGGTAAAGGTCAACGCTGAAC 660
Db 571 AAGCTGCCAACGAGGTCTCTCGCGGATGTCAAAC--A-AGTCAAGGTCACTGTGAAC 627
QY 661 TATCC-ACCA-TA-CATTTCAGAAAGCCAGGATACA--GGTGTCCCGTGGGACAAAAGG 715
Db 528 TATCTCTCCACTATCA---CAGATCCAAGAG--CAATGAAGCCACC-----ACA-----G 673
QY 716 G--GACA--CTGC-----AGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGT 766
Db 674 GACGACAAGCTTCACTCAATGTGAGGCTCGGAGTCCCTGACCTGACTTGTGAGTGT 733
QY 767 ACAGGATGACA-----AAAGACTG--A-----TTGAAGGA--AAGA--AAGGGGTG 807
Db 734 ACCGGATGACACTAGGATAAATAGTCCATGGCCCTTGA--GATTAAGACACGG----- 787
QY 808 AAGTGGAAACACAGACCTTCTCTCAAAAC--TCATCTTTCTCAATGTCTCTGAACATG 865
Db 788 --AG-GG---CCAGTC--TTCC-CT---GACGGTGA---C--CAAGTCACTGAGGAGC 829
QY 866 ACTATGGAACTACACTTGGTGGCTTCCAAAGCTGGGCGCACCAATGCCAGCATCA 925
Db 830 ACTACGGCAACTACACCTGTGTGGCTGCCAACAGCTGGGGGTCCACCAATGCCAGCCTAG 889
QY 926 TGCTATTGTTCCAGGCGCGCTCAGCGAGGTGAGCAACGCGACGCTCGAGGA 976
Db 890 TCCCTTTTTCAGACTGG---GTC-----GGTGA-----GAGGA 918

RESULT 26
US-09-369-364A-1
; Sequence 1, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3002
; TYPE: DNA
; ORGANISM: mus musculus ADAMTS-5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2810)
US-09-369-364A-1

Query Match 42.9%; Score 443.9; DB 4; Length 3002;
Best Local Similarity 37.7%; Pred. No. 1,2e+02;
Matches 889; Conservative 0; Mismatches 103; Indels 1363; Gaps 247;

QY 1 ATG-----AAAACCA-TCCAGC-----CA-AAAATGCAC-AAATTC 32
Db 502 ATGGCGGTACACTCTTAAGCCACTCTCTGGTGGTCTCTGGGAGAGATATGAACAAAT- 560
QY 33 TATCTCTTGGCA---ATCTTTCAG-----GGGCT----- 59
Db 561 TA-----TGGGATGATCTTCCGTCATCTCTGTCATCTCAACCGGAGGCTTTAGCT 615
QY 60 ---GGC-----TG-----CT-CTGTGTC-----TCT-----TCCAG 82
Db 616 TCGAGGCGCTCGGCCACCGCCAGTTCGAGAGACTCTCTGATCCCATCTGGGCCCAA- 674
QY 83 GAGTGGCC---GTGGCGAG-----C--GGAGATGC-CA-C-CT-TCCCCAAAGCT-ATG 126
Db 675 GAGAGCCCTCGGTGACACAGTAGATCTAGGAGAGCGCTCAGCGCTGGCCCCCGAGCTGCTG 734

US-08-179-481-1
; Sequence 1, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARRAWAY, KERMIT L.
; APPLICANT: CAROTHERS CARRAWAY, CORALLIE A.
; APPLICANT: FREGIEN, NEVIS L.
; TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,481
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,521
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-179-481-1

Query Match 42.9%; Score 443.7; DB 1; Length 2603;
Best Local Similarity 42.0%; Pred. No. 50;
Matches 848; Conservative 0; Mismatches 112; Indels 1061; Gaps 231;
Qy 1 ATGA-AAAC-----CATCCAGC-CA-AAAA--TGAC-ATTTCTAT--- 35
Db 290 ATAACCAACGGTGGCCCTTTAAACA-CCAGCGACACTGAAGACTTGCCTGATTTCAATGCC 348
Qy 36 -CT-----CT--TG-----GG-----CAA--TC-----TTACGGGGC--TG 60
Db 349 ACTGGTGCTTACTGATCCAAAATGGCTCCCAAGTCTCAGCCAACTTTGATGGGACAGTG 408
Qy 61 GC--TGCTCTGTG-----TCTCT-----TCCA-----AGGA 84
Db 409 ACCAT-CTCTGTGATGCTCTCTCCAAATCCTTCACGCTCCTCCAGCTGTGAGGA 467
Qy 85 GT---GC--CC-----GTGC-----GCAG-C-GG-----AGATG----- 106
Db 468 GTACCGCAACACACAAAGGGCTTCTGGAGTCTGGAATGACATCCAGAAGATGACTT 527
Qy 107 -----CCACCTTC-CCNA-----AG-----CTA 124
Db 528 CAGATGCCCAATGCTCCACCATCCCTCCAAACGCTCCGAGGAGACTCTTTTCCACTA 587
Qy 125 TG---GACACG-----TGACGG-----TCC--GCGAGG-G-GGAGAGGCCACCC 163
Db 588 TGGATGATCGGAACTAACGGATAGGCTCTCTTGG--GGTAGGACAG-----ACCC 641

Qy 164 TCAGGTGC-----ACT--A-----TTG-----AC-----AAC-----CGGTC 189
Db 542 TC-----TGCTTCTGAGTTTACTCCATCTTCTTGTCCCACTTGGAAACAGACGG--C 696
Qy 190 ACCGGGTG-----G--C-CTGGCT-AAAC-----CGCA-----GCA-----CCATCC 223
Db 697 GCC--GGTGAAGACTTGATCTCTGGGTGCAACGAGGACGACAGTCAAGTTTGCATCC 754
Qy 224 T--CTATGCTGG-----GA-AT--GACAAGTGGTGC-----CTGGATCCT----- 258
Db 755 TGGCCA--CAGGAACAGAGACATCGACAA-----AGCACCAACTCAATCTTTAGACAT 808
Qy 259 --CG--CGTG-----GT-----CCT-T--CT--G-AGCAACA 280
Db 809 TCCGGCAGTGAATGGCAGCTCAACAGTACCACCCCTATCCACTACAGCAGCAAGA 868
Qy 281 CCCAA-----AC-----GC-AGTACAG-----CATGAGAT--CCAG-AACGT--GGATG 319
Db 869 TTCAAGCCTACAGGGCGAGAAACAGTGGCCATTGAGATCACCAGCAAC-TCTAAGGATG 927
Qy 320 T-GTAT--G-----ACGAGGC-----CCTTACACCTGCT-----CGG-----T 350
Db 928 TCGTATTCAGCCTCTCCAAAGTGCAGTGGCCTTTGAGCT-CTTTGAAAACGGGAGTTT 986
Qy 351 GCA-----GACAGACAAACA--CCCA-AAG-----ACC-----TCTA-----GG--GTC 384
Db 987 GCAGCTGGACA-CCAA-CATCCCAGAGAAGACGTACCTGGAGATTCTAGCAAGGGATGTC 1044
Qy 385 CA-CCTCA-TTGTGCA--AGTATCTC--CCAAATTTGTAGA-----GATTTCTTCAAT 432
Db 1045 AAGACTAACTTGT-CATCGGTA-CTCCAGCC-----TG-AGCGGTGGCTTGTCTTC----- 1092
Qy 433 ATCTCCATTAAATGAAGGGAACAATATT-----AGCCTCACTGCATA-----GCAAC 479
Db 1093 -TGT--AGTAAGGA--GGAACAGTGTTTGTACAAGAG-----ACCAGCAAGAGGGCAAC 1143
Qy 480 T-----GGTAGACCAAG-----AG-----CCTACGG-----TT----- 501
Db 1144 TCTTCCACTGAGGT-GACCAAGTGCAGTGGGAGTGCCTTCCGCGCTTGTGTGA 1202
Qy 502 --ACT-----TG-----GAGACA-----CAT----- 515
Db 1203 AACTTAAAGGACCTCTGCACCTGAGCCATGCTTCCCTAATGTGAGCTGCATTCCTGGAA 1262
Qy 516 --CTCTC-----CCAAA--G-C-GG--TTGGC-T--TTGTG-A--GTCAA 546
Db 1263 GGGCTGTGAGCCTGCCCTCAAAACATGACTGGAGATGGCGTCAATGTGTAGCTGTGA 1322
Qy 547 GA---C-GAATACTTG--GAA--ATT-----CAGGGCATCAC-----CC--GG-- 579
Db 1323 GATCTCTGAATTC-TGCCAGAACCATCTCTGTCTGTGTAATTACTGTATAAACCATGCC 1381
Qy 580 -----GAGCA-GTCAGG-----GACTACAG-----TGCA-----G-----TGCTTC 612
Db 1382 ATTGCGA-CATCTCTGGGCTTCCAGACTGCCAGCCCACTTGCACCTCGCCCCCTTC 1440
Qy 613 AATCAGCTGGCGCG-GC--CGTGGTACGAGAGTA-AAGGTCA--CCGTGAACATAT-- 663
Db 1441 ACTG--GTAACCGTGTCTTC-TGG-CCGG-GA--ACAATTTCACTCCCATCATATAA 1493
Qy 664 -----CC-----ACCATACA-----TTTTAG-----AA-GCC---AAG 688
Db 1494 AGAGTTTCCCTTGAGGACCAT-CACGCTCTCTCTCAGGAGGAGCAAAAGCCTCTAACG 1552
Qy 689 GT-ACAGGTGTC--CC-C-GTGGGACAAA-----AG-G-----GGACA----- 720
Db 1553 CTGAC-----GTCAATGCTCGGTGG--CAAAACGTACTAGAGAACTTGACATGCGGGCTT 1606
Qy 721 ----CT-----GC--AGTG-----TGA-----AGCTC-----AG---CAGTC----- 744
Db 1607 TTCTCTCAACAGCTTGTAGTGAAGCTGATACGAACCTTCCCGGAGACCAAGTCTCTGGCA 1666
Qy 745 --CCC--TCAGCA---GAA-----TTCCAGT--GGTACAAGG----- 772

1667 AGCCATTCATCACTGAAGTGGCTCTCCCACTTCAAGTACCGTCCAGGGGACCCCTCA 1726
773 -----A-TG-ACAA--AAGACTGAT-----TGAAGGA----- 795
1727 TCACATATCTGAACACCA--ACTGATAAGCGCGTGGATGGAGGCTTCTCTCTCCAGGC 1784
796 -----AAGAAAGGGGTGA--AGTGAAGA--CAG-----AC-----CT--TTCC--- 829
1785 TCGGAGGAGAGCG--GAAGAGAGTGGAGACCGAGGAGAGACGTCCGCTTCTTCCCA 1843
830 TTTC-A-----AAAC-TCATCTTTCTTCA-----ATGTCTCTGAACATGACTATG--GGA 874
1844 TCTCGAGGGCAGACGTC-----CAGGACGGGATGGCCCTGAACCTTAAGTATGCTGA 1895
875 -----ACTACACTTGG--TGGC-----CT-CCA-----ACA-----AG----- 900
1896 CGAGTACTTCACTGGATGGCTTACAAAGCTACCACTTGGTCTACAGCCGCCAGGATGG 1955
901 -----CT-----GGGC-----CACA-----CCAAATGCCAGCA 922
1956 CGTCACTGTGTCTCCCATGTAGTGGGCTACTGTCAATGGAGGCGCATGCAAGCA 2015
923 TCACTGCTATTGG--TCCAG-----GCG-----CCGTCA-----GCG 952
2016 -CCTGCCAGATGGGCCCCAGTGCACTGGCGCAACCTTCAAGCATCTACACATCTCTGGGGCG 2074
953 A--G--GTGAGC-----AAC-----GGCA--CGTC--GA-----GGAGGCG 980
2075 AACGCTGTGAGCATTAAGCGTGAACCTTGGGCGATCTTTCGGGATCTCTTTGGAGGCC 2134
981 AGGCTG-CGTCTGGCTGCT-GCC-TCTT--C-----TGGTCTTGGAC-----CTGCT 1022
2135 TGGTGCCCTCTTGCTACTGGCACTTAGCATGTGTGTCTTCACTTCTGCGGCTGCT 2194
1023 -----T-----CTCA-AATTTGA 1035
2195 CCATGAACAAGTTCTCTCACTCCCTCTGGACTCGAAGCTGTA 2235

RESULT 28

US-08-179-481-97

Sequence 97, Application US/08179481

Patent No. 5624816

GENERAL INFORMATION:

APPLICANT: CARRAWAY, KERMIT L.

APPLICANT: CAROTHERS CAREWAY, CORALIE A.

APPLICANT: FREGLEN, NEVIS L.

TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/179,481

FILING DATE: 28-DEC-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/922,521

FILING DATE: 30-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 2232 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2232

US-08-179-481-97

Query Match 42.9%; Score 443.5; DB 1; Length 2232;

Best Local Similarity 42.4%; Pred. No. 69;

Matches 845; Conservative 0; Mismatches 113; Indels 1037; Gaps 230;

QY 1 ATGA-AAAC-----CATCCAGC-CA-AAAA-TGCAC-AATTCTAT--- 35
DB 290 ATAACCAACCGTGGCCCTTTAAACA-CCAGCGACACTGAAGACTTGCCTGATTCAATGCC 348
QY 36 -CT-----CT--TG-----GG-----CAA--TC-----TTACGGGGC--TG 60
DB 349 ACTGTGTCTTACTGATCCAAATGGCTCCCAAGTCTCAGCCAATTTGATGGGACAGTG 408
QY 61 GC--TGCTCTGTG-----TCTCT-----TCCA-----AGGA 84
DB 409 ACCAT-CTCTGTGATTGCTCTCTCAACATCCTTCAAGCCTCTCCAGCTGTCAAGGA 467
QY 85 GT--GC--CC-----GTGC-----GCAG-C-GG-----AGATG--- 106
DB 468 GTACCGCAACACACAAAGGGCCCTTCTGGAGTCTTGGAAATGCAATCCAGAAGATGACT 527
QY 107 -----CCACCTTCC--CCAA-----AG-----CTA 124
DB 528 CAGATGCCCATGGCTCCACCTCCCAACAGTCCGAGGAGACTCTTTCCACTA 587
QY 125 TG-----GACAAAG-----TGACGG-----TCC--GGCAGG-G-GGAGAGCGCCACC 163
DB 588 TGGAAATGACATCGGAAACTAAACGGATAGGCTCTCTTGG--GGTGAGGACAG--ACCC 641
QY 164 TCAGGTGC-----ACT--A-----TTG-----AC-----ACG--CGGTC 189
DB 642 TC--TGCCCTTCTGAGTTTACTTCCCATCTTCTTGTGTCACACTGTGGAACAAGAGCGG--C 696
QY 190 ACCCGGGTG-----G-C-CTGGCT-AAAC-----CGCA-----GCATCC 223
DB 697 GCC--GGTGAAGACTTGATCTCTGGGTGCAACGAGGACGACAGTGAAGTTGACATCC 754
QY 224 T--CTATGCTGG-----GA-AT--GACAGTGTGTC-----CTGGATCTCT-- 258
DB 755 TGGCCA--CAGGAACACAGAGACATCGGACAA--AGCACCACCACTCAATCTCTTAGAATC 808
QY 259 --CG--CGTG-----GT-----CCT-T-----CT--G-AGCAACA 280
DB 809 TCCGGCAGTGAATGGCAGCTCAACAGTACCCACCCCTATCCACTACAGCAGCAAGA 868
QY 281 CCCAA-----AC-----GC-AGTACAG-----CATCGAGAT--CCAG-AACGT---GGATG 319
DB 869 TTCAGCCTACAAGGGGCGAGAAACAGTGGCCATTGAGATCACCAGCAAC-TCTAAGGATG 927
QY 320 T-GTAT--G-----ACGAGGC-----CCTTACACTGTCT-----CGG-----T 350
DB 928 TCGTATTCAAGCCTCTCCAAACAAAGTGCAGTGGCCTTTGAGCT-CTTTGAAAAACGGAGTTT 986
QY 351 GCA-----GACAGACAAACA--CCCA-AAG-----ACC-----TCTA-----GG--CTC 384
DB 987 GCAGGTGACA-CCAA-CATCCCCAGAAGAGTACCTGGAGATTTCTAGCAGGAGATGTC 1044
QY 385 CA-CCTCA-TTGTGCA--AGTATCTC-----CCAAAATTGTAGA-----GATTCTTCAGAT 432

Db 1045 AAGACTAACTGT-CATCGGTA-CTCCAGCC-----TG-AGAAGGTGCTTGTCTC----- 1092
QY 433 ATCTCCATTAAAGAGGAGCAATATT-----AGCCTCAGCTGATTA-----GGAAC 479
Db 1093 -TGT-AGTAAGGA--GGAACAGTGTGTGTACACGAG-----ACCAGCAAGAGGGCAAC 1143
QY 480 T-----GGTAGACCAG-----AG-----CCTACGG-----TT----- 501
Db 1144 TCTTCCACTGAGGT-GACCAGCTCAAGTGGGATGGGAATCTCTTCGGCCGCTTGTGTGA 1202
QY 502 --ACT-----TG-----GAGACA-----CAT----- 515
Db 1203 ACACCTTAAGGACCTCTGCACTGAGCCATGCTTCCCTAAATGTGAGCTGCAATCTCTCGGAA 1262
QY 516 ---CTCTC-----CCAAA--G-C-GG---TTGGC-T---TTGTG-A---GTGAA 546
Db 1263 GGGCTGTGAGCCCTGCCCTCAACATGACTGGAGATGGGCGTCATTGTGTAGCTGTGGA 1322
QY 547 GA---C-GAATACTTG--GAA--ATT-----CAGGCACTAC-----CC--GG-- 579
Db 1323 GATCTCTGAATTC-TGCCAGAACCAATCTCTCTCTGTGAATTACTGTATTAACCATGCC 1381
QY 580 ---GAGCA-GTCAGG-----GACTACGAG-----TGCA-----G---TGCTCTC 612
Db 1382 ATTGCGA-CATCTCTGGGCTTCCAGACTGCCAGCCCACTTGCACTGGCCCTGCTTC 1440
QY 613 AATGACGTGCCG-GC--CGGTGTAGGAGGTA--AAGGTCA---CCGTGACTAT-- 663
Db 1441 ACTG--GTAAACCGTGTCTTC-TGG-CCGG-GA--ACAATTTCACTCCCATCTATAA 1493
QY 664 -----CC-----ACCATACA-----TTTCAG-----AA-GCC--AAGG 698
Db 1494 AGAGCTTCCCTTGAGGACCAT-CACGCTCTCTCTCAGGAGGAGGAGAAAGCCTCTACG 1552
QY 689 GT-ACAGGTGC---CC-C-GTGGGCAAA-----AG-G-----GGACA----- 720
Db 1553 CTGAC-----GTCAATGCTCGGTGG--CAAACTGCTAGAGAACTTGCAATCGGGCTT 1606
QY 721 ---CT-----GC--AGTG--TGA-----AGCCTC-----AG--CAGTC----- 744
Db 1607 TTCTCTCCAACTGATGAGCTGATGAGAACTCTCCCGAGGACCACTGCTTGGCA 1666
QY 745 ---CCC--TCAGCA---GAA-----TTCCAGT--GGTACAAGG----- 772
Db 1667 AGCCATTCTACTGGAAGTGTCTCTCCCACTTCAAGTACCGTCCCGAGGGACCCCTCA 1726
QY 773 ---A-----TG-ACAA--AAGACTGAT-----TGAAGGA----- 795
Db 1727 TCCACTATCTGAACAACCA--ACTGATAAGCGCGTGTGAGGCGCTTCTCTCCAGGC 1784
QY 796 ---AAGAAAGGGTGAA---AGTGAATAA--CAG-----AC-----CT--TTCC-- 829
Db 1785 TCGCAGGAGAGGCG-GAAGAGGAGTGGAGAGCCAGAGAAAGCTGCGCTTCTTCCCA 1843
QY 830 TCTC-A---AAAC-TCATCTCTTCA-----ATGCTCTGAACATGACTATG--GGA 874
Db 1844 TCTCGAGGAGAGGCTC-----CAGGACGGGATGCGCTGAACCTAAGTATGCTGGA 1895
QY 875 ---ACTACACTTGG--TGGC-----CT-CCA-----ACA-----AG----- 900
Db 1896 CGAGTACTTCCGTCGATGGCTACAAAGGCTACCACTTGTGTACAGCCCGCCAGGATGG 1955
QY 901 ---CT-----GGGC-----CACA-----CCAATGCCAGCA 922
Db 1956 CGTCACTGTGTGCCCATGTAGTAGGGGTACTGTCAATGGAGGCCAATGCAAGCA 2015
QY 923 TCATGCTATTGG--TCCAG-----GCG---CCGTCA-----GCG 952
Db 2016 -CTGCGAGATGGGCCCGAGTGCAGTGGCGAACTTTCAGCATCTACATCTCTGCGGCG 2074
QY 953 A--G--GTGAGC-----AAC-----GGCA--CGTC--GA-----GGAGGC 980

Db 2075 AACCGTGTGAGCATCTAAGCGTGAACTTGGGCACTTCTTGGGATCCTCTTTGGAGCC 2134
QY 381 AGCGTG-OGTCTGCTGCT-GCC-TCTT--C-----TGCTCTTGCAC-----CTGCT 1022
Db 2135 TGGTGCCCTCTTGTCTACTGCGCATCTTAGCATGTGTGTCTTCTCACTTCTGCGGCTGT 2194
QY 1023 TC-T---CAAATTTT 1033
Db 2195 CCATGAACAAGTTCT 2209

RESULT 29
US-07-596-467-1
; Sequence 1, Application US/07596467
; Patent No. 530862
; GENERAL INFORMATION:
; APPLICANT: Chappell, J.
; APPLICANT: Saunders, Court A.
; APPLICANT: Cuellar, R.
; APPLICANT: Wolf, Fred R.
; TITLE OF INVENTION: Method and Composition for Increasing
; TITLE OF INVENTION: Sterol Accumulation in Higher Plants
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & Milnamow
; STREET: 180 N. Stetson St.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/07596,467
; FILING DATE: 19901012
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 616-5400
; TELEFAX: 312 616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4768 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 164..2827
; US-07-596-467-1

Query Match 42.8%; Score 443.4; DB 1; Length 4768;
Best Local Similarity 38.5%; Pred. No. 2.7e+02;
Matches 888; Conservative 0; Mismatches 107; Indels 1314; Gaps 249;

QY 1 ATGAA-----A---ACCATCC---AGC-----CA--A--AA 21
Db 528 ATGAAGCTTTGGCCCTTTTCTTCTTCTTCTAGACCTTTCTAGAGCGAGTGCCTAGCA 587
QY 22 A---TGCAC-AA-TTCTATCTCT-----T---GGG-CAATCT---TCACGG---GG 57
Db 588 AGTTTCCCTTAAGTTCAAACCTCTCAGGATGAAGTGAAGGAATAATAGCTCGCGAATGG 647
QY 58 ---CTGG-----C---TGCTC-TGTG---TCTCTTCCAA--GGAGT-- 86
Db 648 CAATTCGGGGCCCCCAATTCACCCCTGATGCTCTTGTGGAATGTCTTGAATGGAGTTG 707
QY 87 GC-CC-----GTGCG-CAGC-GGAGAT-----GC--CA-----C 111

Db 1941 TCGGTCTTCTCGTCTGTGATTCTGCAGAGTGAAGCCCTGGCTTGAACACCCGGAAG 2000
QY 655 -----GTGA-----A-----CTATC-----CACATA-C-AATT-----CAGA 680
Db 2001 GGTTCGGGTGATAAAGGAGCGCT-TCGATAGCAC--TAGCAGATTTGCACGCTTACAGA 2057
QY 681 AG-----CCA-----AGG-----GTACA-----GGT-----GTCC----- 700
Db 2058 AGCTTCATGTGACCATGGCAGGGCGCAACCTGTACATCCGTTTCCAGTCCAAGACAGGGG 2117
QY 701 ----CCGTGG-----ACA-A-----AAGGGACACTGCAG-----TGTAAGCCTC 737
Db 2118 ATGCCATGGGATGAACATGATTTCCAAGGG--CACTG-AGAAAGCACTTCTGAAGCTTC 2174
QY 738 AGCAGTCC--CCTCA--GCAGATTC--C--AGTGGT-ACAA--GGA-TGACAA- 779
Db 2175 AGGAGTTCTTCTGAAATGCAG-ATTCTGGCAGTTAGTGGTAACACTGCACTGACAAG 2233
QY 780 AA-----G-----ACT-GATTGA-----AGGAAAGAAAG-----GGGTGA----- 808
Db 2234 AAACCTGCCGCCATAAATCGGATCGAGGGAAGAGGAAAGACAGATTGTGTGAAGCTGTT 2293
QY 809 -----AA-----GTG-----GAA-----AACHAGAC--CTTTC-----CTCTCA----- 834
Db 2294 ATTCCAGCCCAAGGTGCTGAGAGAAGTAATTA-AGACAAC-TACGGAAGCTATGATTGACG 2351
QY 835 -AAAC--T--C--ATC-----TTCTCAATGTCTCTGAACAT--GA--CT----- 868
Db 2352 TAACATTAACAGAATCTTGTGGGTCTGCCATGGCTGGGACATAGGAGGCTACAATG 2411
QY 869 --ATG--GGAA-----CTACACTTGC--GTGGCC----- 891
Db 2412 CCATGCAGCAACATCGTCACCTGCTATCTACA-TTGCATGTGGCCAGGATGCAGCACAG 2470
QY 892 -----TCCBAC-----AAGC---TCGGCCACACCAATG----- 916
Db 2471 AATGTGGGAGTTCAAACTGTATTACTTTAAUGGAAGCAAGTGGTCC-CACGAATGAAGA 2529
QY 917 C-----CA--GCATCATG-----CTAT-----T-----TGGT----- 936
Db 2530 CTTGTATATCAGCTGCACCATGCCATCTATAGATAGGAACTGTGGGTGGTGGGACCAA 2589
QY 937 -----CCA-GGC--GCC-GTC-----A-GCAGGTGAGCAACGGCAAGT-C--GA-- 973
Db 2590 CCTCCTACCACACAGAGCCCTGTCTGCAGATGCTAGGTGTTCAA-GGAGGCTGCAAGACA 2648
QY 974 ----GGAG-----GGCA-GGC-----TGC-----GTCTGG--CT-----GCTG--- 999
Db 2649 ATCCTGGAGAAATGCACGGCAACTGCCGAAATTGTGTGTACTGTAAATGGCTGGGG 2708
QY 1000 -----CCT-----C-TT-----CTTG-----TCTTG-----CACCTGCTTC--- 1024
Db 2709 AGTTGTCTTGTATGGCAGCATTTGGCAGCAGGACATCTTGTAGAGTCAATGGTTCATA 2768
QY 1025 -----TC-----AAATTT-----TG 1034
Db 2769 ACAGATCGAAGATAAATTTACAAAGATCTG 2797

Search completed: May 28, 2004, 21:13:39

Job time : 143.237 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:19:20 ; Search time 2977.63 Seconds
(without alignments)

10379.861 Million cell updates/sec

Title: US-10-017-084a-522_COPY_134_1168

Perfect score: 1035

Sequence: 1 atgaataaccatccagcga...acctgtctcattttga 1035

Scoring table: IDENTITY NUC

Gapop 1.0 , Gapext 0.1

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estl:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estom:*

16: em_estom:*

17: em_estom:*

18: em_estom:*

19: em_estom:*

20: em_estom:*

21: em_estom:*

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24: em_estom:*

25: em_estom:*

26: em_estom:*

27: em_estom:*

28: gb_estl:*

29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.2	84.9	1808	11	AK045973
2	878.2	84.9	1808	11	AK046377
3	866.4	83.7	874	29	AY406347
4	802.5	77.5	1039	10	BE798585

5	757.6	73.2	773	29	AY406348
6	756.8	73.1	856	13	BUI55617
7	724	70.0	874	29	AY406349
8	679	65.6	1085	9	AL533026
9	650.8	62.9	765	14	CD354474
10	639.2	61.8	979	12	BG261691
11	636	61.4	865	12	BI666583
12	585	56.5	3166	11	AK042854
13	580	56.0	759	14	CF737474
14	560.4	54.1	784	12	BI549918
15	541.3	52.3	545	10	BE263639
16	540.8	52.3	732	12	BI551784
17	535.1	51.7	2798	11	AK028345
18	514.6	49.7	580	12	BI548566
19	513.2	49.6	953	12	BM423716
20	503.7	48.7	661	12	BM009450
21	501.7	48.5	1033	12	BM807426
22	500.1	48.3	1083	12	BM809227
23	499.6	48.3	849	12	BI755360
24	497.3	48.0	890	14	CD327172
25	494.1	47.7	1138	12	BM556708
26	485.5	46.9	2768	11	AK030681
27	481.3	46.5	840	13	BUI320256
28	479.8	46.4	1017	29	AY406973
29	476.8	46.1	740	13	BUI368328
30	476.5	46.0	896	13	BQ890272
31	476.4	46.0	1017	29	AY406971
32	475.6	46.0	663	12	BM724307
33	474.7	45.9	2467	11	AK044845
34	473.6	45.8	1015	29	AY406972
35	472.9	45.7	768	9	AU080629
36	467.3	45.1	601	14	CS582386
37	466.7	45.1	1304	12	BM911516
38	460.1	44.5	1953	11	AK030503
39	458.1	44.3	2096	11	AK035218
40	457.4	44.2	524	10	BE014142
41	454	43.9	553	10	BE864555
42	454	43.9	806	9	AU051132
43	445.8	43.1	14278	11	AY318958
44	445.8	43.1	14278	11	AY321317
45	445.6	43.1	5118	11	AK036018
46	445.3	43.0	2650	11	AK044093
47	444.7	43.0	4483	11	AK031352
48	444.5	42.9	3602	11	AK080960
49	444.2	42.9	3590	11	AK036419
50	443.8	42.9	3447	11	BC034177
51	443.8	42.9	3657	11	AK088000
52	443.7	42.9	3678	11	BC023964
53	443.4	42.8	3626	11	BC051109
54	443.2	42.8	4035	11	AK044634
55	443.1	42.8	2650	11	AK044093
56	443.1	42.8	6081	29	AY414808
57	443	42.8	633	12	BG706987
58	442.8	42.8	2892	29	AY412595
59	442.8	42.8	4362	11	AK083908
60	442.7	42.8	4346	11	AK046357
61	442.6	42.8	4014	11	AK049365
62	442.5	42.8	2866	11	AK033729
63	442.5	42.8	3167	29	AY413771
64	442.5	42.8	3525	11	BC015070
65	442.5	42.8	4463	11	AK083374
66	442.5	42.8	7886	11	BC034956
67	442.4	42.7	3473	11	AK051488
68	442.4	42.7	3991	11	AK047198
69	442.3	42.7	3364	11	AK036850
70	442.3	42.7	3971	11	AK054393
71	442.2	42.7	3670	11	AK052437
72	442.2	42.7	4379	11	AK086942
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74	442.1	42.7	4035	11	AK044634
75	442	42.7	2677	11	AK082264
76	442	42.7	2952	11	AK053804
77	441.9	42.7	2963	11	AK082337

REFERENCE	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source

Location/Qualifiers

1..1808

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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/db_xref="MGI:2411779"

/db_xref="taxon:10090"

/clone="B230377K17"

/sex="male"

/issue_type="corpora quadrigemina"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

204..1238

/note="unnamed protein product; NEUROTRIMIN PRECURSOR

(GP65) homolog [Rattus norvegicus] (SWISSPROT Q62718,

evidence: FASTY, 99.4%ID, 92.1%length, match=951)

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VNVPPVISEAKTGVPGVQKGTLOCEASAPSAEFQWPKDKRLVGGKGVKVENRPF
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LIVLHLLALF"

ORIGIN

Query Match 84.9%; Score 878.2; DB 11; Length 1808;
Best Local Similarity 90.5%; Pred. No. 3.5e-10;
Matches 937; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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DB 204 ATGAAACCATCCAGCAAAATGCAATATCTCTTGGGCAATCTTCACGGGGCTG 263
QY 61 GTCGCTCTGTCTCTTCAAGAGTCCCGTGGCAGCGAGAGTCCACCTTCCCAA 120
DB 264 GCGCTCTGTGCTCTTCAAGAGTCCCGTGGCAGCGAGAGTCCACCTTCCCAA 323
QY 121 GCTATGGACAACGTCAGTCCCGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 324 GCTATGGACAACGTCAGTCCCGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 383
QY 181 AACCGGTCACCGGGTGGCTGCTTAACCGGAGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 384 AACCGGAGTCACCGGGTGGCTGCTTAACCGGAGCAGCACCATCTCTATGCTGGGAATGAC 443
QY 241 AAGTGTGCTGTGATCCTCGGTGGTCTCTTGAACAACACCAACGAGTACAGCATC 300
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QY 301 GAGATCCAGAACGTCGATGTATGACGAGGCGCTTACACCTGCTCGGTGCGAGACAGAC 360
DB 504 GAGATCCAGAACGTCGATGTATGACGAGGCGCTTATACCTGCTCGGTGCGAGACAGAC 563
QY 361 AACCAACCAAGACCTCTAGGTCCACCTCATGTGCAAGTATCTCCCAAAATTTAGAG 420
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QY 421 ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGATAGCACT 480
DB 624 ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGATAGCACT 683
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DB 684 GGTAGACAGACGCTACGTTATCTTGAGAGACACATCTCTCTCCCAAGCGCGTGTGGCTTTGTG 743

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QY 601 TGCAGTGCCTCAATGACGTGCGCCCGCGCTGTTACGAGAGTAAAGGTCAACCGTGAAC 660
DB 804 TGCAGGCGCTCCACGACGTCGCGGCACAGTGGTACGAGAGTGAAGGTCAACCGTGAAC 863
QY 661 TATCCACCATACATTTCAAGAGCCAGGTCAGGTGTCCTCGGTGGGCAAAAGGGGACA 720
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QY 721 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTACAAGGATCACAAA 780
DB 924 CTGCAAGTGTGAAGCTTCGCGAGTCCCTTCAGCAGAAATTTCAATGTTCAAGGATGACAAA 983
QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGGAAACAGACCTTCTCTCAAAATCTC 840
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DB 1044 ACCTTTTCAACGTCCTGAACTGACTATGGAACTACACTGTTGGCTTCCCAACAG 1103
QY 901 CTGGGCCACACCAATGCGCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGGAGGTGAGC 960
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QY 961 AACGCGACGTGAGAGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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QY 1021 CTCTCAAAATTTGA 1035
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RESULT 3
AY406347
LOCUS

DEFINITION

Homo sapiens HCM2527 gene, VIRUAL TRANSCRIPT, partial sequence.

AY406347
AY406347.1 GI:39762321

ACCESSION

AY406347

VERSION

AY406347.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

JOURNAL

PUBMED

14671302

REFERENCE

2 (bases 1 to 874)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submision

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..874

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"


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QY 499 GTTACTTGAGACACATCTCTCCAAAGGGTGGCTTTGTCAGTGAAGACGAATACCTG 558
Db 399 GTTACTTGAGACACATCTCTCCAAAGGGTGGCTTTGTCAGTGAAGACGAATACCTG 458
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QY 739 GCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAAGAGTGAATTAAGGAA-A 797
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QY 798 GAAAGGGGTGA-AG-TGGAAACAGAC--TTTCCT-CTCAAACTCAT--CTTC-TTC 849
Db 698 GAAAGGGGTGA-AG-TGGAAACAGAC--TTTCCT-CTCAAACTCAT--CTTC-TTC 758
QY 850 AATGT-CTCTGAA-CAT-GACTAT--GGGAACATACACTTGGCGGCTCCCAACAGCTGG 905
Db 759 AATGTCTCTGANCCATGGACTTGGGAACTACACTTTGGC--GGGCTCCCAAAAGCTGG 817
QY 906 CACACCAATGCCAGATCATGCTAT-----TGGGT-C 937
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QY 960 CAACG-----GCA-----GTCGAG--GAGGCGAGGCT-----GCGTCTGGCTGCTCCTCT 1004
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QY 1005 TCTGTCTTGACCTGCTCTTCAAAATTTTG 1034
Db 987 TCTGG---TGC-CCGG-----TCAATTGTTG 1008

RESULT 5
LOCUS AY406348
DEFINITION Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY406348
VERSION AY406348.1 GI:39762322
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 773)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 773)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
```

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Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..773
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM2527"
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Best Local Similarity 98.4%; Pred. No. 2.6e-08;
Matches 761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;
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QY 228 TGCTGGGAATGACAAGTGGTGCCTGGATCTCTGGGTGGTCTCTTGAGCAACACCCAAAC 287
Db 61 TGCTGGGAATGACAAGTGGTGCCTGGATCTCTGGGTGGTCTCTTGAGCAACACCCAAAC 120
QY 288 GCAGTACAGCATTCAGATCCAGAACGTGGATGTGTATGACAGAGGCGCTTACCTGCTC 347
Db 121 GCAGTACAGCATTCAGATCCAGAACGTGGATGTGTATGACAGAGGCGCTTACCTGCTC 180
QY 348 GGTGCAGACAGACAAACCAACCAAGAGCTCTAGGGTCCACCTATTGCGAAGTATCTCC 407
Db 181 GGTGCAGACAGACAAACCAACCAAGAGCTCTAGGGTCCACCTATTGCGAAGTATCTCC 240
QY 408 CAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 467
Db 241 CAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 300
QY 468 CTGCATAGCACTGTTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAA--- 524
Db 301 CTGCATAGCACTGTTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAA--- 360
QY 525 ---AGCGGTTGGCTTTCTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGA 581
Db 361 CGCAGCGTTGGCTTTCTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGA 420
QY 582 GCAGTACGGGACATACAGTGCAGTGCCTCCAAATGACGTGGCGCGCCGCTGGTACGGAG 641
Db 421 GCAGTACGGGACATACAGTGCAGTGCCTCCAAATGACGTGGCGCGCCGCTGGTACGGAG 480
QY 642 AGTAAAGTCCACCGTGAACCTATCCACCATACATTTACAGAGCCAGGGTACAGTGTCCC 701
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QY 702 CGTGGGCAAAAAGGGGACACTGCGAGTGTGAAGCCTCAGCAGTCCCTTCAGCAAGATTTCCA 761
Db 541 CGTGGGCAAAAAGGGGACACTGCGAGTGTGAAGCCTCAGCAGTCCCTTCAGCAAGATTTCCA 600
QY 762 GTGGTACAGGATGACAAAGACATGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAG 821
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RESULT 6
BUI55617      856 bp      mRNA      linear      EST 03-SEP-2002
LOCUS          AGENCOURT 7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:616839
DEFINITION    5', mRNA sequence.

ACCESSION     BUI55617
VERSION       BUI55617.1 GI:22669149
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     NIH-MGC http://mgi.nci.nih.gov/.
              1 (bases 1 to 856)
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: ATCC/DCTD/DTP
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L14M13527 row: m column: 16
              High quality sequence stop: 593.
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              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_72"
              /note="Organ: Skin; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally. Primer: Oligo dh.
              Average insert size 2 kb. Library constructed by Life
              Technologies."
ORIGIN
Query Match      73.1%; Score 756.8; DB 13; Length 856;
Best Local Similarity 91.2%; Pred. No. 4.1e-08;
Matches 794; Conservative 0; Mismatches 13; Indels 64; Gaps 23;

QY      3 GA-AA-----ACC--ATCCAGCC--AAAATGCACAACTTATCTCTGG 42
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      10 GAGATGGGGGTTCTGGGTACTCTGTCCTGCTGAGAGTGC-----CTCGTG 59
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      43 ----GCAATCT-TCACGGGGCTGGCTCTGTGTCTCTT-----CCA-AGGAGTGCCCGT 92
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      60 TCGTG---TCTCTCA-----GGCTG--CTGT-TC-CTTGATCCACAGGAGTGCCCGT 105
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      93 GCGCAGGGAGATGCCACCTTCCCAAGCTATGGACAAGTGCAGCGTCGGCAGGGGA 152
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      106 GCGCAGGGAGATGCCACCTTCCCAAGCTATGGACAAGTGCAGCGTCGGCAGGGGA 165
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      153 GAGCGCCACCTCAGGTGCATTTACCAACCGGTCACCCGGTGGCTGGCTTAACCG 212
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      166 GAGCGCCACCTCAGGTGCATTTACCAACCGGTCACCCGGTGGCTGGCTTAACCG 225
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      213 CAGCAATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGGTGCTCTTCT 272
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      226 CAGCAATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGGTGCTCTTCT 285
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      273 GAGCAACCCCAACCGATGACGATCGAGATCCAGACGTGGATGTGTATGACGAGGG 332
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      286 GAGCAACCCCAACCGATGACGATCGAGATCCAGACGTGGATGTGTATGACGAGGG 345
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      333 CCCTTACCTGCTCGGTGCAGACACCAACCCAGACCTCTAGGCTCCACTCAT 392
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db      346 CCCTTACACCTGCTCGGTGCAGACACCAACCCAAAGACCTCTAGGGTCCACCTCAT 405
QY      393 TGTGCAAGTATCTCCCAAAATTTCTAGAGATTCTTCTAGATATCTCCATTAATGAGGGAA 452
Db      406 TGTGCAAGTATCTCCCAAAATTTCTAGAGATTCTTCTAGATATCTCCATTAATGAGGGAA 465
QY      453 CAATATTAGCCTCACCTGCATGCAAACTGGTAGACACGACCTACGTTACTTTGGAGACA 512
Db      466 CAATATTAGCCTCACCTGCATGCAAACTGGTAGACACGACCTACGTTACTTTGGAGACA 525
QY      513 CATCTCTCCAAAGCGTTGGCTTTGTAGTGAAGACGAATATCTTGGAAATTCAGGGCAT 572
Db      526 CATCTCTCCAAAGCGTTGGCTTTGTAGTGAAGACGAATATCTTGGAAATTCAGGGCAT 585
QY      573 CACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCAATGACGTGGCCCGCCCGT 632
Db      586 CACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCAATGACGTGGCCCGCCCGT 645
QY      633 GGTACGGAGAGTAAAGGTCAACCGTGAATATCCACCATATTCAGAAAGCCAAAGGTAC 692
Db      646 GGTACGGAGAGTAAAGGTCAACCGTGAATATCCACCATATTCAGAAAGCCAAAGGTAC 705
QY      693 AGTGT-CCCCGTGGGACAAAGGGGACACTGTGAG-TGTGAAGCCTCAGCAGTCCCTCA 750
Db      706 AGTGTGTCCTCCCGTGGGACAAAGGGGACACTGTGAGTGTGTGAACCTCAGCAGTCCCTCA 765
QY      751 GCAG-ATTTCCAGTGTGTACAGGATG-ACAAAGACTGA-TTGAA-GGAAGAAAGGGGT 806
Db      766 GCAGAAATTCAGTGTGTACAGGATGAACAAAGACTGATTTGAAGGAAAAAAGGGGT 825
QY      807 -GAAAGTGG--AAAAACAGACCTTTT-CCTCTC 833
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      826 GGAAGGGGGGAAAAACGAACCTTTCCCTCTC 856

RESULT 7
AY406349      874 bp      DNA      linear      GSS 12-DEC-2003
LOCUS          Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION    genomic survey sequence.
ACCESSION     AY406349.1 GI:39762323
VERSION       AY406349
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
              Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL       Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
AUTHORS       Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
              Direct Submission
              Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT       This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
FEATURES      Location/Qualifiers
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              /db_xref="taxon:10090"
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ORIGIN

Query Match 70.0%; Score 724; DB 29; Length 874;
Best Local Similarity 89.1%; Pred. No. 3.4e-07;
Matches 779; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 168 GTGCACATATGACACCGGGTACCCGGGTGGCTGGCTAAACCGCAGCACCACATCTCTTA 227
Db 1 GTGCACATATGACACCGGGTACCCGGGTGGCTGGCTAAACCGCAGTACCATCTCTTA 60
QY 228 TGCTGGGAATGACACGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 287
Db 61 TGCTGGGAATGACACGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 120
QY 288 GCAGTACAGCATCGACATCCAGAACCTGATGTGTATGACGAGGGCCCTTACACCTGCTC 347
Db 121 CCAGTACAGCATCGACATCCAGAACCTGATGTGTATGACGAGGGCCCTTACACCTGCTC 180
QY 348 GGTGCAGACAGACACCCCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCC 407
Db 181 GGTGCAGACAGACACCCCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCC 240
QY 408 CAAATTTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTCAC 467
Db 241 CAAATTTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTCAC 300
QY 468 CTGCATAGCACTGGTGTAGACCGAGCCTACGTTACTTGGAGACACATCTCTCCCAA--- 524
Db 301 TTGCATAGCACAGGTAGACCGAGCCTACGTTACTTGGAGACACATCTCTCCCAAAGCC 360
QY 525 ---AGCGTTGGCTTGTGAGTGAGACCAATCTTGAAGTGGAGATCCAGGGCATCACTCGGGA 581
Db 361 CGCAGCGTTGGCTTGTGAGTGAGACCAATCTTGAAGTGGAGATCCAGGGCATCACTCGGGA 420
QY 582 GCAGTCAGGGGACTACGAGTCAGTGCCTTCCCAATGACGTGGCGCGCGCTGGTACGAG 641
Db 421 ACAGTCAGGGGACTACGAGTCAGTGCCTTCCCAATGACGTGGCGCGCGCTGGTACGAG 480
QY 642 AGTAAGTTCACCGTGAATCTCCACATATTCACCAATTCAGAACGCAAGGTTACAGGTGTC 701
Db 481 AGTAAGTTCACCGTGAATCTCCACATATTCACCAATTCAGAACGCAAGGTTACAGGTGTC 540
QY 702 CTTGGGACAAAAGGGGACATCTCAGTGTGAGGCTCAGACGTCCTCAGCAGATTTCA 761
Db 541 CTTGGGACAAAAGGGGACATCTCAGTGTGAGGCTCAGACGTCCTCAGCAGATTTCA 600
QY 762 GTGGTAAAGGATGACAAAGACTGATTAAGGAAAGAGGGGTGAAAGTGGAAAACAG 821
Db 601 ATGGTTCAAGGATGACAAAGACTGATTAAGGAAAGAGGGGTGAAAGTGGAAAACAG 660
QY 822 ACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAAATGATGAGTGGAACTACAC 881
Db 661 ACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAAATGATGAGTGGAACTACAC 720
QY 882 TTGGTGGCTCCAAAGAGTGGGACACCAATTCAGCAGCATCATGCTATTGTTGGTCCAGG 941
Db 721 ATGTGTGGCTCCAAAGAGTGGGACACCAATTCAGCAGCATCATGCTATTGTTGGTCCAGG 780
QY 942 CGCGTCAAGGAGTGGACGACGACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1001
Db 781 TGCTGTGAGTGGTCAACAAATGGGACATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 1002 TCTTCTGGTCTTGGACCTGCTCTCAAAATTTGA 1035
Db 841 TCTTCTGGTCTTGGACCTGCTCTCAAAATTTGA 874

RESULT 8
AL533026

LOCUS

DEFINITION AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CSODN005YD20 5-PRIME, mRNA sequence.

ACCESSION

AL533026

VERSION
KEYWORDS
SOURCE
ORGANISM

AL533026.2 GI:31070858

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1085)

J. W. B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12796519.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6387.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODN005DB100P1&cluster=6387.f. Contact :

Peng Liang Email : fliang@lifetech.com URL : CSODN005DB100P1.

http://fulllength.invitrogen.com/ invitrogen Corporation 1600

Paradise Avenue Genoscope sequence ID : CSODN005DB100P1.

Location/Qualifiers

1..1085

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODN005YD20"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Query Match

Best Local Similarity 65.6%; Score 679; DB 9; Length 1085;

Matches 772; Conservative 1; Mismatches 19; Indels 364; Gaps 50;

QY 2 TGAACCAATCATCCAGCCAA-AAA--TGACAAATTTCTATCTCTGGGCAATCTTTCACGGGGC 58

Db 2 TGAAC--AT--AG--AACAAATTTGTACAA---A-----AAAC--CA---NGC 35

QY 59 TGGCTGTCTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTCAGGTGCACTATTG 118

Db 36 TNNTTAC---NNGTC---CNNA--ATT--CC-----CGG-GATG----- 63

QY 115 AAGCTATGGACAAGCTGACGCTCGGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTG 178

Db 64 --GCTA-----GGAGA-----A-----CAG-----CTATT-- 81

QY 179 ACAACCGGGTCAACCGGGTGCCTGGCTAAACCGCAGCAGCATCTCTATGCTGGGAATG 238

Db 82 ---C---CA---GTG---T---T---GCG------TA-----GAAT-- 99

QY 239 ACAAGTGGTGGATCTCGGTGTGTC--TTCTGAGCAACACCCAAACGAGTACAGC 297

Db 100 -----T---T---AT--TC-----CCATTCGGA-----C 115

QY 298 ATCGAGATCCAGAACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACACA 357

Db 116 -TC-----CTTG-ACCT--TGCT-----TTAAA-----TAGG---AG--- 141

QY 358 GACCAACCAACCAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCAAAATTGTA 417

Db 142 GA-AA-----TCAAAG---CTA-----A---ATT---AAAGTATCTCCAAAATTGTA 179

QY 418 GAGATTCTTCAGATATCTCATTAATGAAGGAAACAAATATTAGCTTCACCTGCATGACGA 477


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Db 180 GAGATTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTACCTCCATCAGCA 239
QY 478 ACTGGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTT 537
Db 240 ACTGGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTT 299
QY 538 GTGAGTGAGACAGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTAC 597
Db 300 GTGAGTGAGACAGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTAC 359
QY 598 GAGTGCAGTGCCTCCATGACGTGGCGCGCCCGTGTACGAGAGTAAAGGTACCGGTG 657
Db 360 GAGTGCAGTGCCTCCATGACGTGGCGCGCCCGTGTACGAGAGTAAAGGTACCGGTG 419
QY 658 AACTATCCACCATACATTTTCAGAAAGCAAGGTCAGAGTGTCCCCGTGGGACAAAAGGGG 717
Db 420 AACTATCCACCATACATTTTCAGAAAGCAAGGTCAGAGTGTCCCCGTGGGACAAAAGGGG 479
QY 718 AACTGCAGTGTGAGCCTCAGCAGTCCCTCAGCAGATTCAGAGTGTACAGAGTAC 777
Db 480 AACTGCAGTGTGAGCCTCAGCAGTCCCTCAGCAGATTCAGAGTGTACAGAGTAC 539
QY 778 AAAA----- 781
Db 540 AAAAGAGCTGAAATCTCATTACAGTGTGTTATGATGGGAAAGCTTCTCCCATGGTG 599
QY 782 ----- 781
Db 600 GAGCAATGGTGTCAAAGCGCCAGTGGGATCAATCAGCCTGACTTGTCTGGCAGAACTCTC 659
QY 782 --GACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACT 839
Db 660 CCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACT 719
QY 840 CATCTTTCAATGTCTTGAACATGACTATGGGAACTACATTTGGTCCAGGCGCGGTGAG 959
Db 720 CATCTTTCAATGTCTTGAACATGACTATGGGAACTACATTTGGTCCAGGCGCGGTGAG 839
QY 900 GCTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGTGAG 959
Db 780 GCTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGTGAG 839
QY 960 CAACGGCAGCTCGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
Db 840 CAACGGCAGCTCGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 1020 GCTTCTCAAAATTTGA 1035
Db 900 GCTTCTCAAAATTTGA 915
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RESULT 9
CD354474
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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CD354474 765 bp mRNA linear EST 15-JUL-2003
UI-N-GMO-cydg-9-16-0-UI.r1 NIH BMAP_GMO Mus musculus cDNA clone
IMAGE:30361215 5', mRNA sequence.
CD354474
CD354474.1 GI:31146975
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 765)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Dr. Jim Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouseefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyx-5.

FEATURES
source
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30361215"
/dev_stage="1, 5 and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_GMO"
/note="Organ: Brain; Vector: pyx-Asc; Site:1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction, ligated with EcoR
I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 62.9%; Score 650.8; DB 14; Length 765;
Best Local Similarity 90.4%; Pred No. 1.9e-05;
Matches 697; Conservative 0; Mismatches 68; Indels 6; Gaps 6;
QY 15 GCCAAAATGCAATTTCTTCTTGGGCAATCTTTCAGGGGGCTGGTCTCTGTGCT 74
Db 1 GGCAAAATGCAATTTCTTCTTGGGCAATTTTCAGGGGGCTGGGCTCTGTGCT 60
QY 75 CTTTCAAGAGTGGCGGTGGCGGAGATGCCACCTTCCCAAGCTATGGAACAAGT 134
Db 61 CTTTCAAGAGTGGCGGTGGCGGAGATGCCACCTTCCCAAGCTATGGAACAAGT 120
QY 135 GACGCTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGGTCAACCG 194
Db 121 GACGCTCAGGCGAGGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGGTCAACCG 180
QY 195 GGTGGCTGGCTAAACCGGAGCACCATCTCTATGCTGGGAATGACAAGTGGTCTGGA 254
Db 181 GGTGGCTGGCTAAACCGGAGCACCATCTCTATGCTGGGAATGACAAGTGGTCTGGA 240
QY 255 TCCTCGCTGGTTCCTTCTGAGCAACACCCAGCAGTACAGCATCGAGATCCAGAACT 314
Db 241 TCCTCGCTGGTTCCTTCTGAGTAACCCAGACCCAGTACAGCATCGAGATCCAGAACT 300
QY 315 GAGTGTGATGACGAGGGCCCTTTACACCTGCTCGGTGAGAGATGACAAGTGGTCTGGA 374
Db 301 GAGTGTGATGAGGGCCCTTTATCTCTGCTGAGTACAGACCAACCCCTTAAAGC 360
QY 375 CTCAGAGTCCACCTCATGTTGGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATAT 434
Db 361 CTCAGAGTCCACCTCATGTTGGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATAT 420
QY 435 CTCCAATTAATGAAGGAAACAATATTAGCCTCACCTGCACTACCACTGTAGACAGGCC 494
Db 421 CTCCAATTAATGAAGGAAACAATATCAGCCTCCTTGTGATGAGTGAAGGAAATA 554
QY 495 TACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGGAAATA 540
Db 481 TACAGTAACTGGAGACATATTTCTCCCAAGCGGTGGCTTTGTGAGTGAAGTGAATA 540

QY 555 CTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTCCAA 614
 Db |||||
 541 CTTGGAGATCCAGGGCATACTCGGGAACAGTCAAGGGGAGTGCAGCGCCTCCAA 600
 QY 615 TGAGTGGCGCGCCCGTGGTACGAGAGTAAAGTCAACCGGTCACTATCCACCATACAT 674
 Db |||||
 601 CGAGTGGCGGCCACCACTGGTACGAGAGTGAAGGTCACTGTAATCCACATACAT 660
 QY 675 TTCAAGACCAAGGTTACAGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGC 734
 Db |||||
 661 CTCAAGAGCTAAGGGCACAGTGTCCCGTGGGACAGAGGACTCTGCAGTGTGAAGC 720
 QY 735 CTCAAGAGTCCCTCAGCAGATTCAGTGTGATCAAGGATGACAAAGACT 785
 Db |||||
 721 TTC-GCAGT-CCTTCAGCAGATTTCA-TGGT-C-NGGATGAC-AAAGACT 765

RESULT 10

LOCUS BG261691 979 bp mRNA linear EST 13-FEB-2001
 DEFINITION 602373361F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4480983 5', mRNA sequence.
 ACCESSION BG261691
 VERSION BG261691.1 GI:12771416
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://img.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM10315 row: i column: 16
 High quality sequence stop: 715.

FEATURES

source
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 /db_xref="taxon:10090"
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 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_94"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 61.8%; Score 639.2; DB 12; Length 979;
 Best Local Similarity 73.3%; Pred. No. 0.0001;
 Matches 792; Conservative 0; Mismatches 88; Indels 200; Gaps 80;
 3 CA-AA-----ACC--ATCCAGCC--AAAAATGCACAAATCTATCTTGG 42
 39 GAGAAATGGGGTCTGTGGGTACCTGTCTCCCTCGGAAGTGC-----CTCGTG 88
 43 ----GCAATCT-TCAAGGGGCTGCTGTCTGTCTT-----CCA-AGGAGTGGCGGT 92
 89 TCGTG---TCTCTCA-----GGCTGTAT---TC-CTTGATCCCAAGAGTSCCGGT 134
 93 GCGCAGCGGAGATGCCACCTTCCCAAGACTATGGAACAACGTGACGTCCGGCAGGGGGA 152

Db |||||
 135 GCGTAGCGAGATGCCACCTTTCCCAAGCTATGGACAAGTGCAGTGCAGCGAGGGGA 194
 QY |||||
 153 GAGCGCCACCTCAGTGCAGTATTGACAACCGGGTCAACCGGGTGGCTGGCTAAACCG 212
 Db |||||
 195 GAGCGCCACCTCAGTGCAGTATTGACAACCGAGTCAACCGGGTGGCTGGCTAAACCG 254
 QY |||||
 213 CAGCAACATCTCTATGCTGGGAATGACAAGNGTGCCTGGATCTCCGCGTGGTCTTCT 272
 Db |||||
 255 CAGTACCATCTCTATGCTGGAAATGA CAAGTGGTCCCTAGATCTCTGCTGGTCTCT 314
 QY |||||
 273 GAGCAACCCCAACCGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGG 332
 Db |||||
 315 GAGTAACACCCAGACCCAGTACAGCATTCAGATCCAGAAATGTGGATGTGATGATGAGG 374
 QY |||||
 333 CCCTTACACCTGCTCGGTGACAGACACCAACCAAGACCTCTAGGGTCCACTCAT 392
 Db |||||
 375 CCCTTATACCTGCTCGGTACAGACACCAACCAACCTTAGACCTCCA-GGTCCACTCAT 433
 QY |||||
 393 TGTCAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGA 452
 Db |||||
 434 TGTACAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGA 493
 QY |||||
 453 CAATATTAGCTCACTCGATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGAGACA 512
 Db |||||
 494 CAACATCAGCTCACTTGCATAGCCACAGTAGACCGGAGCTACAGTAACCTGAGACA 553
 QY |||||
 513 CATCTCTCCCAAGCGTGGCTTGTGAGTGAAGACCAATACTTGGAAATTCAGGGCAT 572
 Db |||||
 554 TATTTCTCCCAAGCGCTTGTGAGTGAAGATGAGTTCTTGGAGATCTCTGAGATCCAGACAT 613
 QY |||||
 573 CACCGGGAGCAGTCAAGGGGACTACAGTGCAGTCCCTCAATGACGTGGCGCGCCCGT 632
 Db |||||
 614 CACTCGGGAACAGTCAGCGGAGTACAGTGCAGCG-CT-CAACGACGTGG-CG-GACCGT 669
 QY |||||
 633 GGTACGAGAGTAAAGTCAACCGTGAATTCACCAATACATTCAGAAAGCAAGGTA 691
 Db |||||
 670 GGTACGAGAGTGAAGTTC-CCGTGAATAT-CACCATACATTCACAGAAG-TTAGGG-C 725
 QY |||||
 692 CAGGTGTCCTCGT-GGGACAAAGGGGACACTGCAAGTGTGAAGCTCAGAGTCCCTCA 750
 Db |||||
 726 CCGGTGT-CCCGTGGGGCAGAGGGG-CTCTGAGTGTG-AGCTTC-G-AGTCCCTTC- 779
 QY |||||
 751 GCAGAAATTCAGTGTACAAAGATG---ACAAAAG-ACTGATTGAAG---GAAAGAAAGG- 803
 Db |||||
 780 GCCGGAAT-CA-T-GTCC--GG-TGGCCAC-----GCACGTG-----CGCCGA---AAAGGC 821
 QY |||||
 804 ----GGTGAAGTGGAAACAGACCTTTCTCTCAAACTCATTTCTTCAATGTCTGT 859
 Db |||||
 822 TCCCG-----GG--AACA-AC--TTCCT-T--AAA-TC--C--CTTTA--G-GTCTG 857
 QY |||||
 86C AACATGACTATGGAACTACACTTGGCTGGCTCCCAACAGCTGGGCGCACCAATGCCA 919
 Db |||||
 858 -AC-TG--TATGG--AC-A-ACTTG-GTGCC-CCA-----GGG-CACAC-----CCG 894
 QY |||||
 920 GCATCATGTATTGTGTCAGGCGCTCAGC-GAGGTGAGCAACCGCAGCTCGAGAGG 978
 Db |||||
 895 G-----TG--AT--GT-----GGCGC-----GCGAG--GA-CAACAGAAC--AGAGGGGG 931
 QY |||||
 979 GC-----AGGCTGGGTGCTGCTGCTGCTCTTCTGCTTGTGCTTGTGCAAC--CTGC 1021
 Db |||||
 932 GCCTGAAAGCCGAAGTAGGC-GCG--AGG--G--GC-----CAAGAAATACACAACAGC 979

RESULT 11

LOCUS BI666583 865 bp mRNA linear EST 12-SEP-2001
 DEFINITION 603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5', mRNA sequence.
 ACCESSION BI666583
 VERSION BI666583.1 GI:15580816
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 865)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strauberg, Ph.D.
 Email: rstraub@xmail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Pietro Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLAM11787 row: j column: 18
 High quality sequence stop: 742.
 Location/Qualifiers
 1. .865
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5310833"
 /tissue_type="hypothalamus"
 /lab_host="DH108"
 /clone_lib="NIH MGC 96"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTT-3', size-selected for average
 insert size 2.3 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN
 Query Match 61.4%; Score 636; DB 12; Length 865;
 Best Local Similarity 96.3%; Pred. No. 7.7e-05;
 Matches 658; Conservative 0; Mismatches 11; Indels 14; Gaps 14;
 QY 1 ATGAACACCATCCAGCAAAATGCAATTTCTTTGGGCAATCTTCACGGGGCTG 60
 DB 183 ATGAACACCATCCAGCAAAATGCAATTTCTTTGGGCAATCTTCACGGGGCTG 242
 QY 61 GCTGCTCTGTGTCTCTTCCAGGAGTGGCGCGGAGATGCCACCTTCCCAAA 120
 DB 243 GCTGCTCTGTGTCTTCCAGGAGTGGCGCGGAGATGCCACCTTCCCAAA 302
 QY 121 GCTATGGAACAGTCAAGTCCGGTCCGGAGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
 DB 303 GCTATGGAACAGTCAAGTCCGGTCCGGAGGAGAGCGCCACCTCAGGTGCACTATTGAC 362
 QY 181 AACCGGTCACCGGGTGGCTGCTTAACCGCAGACCATCTCTATGCTGGGAATGAC 240
 DB 363 AACCGGTCACCGGGTGGCTGCTTAACCGCAGACCATCTCTATGCTGGGAATGAC 422
 QY 241 AAGTGGTGGTGGATCTCTGCTGGTGGTCTTCTGAGCAACCCCAACCGCAGTACGATC 300
 DB 423 AAGTGGTGGTGGATCTCTGCTGGTGGTCTTCTGAGCAACCCCAACCGCAGTACGATC 482
 QY 301 GAGATCCAGAACGTTGTATGATGACGAGGCGCTTACACCTGCTCGGTGACAGACAC 360
 DB 483 GAGATCCAGAACGTTGTATGATGACGAGGCGCTTACACCTGCTCGGTGACAGACAC 542
 QY 361 AACACCCCAAGACCTTAGGTTCACCTCTATTGCAAGTATCTCCCAAAATTGTAGAG 420
 DB 543 AACACCCCAAGACCTTAGGTTCACCTCTATTGCAAGTATCTCCCAAAATTGTAGAG 602
 QY 421 ATTTCTTCAGATATCTCCATTAAATGAAGGAAC-AATATTAGCTCCTCAGTCAAGCAAC 479

Db 603 ATTTCTTCAGATATCTCCATTAAATGAAGGAACAATATAGCTCAGTCAAGCAAC 662
 QY 480 TGGTAGACAGAGCCTACCGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGT 539
 Db 663 TGGTAGACAGAGCCTACCGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGT 722
 QY 540 GAGTGAAGACGAA-TACTT-GGAAATTCAGGG-CATCACCCCGGAG-CAGTC-AGGGGAC 594
 Db 723 GAGTGAAGACGAACTACTTTGGGAATCTTCAGGGCCATCTCCCGGAGCCAGTCAAGGGGAC 782
 QY 595 T-ACGAG-TG-CAGTGCCTCCAAAT-GACGTGGCCGG-CGCCGTGGTACGGAG-AGTA-AA 647
 Db 783 TAACGAGTTGGCAGTGCCTCCAAATGGACGTTGGCGGCCCGCTGGTACGGAAGTACAC 842
 QY 648 GGTCAACGTGA-ACTATCCACCA 669
 Db 843 AGTCCACGGGATATTTTCCACCA 865

RESULT 12
 LOCUS AK042854
 DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:A73031E08 product:NEUROTRIMIN PRECURSOR
 (GP65) homolog (Rattus norvegicus), full insert sequence.
 ACCESSION AK042854
 VERSION AK042854.1 GI:26089310
 KEYWORDS HTG; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 2
 99279253
 10349636
 3
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 :1042159
 4
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multipillar sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 5
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 6
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3166)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
1. 3166
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="FANTOM_DB:A730031E08"
/db_xref="MGI:2407957"
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/tissue type="cerebellum"
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/dev_stage="7 days neonate"
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1. 3166
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ORIGIN

Query Match 56.5%; Score 585; DB 11; Length 3166;
Best Local Similarity 45.8%; Pred. No. 0.24;
Matches 899; Conservative 0; Mismatches 99; Indels 966; Gaps 158;

QY 1 ATGAAACCATCCAGCCAAATGCAATTTCTCTCTGGGCAATCTTTCAGGGGCTG 60
DB |||||
QY 206 ATGAAACCATCCAGGCAAAATGCAATTTCTCTCTGGGCAATCTTTCAGGGGCTG 265
DB |||||
QY 61 GCTGCTGTGTCTCTTCCAGGAGTGCCGCTGGGAGGAGATGCCACCTTCCCCAAA 120
DB |||||
QY 266 GCGGCTGTGTGCTCTTCCAGGAGTGCCGCTGGGAGGAGATGCCACCTTCCCCAAA 325
DB |||||
QY 121 GCTATGGACACGTCAGCTCCGCGAGGGAGAGCGCCACCTCAGTGCATATTGAC 180
DB |||||
QY 326 GCTATGGACACGTCAGCTCCGCGAGGGAGAGCGCCACCTCAGTGCATATTGAC 385
DB |||||
QY 181 AACCGGCTCACCGGGTGGCTTGGTAAACCGAGCACCATCTCTATGCTGGGAATGAC 240
DB |||||
QY 386 AACCGAGTCACCGGGTGGCTTGGTAAACCGAGCACCATCTCTATGCTGGGAATGAC 445
DB |||||
QY 241 AAGTGGTCCCTGGATCTCTCGGCTGGTCTCTTGAGCAACACCCAAACGAGTACGATC 300
DB |||||
QY 446 AAGTGGTCCCTGGATCTCTCGGCTGGTCTCTTGAGCAACACCCAAACGAGTACGATC 505
DB |||||
QY 301 GAGATCCAGACGTCGATGTCATGACGAGGGCCCTTACCTGCTCGGTGACAGAC 360
DB |||||
QY 506 GAGATCCAGACGTCGATGTCATGACGAGGGCCCTTACCTGCTCGGTGACAGAC 565
DB |||||

QY 361 AACCAACCAAGAGCTCTAGGCTCCACCTCATTTGTGCAAG----- 400
DB |||||
QY 566 AACCAACCTTAAGACCTCCAGGCTCCACCTCATTTGTAAGGTTGGGTGGGTGGCTGGG 625
DB |||||
QY 401 -----TATC-----TC-----C 407
DB |||||
QY 626 AGGCTGAGTGGGTGGCTGGGAATATCAACATTACTGATTTTTTTTCCACATCTTAATC 685
DB |||||
QY 408 CAA-----AA-----TTG-----TGA- 419
DB |||||
QY 686 CAAGCTAGTGGGTGGTCTCCCGCAGCAAGTCTCTCTGGTGGTCACTCTGAAGCTAGAC 745
DB |||||
QY 420 ---GA---TTTCTTCA-----GA-----TATCTCC-ATT-A-ATG 445
DB |||||
QY 746 ACGGACGCTTTCATCAATTTACTTTTTCAGTTGAACGATTTTCTCTATTCAGATTT 805
DB |||||
QY 446 AAG---GGAACAATATTA-----G---CCT-----CACCT-----GCA 472
DB |||||
QY 806 ATGTTTGTACAAAATTAATGCTAAATATTGTTTCCCTTGGCTTTTCTCTCTCTAGCA 865
DB |||||
QY 473 T-----A-G-----CAACT-----G---GT-----AGACGGA-----G- 492
DB |||||
QY 866 TTTTAAATGTTTCAACAACTCAAGTTTGTATTATTAAAGCACAAGATTTTAATGT 925
DB |||||
QY 493 CCTACGGTTACT-----TG-----GA-GACA----- 512
DB |||||
QY 926 TCTTCGGTGTGTACATATATATACATGATGATGATGATGATGATGATGATGATGATGAT 985
DB |||||
QY 515 -----CATCTCT-----CCCA-----AAAG----- 526
DB |||||
QY 986 AGAAACAGTACCCAGGATCTTATCGCAACCATCTCTCCACACACCATTTATAAGTAG 1045
DB |||||
QY 527 -----CGG---TTGGCTT-----TG-----TG---AGTGAA 546
DB |||||
QY 1046 GGTCTTGTCTCTCTCCATCCATCCAGTTTGGCTTCCCAATGCTCTGCTA-T-AA 1103
DB |||||
QY 547 GAC-----GA-----ATACTT-----GG---AA 561
DB |||||
QY 1104 GACTGGATTCAGAGTCTCTTCTCTATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1163
DB |||||
QY 562 -----ATT-----CAGG----- 568
DB |||||
QY 1164 TGTTTGTGGGTCTCCCGTGTGTTTGTGGGCTTTGTGGCATTTCTCCAGTTCTCA 1223
DB |||||
QY 569 -----GC-----ATCAC-----CGG-G---AGC-----AGTCAG----- 589
DB |||||
QY 1224 TCTCTCTCTCTCATATCAGGTCTGGTGTTCAGCCCTTTTCAAAATCAGATGTTCC 1283
DB |||||
QY 590 ---GG-----GACTAC-----G-AG-TG-----C-AGTGCCTCCAATGAC-G---T 620
DB |||||
QY 1284 TGAGGACAGCAGCAACATTTAAACAGTAGATGAATTTCTAGTTACT-GAACACAGCTTT 1342
DB |||||
QY 621 GCGCGC-----GCCGTGGT---ACGGAGTAAGGTCAACGTCGTCGTCAT---C-CAC 667
DB |||||
QY 1343 GG---GCTACATTTGTCTGTTTCTGACGGAGAG-AAAG---CC-TCAATATTACTGCA 1395
DB |||||
QY 668 CATAC-----ATTTC-----AGAAGCA-AGGTACAGGT---GTCCCGTGGG----- 707
DB |||||
QY 1396 C---CCTGGGCTTTTCTTGGCA---ATAGGTAATGAGG---AGTGGGTGAA 1445
DB |||||
QY 708 ---ACA---AAG---GGGACACT---GC---AGTGTGAA-GCCTCAGCACT----- 743
DB |||||
QY 1446 GATTACATTATATGATAGGTAAACTAAAGCCCTTAG-GAGAGGCTTCACTCTGGAGGA 1504
DB |||||
QY 744 -----CC-----CCTCA-GC-----A-----GAATTC-----CAG 762
DB |||||
QY 1505 CTATTTACCTGTTGTCTATCATCATGCTATGATGTCCTCCCTTTTGAATCTTTTCAATAC 1564
DB |||||
QY 763 TG-----GT---ACA---AG-GATG-----ACA-AAAGAC-TGATT----- 789
DB |||||
QY 1565 TGAATATTTTAAACATTTAGTCATCTTTTATAGTAATTAATATCTGTTTGTCTCTCT 1624
DB |||||
QY 790 --GAAGAAAGA-A--AGGGGTGAAAGTGGAAA--C-----AGA----- 822
DB |||||

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Db      1625 GAGACTAAACATACCA-----TG-AAGT---AAAATCTTGTGGATTTTTTGTGGGTTTC 1677
QY      823 -CCT-TTCCTC-TCAAACTCATCTCT-----TC-AAT-----G-----TC-TC-- 857
Db      1678 TCCTGCTCTCGT-----CTCCCTCTCTTCTTAGTCTAATCCCTGCTTCTCTCATCCA 1733
QY      858 ---TGA-----A-CATGA-----CT-----A-----TG-----G 872
Db      1734 GCATGATGGCAGGTGTTCAGCAGAGCCATGAAGTTCCTCTTGCACAGCCCTGCTTCTG 1793
QY      873 GAATACATCTT---GCTG-GG-----CCT-----C-----CACACAG----- 900
Db      1794 GAATACATCTTGAAGTAGATGAATGAACCTGAGTGACTGAGAGAGACAAAGAATAG 1853
QY      901 -----C-----TGG-----GCCAC-----ACC 912
Db      1854 GGGATTGAGAAGACAAATTTGAGAGAGTGCAGGAGCCACTGTGACGAGAGAGGAAGC 1913
QY      913 --AATGCCAGCAT-----CA-TGCTA-----T-----TTGGTCAGGC-GCC----- 945
Db      1914 AGAATGCCATCATGAACCAACAGAGCTACGAGAGTAGAATGGGGCAAGCAGCCATGAG 1973
QY      946 -----GTCAG--CGAGG-----TGAGCA-ACG---GCACGTGAGG---AGG- 978
Db      1974 ATGAGACTATGTTAGATGAGGGGACACTTGTAGCATATGTAG-AGG--GAGGTGAAGGT 2030
QY      979 -GCAG--G-CT-GC--G-TCTGGCTGCTG-----CCTC-----TTCTGGTC 1011
Db      2031 AGCAGCTGACTGGCAATGATCAGCTG-TGGTAGAGTATGTTGACCTCAGGTTT-TTATC 2088
QY      1012 ---TTGCAC-CTGCT---CTCTC-----AAATTTCGA 1035
Db      2089 ACTTTTGTCTGCTGCTTTTCTCTCTCCCCCAAGGAAGATGA 2132

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RESULT 13

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LOCUS      CF737474
DEFINITION UI-M-HD0-cks-o-09-0-UI.r1 NIH BMAP_HD0 Mus musculus cDNA clone
IMAGE:30614264 5', mRNA sequence.
ACCESSION  CF737474
VERSION     1 (bases 1 to 759)
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 759)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mouseefl.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
Seq primer: pYX-5

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FEATURES

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1..759
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30614264"
/tissue_type="whole eye"
/dev_stages="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"

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/clone lib="NIH_BMAP_HD0"
/note="Organ: Eye; Vector: pYX-Asc; Site: 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTTATGAAGT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

```

ORIGIN

```

Query Match      56.0%; Score 580; DB 14; Length 759;
Best Local Similarity 83.5%; Pred. No. 0.0015;
Matches 642; Conservative 0; Mismatches 71; Indels 56; Gaps 15;

QY      3 GA-AA-----ACC--ATCCAGC--AAAAATGCACAAATCTATCTCTTGG 42
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QY      43 ----GCATCT--TCACGGGGTGGTGTCTGTCTCTCTT---CCA-AGGAGTGCCTT 92
Db      67 TCGTG---TCTCTCA-----GGCTGTCTAT---TC-CTGTACCCACAGGAGTGCCT 112
QY      93 GGCAGCGGAGATGCACTTCCCAAGCTATGACACACGTGACGCTCCGGCAGGGGGA 152
Db      113 GGGTAGCGGAGATGCCACCTTTCCCAAGCTATGACACACGTGACGCTCAGGCGGGGA 172
QY      153 GAGGCGCCCTCAGTGCATATTGACAAACGGGTGACCCGGGTGCTGGTAAACCG 212
Db      173 GAGCGCCCTCAGTGCATATTGACAAACGGGTGACCCGGGTGCTGGTAAACCG 232
QY      213 CAGCACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTGGATCTCGGCTGCTCTTCT 272
Db      233 CAGTACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTGGATCTCGGCTGCTCTCT 292
QY      273 GAGCAACACCCAAACCGAGTACAGATCCAGATCCAGAACCGTGGATGTGTACGAGGG 332
Db      293 GAGTAACACCCAGACCCAGTACAGCATTTGAGATCCAGAAATGTGGATGTGTACGAGGG 352
QY      333 CCCTTACACCTGCTCGGTGACAGACAAACCCAGACCTCTAGGCTCCACTCAT 392
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QY      393 TGTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGATATCTCATTAATGAAGGAA 452
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QY      453 CAATATTAGCTCCTCATGATAGCAACTGGTAGACAGCCTACGGTTACTTTGAGAGACA 512
Db      473 CAACATCAGCTCCTCATGATAGCAGAGTAGACCGGAGCTACAGTAACCTGGAGACA 532
QY      513 CATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGCAT 572
Db      533 TATTTCTCCCAAGCGGTGGCTTTGTGAGTGAAGTACCTGGAGATTCAGGGCAT 592
QY      573 CACCGGGAGCAGTACAGGGGACTACGAGTGCAGTGCCTTCCCAATGACGTGGCGGCCCGT 632
Db      593 CACTCGGGAACAGTCAGGAGTACGAGTGCAGGCTCCCAACGACGTGGCGGCCAGCT 652
QY      633 GGTACGAGAGTAAAGTTCACCGTGAATCTCACCATAATTTCAAGAGCCAAAGGTTAC 692
Db      653 GGTACGAGAGTAAAGTTCACCGTGAATCTCACCATAATTTCAAGAGCCAAAGGTTAC 712
QY      693 AGGTGTCTCCCGTGGGACAAAGGGGACACTGCACTGAGTGTGAAGCTTCAGCA 741
Db      713 AGGTGTCTCCCGTGGGACAAAGGGGACAAAGGGGACACTGCACTGAGTGTGAAG-CTCCGCA 759

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```

RESULT 14
BI549918
LOCUS
DEFINITION
603194765F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274161 5',
mRNA sequence.
BI549918
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 784)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
CDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
Toshnyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM11692 row: b column: 18
High quality sequence stop: 726.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5274161"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
ORIGIN
Query Match 54.1%; Score 560.4; DB 12; Length 784;
Best Local Similarity 96.5%; Pred. No. 0.0059;
Matches 577; Conservative 0; Mismatches 5; Indels 16; Gaps 12;
QY 1 ATGAAACCATTCAGCCAAATGCAATTTCTTCTTGGCAATCTTTCACGGGGCTG 60
DB 193 ATGAAACCATTCAGCCAAATGCAATTTCTTCTTGGCAATCTTTCACGGGGCTG 252
QY 61 GCTGCTCTGTCCTCTTCCAGGAGTCCCGTGGCGAGCGGAGATGCCACTTCCCAAA 120
DB 253 GCTGCTCTGTCCTCTTCCAGGAGTCCCGTGGCGAGCGGAGATGCCACTTCCCAAA 312
QY 121 GCTATGACCAACGTGACGGTCCGGCAGGGGAGCGCCCTCAGTGCATTTATGAC 180
DB 313 GCTATGACCAACGTGACGGTCCGGCAGGGGAGCGCCCTCAGTGCATTTATGAC 372
QY 181 AACCGGTGACCCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 373 AACCGGTGACCCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 432
QY 241 AAGTGGTGCTGGATCTCTCGGGTGGTCTTCTTGTAGCAACCAACCAACGCAATC 300
DB 433 AAGTGGTGCTGGATCTCTCGGGTGGTCTTCTTGTAGCAACCAACCAACGCAATC 492

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QY 301 GAGATCCAGACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 360
DB 493 GAGATCCAGACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 552
QY 361 AACCAACCAAGACCTCTAGGTCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 553 AACCAACCAAGACCTCTAGGTCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAG 611
QY 421 ATTCTTCAGATATCTCCATTAAATGAAGGAAACATATTAGCCTCA-CTGCAATAGCAAC 479
DB 612 ATTCTTCAGATATCTCCATTAAATGAAGGAAACATATTAGCCTCACTGCAATAGCAAC 671
QY 480 TGGTAGACAGAGCTCAGGTTACTTTGAGACA-CATCTCTCCC--AAAGCGTTGGCTT 536
DB 672 TGGTAGACAGAGCTCAGGTTACTTTGAGACA-CATCTCTCCC--AAAGCGTTGGCTT 731
QY 537 TGTGA-GTGAAGA-CGAATACCTT-GGA-AAATTCAGGGC-ATCA-CCCGGAGCAGTCA 588
DB 732 CGGACATGAAGACCGAATCTTGGACAATTC--GGCGATCACCCCGGGAAC---CA 784

RESULT 15
BE263639
LOCUS
DEFINITION
601192064F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536127 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 545)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Plate: LHM217 row: p column: 16
High quality sequence stop: 545.
Location/Qualifiers
1..545
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3536127"
/tissue_type="small cell carcinoma"
/cell_line="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 52.3%; Score 541.3; DB 10; Length 545;
Best Local Similarity 99.6%; Pred. No. 0.0049;
Matches 543; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 271 CTGAGCAACCCCAACAGCAGTACAGATCGAGATCCAGACGTGATGATGATGACGAG 330
DB 1 CTGAGCAACCCCAACAGCAGTACAGATCGAGATCCAGACGTGATGATGATGACGAG 60
QY 331 GCCTCTTACCTGCTCGGTGAGACAGACCAACCAACCAACCAACCAACCAACCACTTC 390
DB 61 GCCTCTTACCTGCTCGGTGAGACAGACCAACCAACCAACCAACCAACCACTTCACCTC 120

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391 ATTGTGCAAGTATCTCCCAAAATGTAGAGTATCTTTAGATATCTCCATTAATGAAGGG 450
 121 ATTGTGCAAGTATCTCCCAAAATGTAGAGTATCTTTAGATATCTCCATTAATGAAGGG 180
 451 AACAAATATTAGCTCAGCTCATAGCACTGTTAGACAGAGCTTACCTTGTAGAG 510
 181 AACAAATATTAGCTCAGCTCATAGCACTGTTAGACAGAGCTTACCTTGTAGAG 240
 511 CACATCTCTCCCAAGCGGTGGCTTGTGAGTGAAGCAATACCTTGGAAATTCAGGGC 570
 241 CACATCTCTCCCAAGCGGTGGCTTGTGAGTGAAGCAATACCTTGGAAATTCAGGGC 300
 571 ATACCCGGGAGAGTACAGGGGACTAGAGTGCAGTGCCTCCCAATGACGTCGGCGGCC 630
 301 ATACCCGGGAGAGTACAGGGGACTAGAGTGCAGTGCCTCCCAATGACGTCGGCGGCC 360
 631 GTGGTACGAGAGTAAAGGTCAAGGTGCAAGTGCAGTGCCTCCCAATGACGTCAGGGT 690
 361 GTGGTACGAGAGTAAAGGTCAAGGTGCAAGTGCAGTGCCTCCCAATGACGTCAGGGT 420
 691 ACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCTTCAGCAGTCCCTCA 750
 421 ACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCTTCAGCAGTCCCTCA 480
 751 GCAGAAATTCAGTGTGACAGGATGACAAAGAGTGAAGTGAAGGAA - GAAAGGGGTGAA 809
 481 GCAGAAATTCAGTGTGACAGGATGACAAAGAGTGAAGTGAAGGAA - GAAAGGGGTGAA 540
 810 AGTGG 814
 541 AGTGG 545

RESULT 16
 BI551784
 LOCUS
 DEFINITION
 603197479F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277115 5',
 mRNA sequence.
 BI551784
 BI551784.1 GI:15439096
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbb-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11699 row: m column: 20
 High quality sequence stop: 732.
 Location/Qualifiers
 1. 732
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:5277115"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 95"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

FEATURES

source
 AK028345 2798 bp mRNA linear HTC 18-SEP-2003
 Mus musculus 12 days embryo embryonic body below diaphragm region
 cDNA, RIKEN full-length enriched library, clone:3732419F12
 product:weakly similar to OPIOID BINDING PROTEIN/CELL ADHESION
 MOLECULE PRECURSOR (OBPM) (OPIOID-BINDING CELL ADHESION MOLECULE)
 (OPCML) [Homo sapiens], full insert sequence.
 AK028345
 AK028345.1 GI:26390423
 HTCC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning

(gtcag): Oligo-dT primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected for average
 insert size 2.5 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

ORIGIN

Query Match 52.3%; Score 540.8; DB 12; Length 732;
 Best Local Similarity 99.5%; Pred. No. 0.015;
 Matches 543; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 QY 1 ATGAAACCATCCAGCAAAATGCAATTTCTTCTTGGCAATCTTACGGGGCTG 60
 Db 188 ATGAAACCATCCAGCAAAATGCAATTTCTTCTTGGCAATCTTACGGGGCTG 247
 QY 61 GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCGAGGAGATGCCACCTTCCCAA 120
 Db 248 GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCGAGGAGATGCCACCTTCCCAA 307
 QY 121 GCTATGGAACAAGTGCAGTCCCGGAGGAGAGCGCCACCTCAGGTGCATTTGAC 180
 Db 308 GCTATGGAACAAGTGCAGTCCCGGAGGAGAGCGCCACCTCAGGTGCATTTGAC 367
 QY 181 AACCGGGTCAACCGGGTGGCTTAAACCGAGGAGATCTCTATGCTGGGAATGAC 240
 Db 369 AACCGGGTCAACCGGGTGGCTTAAACCGAGCAGCACCCTCTATGCTGGGAATGAC 427
 QY 241 AAGTGTGCTGATCTCGCTGCTCTTCTGAGCAACACCAACGAGTACAGCATC 300
 Db 423 AAGTGTGCTGATCTCGCTGCTCTTCTGAGCAACACCAACGAGTACAGCATC 487
 QY 301 GAGATCCAGAACGTGGATGTGTATGACGAGGCGCTTACACCTGCTCGGTGAGACAG 360
 Db 488 GAGATCCAGAACGTGGATGTGTATGACGAGGCGCTTACACCTGCTCGGTGAGACAG 547
 QY 361 AACCAACCAAGACCTCTAGGTCACCTCTTGTGCAAGTATCTCCCAAAATTTAGAG 420
 Db 548 AACCAACCAAGACCTCTAGGTCACCTCTTGTGCAAGTATCTCCCAAAATTTAGAG 607
 QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCTCCTCAGCTGATCAACT 480
 Db 608 ATTTCTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCTCCTCAGCTGATCAACT 667
 QY 481 GGTAGACAGAGCCCTACGTTACTTGG-AGACACATCTCTCCCAAGCGGTGGCTTGT 539
 Db 668 GGTAGACAGAGCCCTACGTTACTTGG-AGACACATCTCTCTCCCAAGCGG-TGGCTTGT 726
 QY 540 GAGTGA 545
 Db 727 GAGTGA 732

586 QY -----TCAG-----GGGA---CT-----595
 777 Db AAAAATTACCTAAATATCTCTCAGCTTTCTTTTCATGACTTGGGAAGCTTTGTTTTC 836
 596 QY -----GAGTG---CAGT-GC---CTCCATG---AC-----G-TG 621
 837 Db AACTGAAGGAAGAGTGTGTGAGTAGCTTTTGTGTGATGATAGTAACCTGTGTGGAGATG 896
 622 QY GCGCGCGCC-----GTGTACGAGAG-GT-AAAGGTCA---CC-GTGAACCT---661
 897 Db GATGTGCGCTTTCTTATGTGGT---GGTATGTTCAG---CATGCCCTGGGAACCTTTG 952
 662 QY --AT--C-----ACCATC-----A-TTTCAGAAGCCA-----685
 953 Db ACATTACTGTATGTACTAAAGAAACCATACCTGCTTGTATTTTCAGAA---CAGTTT 1010
 686 QY AG-G-----GTA-CAGGTG---TCCCC---GTGGGACAAA-----A---GGGA---718
 1011 Db AGAAGACTGTATCTGTTGAT---CTGATGTGGGGGAAGGTGAGTGGAGTGGGGATTTG 1067
 719 QY CA---CTGCA-----GTGTGAAGC-----CTCAGCAGT---CC---745
 1068 Db CACTCTGCATGACCTTGTCTGGGTGTTTCAGCAATTGTTATTAACATCATCAGTACTACAT 1127
 746 QY C-CTCA-----GCAG---AAT-----TCC-----A 761
 1128 Db CTCTCACTAAATATGAAGGAATCTAAAGACATGGGTTCTTATCTCTTGGAAATAAA 1187
 762 QY -GTGGT-----A---CAAGGATG-----ACA-----778
 1188 Db CTGTGTCACACTTGAATTTCAAGATGGGCACAGACCATCTGATATATTACCTGTTG 1247
 779 QY -----AAA---GACTGATT---GA-----AGGAAGAA-----AGG-----803
 1248 Db CCAGCAAACTATGATTGTTTTCAGATATATACAGGAATCAAGTGTCTCCCTCAGGATTA 1307
 804 QY G-----GTGAA---AGT-----GGAACACAGACT-TTCTCT-----CAA 835
 1308 Db GAAAACACAAACGTGAACACGACTAGTAGAAATAACATATGCTGTGTGAATGTA 1367
 836 QY AACT-----CATCT-----AT-----GGG-----AAC--TA-C--ACTT 883
 1368 Db AACTAATGCATCTCAAGAAGACAGGAGCTT-AATCTCAGTAACTTTGAGAAGGCA 1426
 864 QY TGA---CT-----AT-----GGG-----AAC--TA-C--ACTT 883
 1427 Db -GAGATCTCAAAATACAAAATTCCTCTCCCTGAGAAGGGAAGAAACAAATAGCAGACTT 1485
 884 QY GGTG-GCCTCCACA-AGCTGGCC--ACACCAATGC-----CAGCA---TCATG---927
 1486 Db GCTTGAAGCTTCC--CAGGCT--GCCTAGCCAGTGCAAAAATAGAAAATTTTCATGAA 1541
 928 QY -----CTATT---TGCTCAGGC---GCCGTGAGGAGTGGAGTGGTCTCTCT 1652
 1542 Db AFAAATGGAATGTACTCTCTCTTCTGCTGG---AGGCTGTG-TGTCA---AAGGT---C 1592
 961 QY AA--C--GG-CAGTCTGA-----G-GAGGG-----979
 1593 Db AAATCATGCCAGGTTGATTTCTCTCTTAGCTGTGATGGACAATCTTGTCTCTCTCT 1652
 980 QY -----CAGGC-TGCGCTGGC-----TGCTGCC 1001
 1653 Db TCCCTCCCTCCT 1710
 1002 QY TCTTCTGCTCT-TG---CA-CCT-----GC-TTCT-----CAAA---1029
 1711 Db TCTT-AGGTCTCTGCT 1769
 1030 QY -----TTTTGA 1035
 1770 Db TCCCTCTTTTA 1780

RESULT 18
 BI548566
 LOCUS

DEFINITION
 mRNA sequence.

ACCESSION
 BI548566

VERSION
 BI548566.1

KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 580)

AUTHORS
 NIH-MGC

TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
 Unpublished (1999)

COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Yoshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLML1657 row: d column: 02
 High quality sequence stop: 580.

FEATURES
 Location/Qualifiers

1..580

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5260753"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH MGC 95"

/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI), National Institutes of Health. Note: this is a NIH MGC Library."

ORIGIN

Query Match

Best Local Similarity 49.7%; Score 514.6; DB 12; Length 580;

Matches 518; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY - ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTGGGCAATCTTCACTGGGGCTG 60

Db 60 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTGGGCAATCTTCACTGGGGCTG 119

QY 61 GCTGCTGTCTCTTCCCAAGGAGTGCCTGTGGCAGGAGATGCCACCTTCCCAAA 120

Db 120 GCTGCTGTCTCTTCCCAAGGAGTGCCTGTGGCAGGAGATGCCACCTTCCCAAA 179

QY 121 GCTATGGAC-AACTGACGGTCCCGCAGGGGAGAGGCCACCTCAGGTGCTACTATGA 179

Db 180 GCTATGGACAACTGACGGTCCCGCAGGGGAGAGGCCACCTCAGGTGCTACTATGA 239

QY 180 CAACCGGCTACCCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTATGCTGGGAATGA 239

Db 240 CAACCGGCTACCCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTATGCTGGGAATGA 299

QY 240 CAAGTGTGCTGTGATCTCTCGGTGGTCTTCTGAGCAGACCCCAACCGCAGTACAGCAT 299

Db 300 CAAGTGTGCTGTGATCTCTCGGTGGTCTTCTGAGCAGACCCCAACCGCAGTACAGCAT 359

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QY 300 CGAGATCCAGAACGCTGGATGTGTATCAACAGAGGCCCTTACACCTGCTCGGTGCAGACAGA 359
Db 360 CGAGATCCAGAACGCTGGATGTGTATCAACAGAGGCCCTTACACCTGCTCGGTGCAGACAGA 419
QY 360 CAACACCCCAAGACCTCTAGGCTCACTTATGTCAGAGTATCTCCCAAAATTGTAGA 419
Db 420 CAACACCCCAAGACCTCTAGGCTCACTTATGTCAGAGTATCTCCCAAAATTGTAGA 478
QY 420 GAATTTCTTCAGATATCTCCATTAATGAAGGACAAATATTAGCTCCTCAGCTGCATAGCAAC 479
Db 479 GAATTTCTTCAGATATCTCCATTAATGAAGGACAAATATTAGCTCCTCAGCTGCATAGCAAC 538
QY 480 TGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCC 521
Db 539 TGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCC 580

RESULT 19
LOCUS BM423716
DEFINITION AGENCOURT_G39987 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5516929
5', mRNA sequence.
ACCESSION BM423716
VERSION BM423716.1 GI:18319128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/Drp
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2018 row: f column: 02
High quality sequence start: 10
High quality sequence stop: 571.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5516929"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site: 1; XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Query Match 49.6%; Score 513.2; DB 12; Length 953;
Best Local Similarity 87.9%; Pred. No. 0.23;
Matches 529; Conservative 0; Mismatches 3; Indels 70; Gaps 7;
QY 467 CCTCATAGCAACTGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCCCAAG 526
Db 2 CCTG-----GGTGG-----CGATTAC--GG-----GAG 25

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QY 527 CGTTTGGCTTTGTGAGTGAAGCAATATTCTGGAATTCAGGGCATCACCOCGGAGCAGT 586
Db 26 -GTTTGGCTTTGTGAGTGAAGCAATATTCTGGAATTCAGGGCATCACCOCGGAGCAGT 84
QY 587 CAGGGGACTACAGTGCAGTGCCTCCAATGACGTGGCCGCGCGGTGCTAGCGAGAGTAA 646
Db 85 CAGGGGACTACAGTGCAGTGCCTCCAATGACGTGGCCGCGCGGTGCTAGCGAGAGTAA 144
QY 647 AGGTCAACCTGAATATCCACCATACATTTCAGAGGCCAAGGGTACAGTGTCCCGGTGG 706
Db 145 AGGTCAACCTGAATATCCACCATACATTTCAGAGGCCAAGGGTACAGTGTCCCGGTGG 204
QY 707 GACAAAAGGGGACACTGTCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCACAGTGT 766
Db 205 GACAAAAGGGGACACTGTCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCACAGTGT 264
QY 767 ACAAGGATGACAAAAGACTGATTGAAGGAAAGAGGGGTGAAAACACACACTT 826
Db 265 ACAAGGATGACAAAAGACTGATTGAAGGAAAGAGGGGTGAAAACACACACTT 324
QY 827 TCCTCTCAAAACTCATCTTCTCAATGTCTGACATGACTATGGGAACATACATTGCG 886
Db 325 TCCTCTCAAAACTCATCTTCTCAATGTCTGACATGACTATGGGAACATACATTGCG 384
QY 887 TGGCTTCCAAACAAGCTGGGCCACACCAATGCCAGCATCATCTATT----- 933
Db 385 TGGCTTCCAAACAAGCTGGGCCACACCAATGCCAGCATCATCTATTGGAAGTGAATACTA 444
QY 934 -----GGTCCAGCGCGCTGAGCGAGTGGAGCAACCGCAGCTCGA 973
Db 445 CAGCCCTGACCCCTTGGAAAGGTCAGGCGCGCTGAGCGAGTGGAGCAACCGCAGCTCGA 504
QY 974 GGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1033
Db 505 GGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
QY 1034 GA 1035
Db 565 GA 566

RESULT 20
LOCUS BM009450
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mRNA sequence.
ACCESSION BM009450
VERSION BM009450.1 GI:16523804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/Drp
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1921 row: 1 column: 16
High quality sequence stop: 659.
FEATURES
Location/Qualifiers
1..661
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/mol_type="mRNA"
/db_xref="taxon:9606"

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/clones="IMAGE:5443743"
/tissue_type="amelanotic melanoma, cell line"
/lab_hosts="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

```

ORIGIN

```

Query Match 48.7%; Score 503.7; DB 12; Length 661;
Best Local Similarity 93.9%; Pred. No. 0.11;
Matches 508; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 528 GGTGGCTTTGTGAGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTC 587
Db 1 GGTGGCTTTGTGAGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTC 60
QY 588 AGGGGACTAGAGTCAGTGCCTCCCAATGACGTGGCGCGCGCGTGTACGAGAGTAA 647
Db 61 AGGGGACTAGAGTCAGTGCCTCCCAATGACGTGGCGCGCGCGTGTACGAGAGTAA 120
QY 648 GGTCCCGTGAACTATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGG 707
Db 121 GGTCCCGTGAACTATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGG 180
QY 708 ACAAAGGGGACATGTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 767
Db 181 ACAAAGGGGACATGTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 240
QY 768 CAGGATGACAAAGACATGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 827
Db 241 CAGGATGACAAAGACATGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 300
QY 828 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGATATGGAACTACATTCGCT 887
Db 301 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGATATGGAACTACATTCGCT 360
QY 888 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTT----- 933
Db 361 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTTGAAGTGAAGAACTAC 420
QY 934 -----GGTCCAGGCGCGTTCAGCGAGGTGAGCAACGGCAGTCGAG 974
Db 421 AGCCCTGACCCCTTTGGAAGGTCAGGCGCGCTCAGCGAGGTGAGCAACGGCAGTCGAG 480
QY 975 GAGGCGAGGCTGGCTGTGGCTGTGCTTCTTCTGCTTTCGCTTTCGCTTTCGCTTTCGCT 1034
Db 481 GAGGCGAGGCTGGCTGTGGCTGTGCTTCTTCTGCTTTCGCTTTCGCTTTCGCTTTCGCT 540
QY 1035 A 1035
Db 541 A 541

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RESULT 21
BM807426
LOCUS
DEFINITION
  AGENCOURT 6581928 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471935
  5', mRNA sequence.
ACCESSION
  BM807426
VERSION
  BM807426.1 GI:19124249
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1033)
  NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS

```

TITLE JOURNAL COMMENT

```

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1981 row: c column: 08
High quality sequence stop: 639.

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FEATURES source

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1..1033
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  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH_MGC_41"
  /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
  EcoRI; cDNA made by oligo-dT priming. Directionally cloned
  into EcoRI/XhoI sites using the following 5' adaptor:
  GGCAGGAG(G). Library constructed by Ling Hong in the
  laboratory of Gerald M. Rubin (University of California,
  Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
  Superscript II RT (Life Technologies). Note: this is a
  NIH_MGC Library."

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ORIGIN

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Query Match 48.5%; Score 501.7; DB 12; Length 1033;
Best Local Similarity 93.9%; Pred. No. 0.64;
Matches 506; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 530 TTGGCTTTGTGAGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAG 589
Db 1 TTGGCTTTGTGAGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAG 60
QY 590 GGGACTAGAGTCAGTGCCTCCCAATGACGTGGCGCGCGTGTACGAGAGTAAAGG 649
Db 61 GGGACTAGAGTCAGTGCCTCCCAATGACGTGGCGCGCGTGTACGAGAGTAAAGG 120
QY 650 TCACCGTGAACTATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGGAC 709
Db 121 TCACCGTGAACTATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGGAC 180
QY 710 AAAAGGGGACATGTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTACA 769
Db 181 AAAAGGGGACATGTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTACA 240
QY 770 AGGATGACAAAGACATGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTTCC 829
Db 241 AGGATGACAAAGACATGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTTCC 300
QY 830 TCTCAAACTCATCTTCTTCAATGTCTTGAACATGATATGGAACTACATTCGCTATTTT 889
Db 301 TCTCAAACTCATCTTCTTCAATGTCTTGAACATGATATGGAACTACATTCGCTATTTT 360
QY 890 CTTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTT----- 933
Db 361 CTTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTTGAAGTGAAGAACTACAG 420
QY 934 -----GGTCCAGGCGCGTTCAGCGAGGTGAGCAACGGCAGTCGAGGA 976
Db 421 CCGTGAACCCCTTTGGAAGGTTCCAGGCGCGTTCAGCGAGGTGAGCAACGGCAGTCGAGGA 480
QY 977 GGGCAGGCTGGCTGTGGCTGTGCTTCTGCTTCTGCTTTCGCTTTCGCTTTCGCTTTCGCT 1035
Db 481 GGGCAGGCTGGCTGTGGCTGTGCTTCTGCTTCTGCTTTCGCTTTCGCTTTCGCTTTCGCT 539

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RESULT 22

BM809227
 LOCUS
 DEFINITION
 AGENCOURT 6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 1083)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: DCTD/DP

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1971 row: h column: 14
 High quality sequence stop: 656.
 Location/Qualifiers
 1. 1083

FEATURES
source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5468221"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 41"
 /note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 48.3%; Score 500.1; DB 12; Length 1083;
 Best Local Similarity 93.7%; Pred. No. 0.85;
 Matches 505; Conservative 0; Mismatches 1; Indels 33; Gaps 1;
 QY 530 TTGGCTTTGTGAGTGAACGAAATCTTGAATTCAGGCGATCACCCGGAGCGTCAG 589
 Db 1 TTGGCTTTGTGAGTGAACGAAATCTTGAATTCAGGCGATCACCCGGAGCGTCAG 60
 QY 590 GGGACTACGAGTGCAGTGCCTCCAACTACGTCGGCGCCCGTGGTACGGAGTAAGG 649
 Db 61 GGGACTACGAGTGCAGTGCCTCCAACTACGTCGGCGCCCGTGGTACGGAGTAAGG 120
 QY 650 TCACCGTGAATATCCACCAATACATTTCAAGCCAGGGGTACAGGTGTCCCGTGGAC 709
 Db 121 TCACCGTGAATATCCACCAATACATTTCAAGCCAGGGGTACAGGTGTCCCGTGGAC 180
 QY 710 AAAAGGGGACATGTCAGTGTGAAGCCTCAGACGTCCCTCAGCAGATTCAGTGGTACA 769
 Db 181 AAAAGGGGACATGTCAGTGTGAAGCCTCAGACGTCCCTCAGCAGATTCAGTGGTACA 240
 QY 770 AGGATGCAAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCC 829
 Db 241 AGGATGCAAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCC 300
 QY 830 TCTCAAACTCATCTTCTTCAATGTCTTGAACATGACTATGGGAACTACACTTGGGTGG 889
 Db 301 TCTCAAACTCATCTTCTTCAATGTCTTGAACATGACTATGGGAACTACACTTGGGTGG 360

QY 890 CCTCCAAAGCTGGCCACACCAATGCGAGCATCATCTATTT----- 933
 Db 361 CCTCCAAAGCTGGCCACACCAATGCGAGCATCATCTATTTCAAAGTGAATACTACAG 420
 QY 934 -----GTTCCAGGCCCTTCAGGAGGTGAGCAACGGACGTCGAGGA 976
 Db 421 CCCTGACCCCTTGAAGAAGTCCAGGCCGTCAGGAGGTGAGCAACGGACGTCGAGGA 480
 QY 977 GGGCAGGCTGCTGCTGCTGCTCTTCTGCTGCTTTCGACCTCTCTCAAAATTTGA 1035
 Db 481 GGGCAGGCTGCTGCTGCTGCTCTTCTGCTGCTTTCGACCTCTCTCAAAATTTGA 539

RESULT 23

BI755360 849 bp mRNA linear EST 25-SEP-2001
 603024964F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195750 5',
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 849)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11489 row: o column: 15
 High quality sequence stop: 848.
 Location/Qualifiers
 1. 849

FEATURES
source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5195750"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dr
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 48.3%; Score 499.6; DB 12; Length 849;
 Best Local Similarity 75.3%; Pred. No. 0.35;
 Matches 622; Conservative 0; Mismatches 118; Indels 86; Gaps 43;
 QY 2 TGAAGA--ACCATCCAGC--CAAAATGACAAATTCATCTTTGGGCAATCTTCAGGGG 57
 Db 65 TGAGAGACCC--GCAGCGTC--GAGATGTACCATCTGCTCTCTCTCTCGGG 121
 QY 58 ----CTG-GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCAGCGAGATGCCACT 112
 Db 122 ACAACTGCCCTGCTT-----TCATCCAGGAGTCCCGTGGCAGCGAGATGCCACT 176
 QY 113 TCCCAAGACTATGGACAACTGACGTCCTCCGAGGGGAGAGCCGCCCTCAGGTGCA 172


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QY 692 CA--GGTG-TCCCGTGGGCAAAAG--GGGACACTCAGTGTGAAGCCTCAGCAGTCCCC 747
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QY 748 TCAG-CAGAAATTC--CAGTGGTACAGGATGACAAAGACTGATTCG---A-GGAAAGAA 800
Db 807 GCAGCCGACTTCTTC--TGTACAGGAGAGACAAAGGCTGAGTGATTCATGGAGG-- 862
QY 801 AGGGGTGAAGT---GGAA---AACGAGAC 823
Db 863 -GGGGTCAAAAGTAGAGGAAACCCGAGAGAC 890

RESULT 25
LOCUS BM556708
DEFINITION AGENCOURT_6578223 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5467479
5', mRNA sequence.
ACCESSION BM556708
VERSION BM556708.1 GI:18798153
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1138)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTP/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLCM1969 row: i column: 16
High quality sequence start: 8
High quality sequence stop: 517.
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/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
source
Query Match 47.7%; Score 494.1; DB 12; Length 1138;
Best Local Similarity 86.1%; Pred. No. 1.5;
Matches 520; Conservative 0; Mismatches 11; Indels 73; Gaps 12;

QY 467 CTTGCATAGCACTGGTAGACGAGCCTACGGTACTTGGAGACACATCTCTCCCAAG 526
Db 3 CCTG-----GGT-----G-GC-----GTT-CTCG-----CAC-----GAG 26
QY 527 CGGTTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGCATCACCCGGAGCAGT 586
Db 27 -GGTTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGCATCACCCGGAGCAGT 85

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QY 587 CAGGGGACTACAGTGCAGTGCCTCCAATGACGTGGCCGCGCCGCTGGTACGGAGATAA 646
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QY 647 AGGTCAACCGTGAACACTATCCACCATACATTTCAAGAGCCAAAGGTTACAGGTGTCGCCGTGG 706
Db 146 AGGTCAACCGTGAACACTATCCACCATACATTTCAAGAGCCAAAGGTTACAGGTGTCGCCGTGG 205
QY 707 GACAAAGGGGACACTCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGT 766
Db 205 GACAAAGGGGACACTCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGT 265
QY 767 ACAAGGATGACAAAGACTGATTGAAGAGAAAGAGGGGTGAAGTGGAAAAACACACTT 826
Db 265 ACAAGGATGACAAAGACTGATTGAAGAGAAAGAGGGGTGAAGTGGAAAAACACACTT 325
QY 827 TCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACACTTCG 886
Db 326 TCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACACTTCG 385
QY 887 TGGCCTCCAAAGCTGGGCCACACCAATGCAGCATCATGCTATTT----- 933
Db 386 TGGCCTCCAAAGCTGGGCCACACCAATGCAGCATCATGCTATTTGAAGTGAAGAACTA 445
QY 934 -----GGTCCAGGCGCGTCAGCGAGTGTGAGCAACCGCAGCTCGA 973
Db 446 CAGCCCTGACCCCTTGGAAAGTTCAGGCGCGTCAGCGAGTGTGAGCAACCGCAGCTCGA 505
QY 974 GGAGGCGAGGTGGCTGTGGCTGTGGC-TCT-TCTGGTCTTGACCTGCT-TCTCAAAAT 1030
Db 506 GGAGGCGAGGTGTGATCTGTGGCTGTGGCTTCTCCTCGGCTGGCAGCATGCTGTCCCACT 565
QY 1031 TTTG 1034
Db 566 CTTG 569

RESULT 26
LOCUS AK030681
DEFINITION Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
library, clone:5430428I19 product:LTMBIC SYSTEM-ASSOCIATED MEMBRANE
PROTEIN PRECURSOR (LSAMP) homolog [Rattus norvegicus], full insert
sequence.
ACCESSION AK030681
VERSION AK030681.1 GI:26081944
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

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TITLE	RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2768)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/
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	/clone="5430428119"
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	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="6 days neonate"
misc_feature	341..1358
	/note="LIMBIC SYSTEM-ASSOCIATED MEMBRANE PROTEIN PRECURSOR (LSAMP) homolog [Rattus norvegicus] (SWISSPROT Q62813, evidence: FASTY, 100%ID, 90.5length, match=918) putative"
polyA_signal	2747..2752
	/note="putative"
polyA_site	2768
	/note="putative"
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Best Local Similarity	60.7%; Pred. No. 72;
Matches 718; Conservative	0; Mismatch 170; Indels 295; Gaps 103;
QY	7 ACCA--TCCAGCCAAAATG--CACAAAT--TCATATCTTTGGGCAATCTCA-----C 53
	321 ACCAATC--GCGA-----GGCCACCATGGTC-----GGG-AGAGTTACGCCGATC 365
QY	54 GG-----G--GCTGG-----CTGCTCTGTGTCTCTT--CCA-AGAGTGGCCC 90
Db	
	366 GGAAACAGTTGCGCGTGGTCTTACTGAGACTGCTCTGCCT-TCTTCCCACAGAGCTGCC 424
QY	91 G-TGGCGCAGGAGATGCCACCTTCCCAGAACTATGGCAACGTTGACGTCGGCAGGG 149
Db	
	425 GTTTCGACGCTGGAT-----TTTAAACCGAGC-ACGGACAACATCACCGTGACAGGG 478
QY	150 GGAGAGCGCCACCTCAGGTGCATAT--T-----GACAAACCGG--TCACCCGGGTGGC 200
Db	
	473 GGACACGGCCATCTTCAGGTG--TGTGTAGAAGACAA-----GAATCA--AGAGTGGC 529
QY	201 CTGGCTAAACCGC-----AGCACCATCTTATGCTGGGAATGACAAAGTGGTCTGGATCC 257
Db	
	530 CTGGTTGAACCGCTCTGGCATCATCTTC-----GCTGGACATGACAAAGTGGTCTTGACCC 586
QY	258 TCGCGTGTCTCTCTGAGC-----AA-CACCAACAGC-----AGTACAGCAT-CGAGAT 305
Db	
	587 TCG-----GGT-----TGAGCTGGAGAAGCGCC-----ATGCTCTGGAATACAGCGCTCGCA-AT 634
QY	306 CCAGAACCTGGATGTGTATGACGAGG--CCCTTACACCTGCTCGTGCAGACAGACACAC 363
Db	
	635 CCAGAAAGTGGATGTCTATGATGAAGATCC--TACACATGCTCAGTTTCAGAC--AC-AG 689
QY	364 CA-----CCAAAGACCTCTAGGTGCC-----ACCTCATTTGTGCAAGTATCTCCCAA-A 412
Db	
	690 CATGAGCC--AAGACCTC-----CCAAGTTTACTTGTATCGTCAAGT-TCCACCAAGA 741
QY	413 T-TGTAGAGATTCTTTCAGATATCTCCATTAATGAGGACAAATATAGCTCACCTGCG 471
Db	
	742 TCTCCA-ACATCTCTCGATGTCACTGTGAATGAGGACCAATGTAACCTCGTGTGTC 800
QY	472 ATACCAACTGGTAGACAGACGCTACCGTT---ACTTGGAGACACATCTCTC-CCA---- 523
Db	
	801 ATGGCCAATGGCGCCCTGAACCT---GTTATCACTTGGAGACAC--CTTACACCATAG 855
QY	524 -AAGCG-GTTGGCTTTGTGA--GTGAAGACGAATATCTTGGAAATTCAGGCGCATCACCCGG 579
Db	
	856 GAAGAGAATT-----TGAAGGAGAAGAAATATCTGGAGATCTTAGGCATCACCCAGG 908
QY	580 GAGCAGTTCAGGGGACTACAGTCAAGTGCCTCCAAATGACGTGGCGCGCCCGTGGT---A 636
Db	
	909 GAACAGTCAGGCAATATGATGCAAGCTGCCAACAGGTTCTCTCGCGGATGTCTCAA 968
QY	637 CGGAGAGTAAAGTTCACCGTGAACATATCCACCATACA-TTTC-CAAAG-CCAAG-GGTAC 692
Db	
	969 C--A-AGTCAAGGTCACTGTGNACTATCCACC---CACTATCAGGAGTCCAGAGCAAC 1022
QY	693 --AGGTGTC--CCGTGGGACAAAGGG--GACA--CTGC-----AGTGTGAAGCCTCAGC 740
Db	
	1023 GAAG-----CCACC-----ACA-----GGACGACAAGCTTCCCTCAAATGTGAAGCCTCAGC 1069
QY	741 AGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAAGACTGATTGAAGGAAG-- 798
Db	
	1070 GGTGCTGACCTGACCTTGTGATGTTGATACCGGATGACACCAG---GAT--AA--ACAGTG 1122
QY	799 -AAAGGG--GTGAAGTGGAA-A--ACAGA---CCTTTCTCTCAAACTCA---T--CT 844
Db	
	1123 CAAATGCGCTTGAGATT--AAGAGCACTGAGGCGCAGTCTC-C-----CTGACGGTGAC- 1174
QY	845 TCTTCAATGCTCT---GAACATGACTATGGGAACATACCTTCGCTGGCTCCAAAGC 901
Db	
	1175 ----CAATGTCACTGAGAAC---ACTATGGCAACTATATACCTGTGTGGTCCCAACAGC 1227
QY	902 TGGGCCACCAATGCGCAGCATCATGCTATTTGGTCCAGCGCC--GTCAGCAGGTGAG 959
Db	
	1228 TCGGTGTCAACCATGCGCAGCTAGTCT-TTT-----CAGAC-CCGGGTC-----GGTAG 1276
QY	960 -----CAACGGCA--CGTCGAGGAGGCGAGGTG--CGT-----C--TGGCTCT-----G 999

Query Match	46.4%	Score 479.8	DB 29	Length 1017
Best Local Similarity	61.7%	Prod. No. 2.4		
Matches 709	Conservative 0	Mismatches 173	Indels 267	Gaps 101
QY	22	ATG-C--ACAATCTATCTC--TTGGGCAATC--TT--CACGG--GCTG-G-CTG 64		
DB				
	1	ATGGTCGGAGAGTTC-AGCCGATCG--AAACAGTTGCCGTGGTCTTACTGAGACTG 57		
QY	65	CTCTGTGTCCTTT-CCA-AGGAGTGCCTGTCGCGAGCGAGAGATGCCACCTTCCCAAAGC 122		
DB	58	CTCTGCT-TCCTCCCAAGAGACTGCCCGTTCGACGGTGGAT-----TTTAAACGAGGC 111		
QY	123	TATGGACAAGCTCACGGTCCGGCAGGGGGAGAGCGCACCTCAGTGTCATAT--T--- 177		
DB	112	-ACGGACAACATCACCGTGGACAGGGGGACACGGCCATCTCAGGTG---TGTGTTAGA 167		
QY	178	-GACAAACCGGG---TC---ACCCGGGTGGCTCGCTTAAACCGC---AGCACCATCTCTTA 227		
DB	168	AGACAA-----GAACTCAAAA-----GTGGCTGGTTGAACCGCTTGGCATCATCTTC-- 216		
QY	228	TGCTGGGAATGACAAGTGGTGCTTGATCTCTCGCTGGTCTTCTGAGC-----AA-CAC 281		
DB	217	-GCTGGACATGACAAGTGGTCTCTGACCTCG-----GGT-----TGAGTCGGAGAAGCGC 267		
QY	282	CCAAACGC-----AGTACAGCAT-CCAGATCCAGAACGTGGATGTGTATGACGAGG--C 333		
DB	268	C---ATGCTCTGGAATAAGCTCCG-ATCCAGAAAGTGGATGTCTATGATGAAGATC 323		
QY	334	CCTTACACCTGCTCGGTGGAGACAGAACCA-----CCCAAAGACCTCTAGGGTCC--- 385		
DB	324	C--TACACATGTCTAGTTGAGAC--AC-AGCATGAGCCC-AGACCTC-----CCAAGT 371		
QY	386	--ACCTCATTTGTGCAAGTATCTCCAAA--AT--TGTAGAGATTCTTTCAGATATCTCCATT 441		
DB	372	TTACTTGTATCGTACAAGT--TCCACCAAGATCTCA-ACATCTCTCGGATGTCACTGTG 429		
QY	442	AATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTGTAGACCAGAGCTCAGGTT 501		
DB	430	AATGAGGGCAGCAATGTAAACCTGGTGTGCTATGGCCATGGCGGCCCTGAACCT---GTT 486		
QY	502	---ACTTCGAGNACATCTCTC-CCA-----AAGCG--TTGGCTTTGTGA--GTGAAGAC 549		
DB	487	ATCACCCTGGAGAC--CTTACACCACTAGGAAGAGAATT-----TGAAGGAGAAGAA 537		
QY	550	GAATATTGGAAATTTCAGGGCATCACCGGAGCAGTCAAGGGACTACGAGTGCAAGTCC 609		
DB	538	GAATATCTGGAGATCTTAGGCATCACCAAGGACAGTCAAGGCAATATGATGTGCAAGCT 597		
QY	610	TCCAATGAGTGGCGCGCCGTGGT---ACGGAGGTAAAGGTCACCGTGAACCTATCCCA 666		
DB	598	GCCAACGAGGTCTCTCTCGCGCGATGTCAAAC--A-AGTCAAGGTCACCTGTGAACCTATCCA 654		
QY	667	CCATACA--TTTCA-GAAG-CCAAG-GGTAC--AGGTGTCC--CCGTGGGACAAAAGGG--G 717		
DB	655	CC---CACTATCAAGGATCGAGAGCAACGAAG-----CCACC-----ACA---GGACG 698		

Qy	9	CATCCAGCCAAA-----ATGCAC---AA-TT-----CTATC-----TCT- 39
Db	1	CGTCGG-----AATTCGGGATGTTGGGGAGTGTGGCTGTGGAATGGGGGTCTG 56
Qy	40	TGGGCA-ATCTTC-----A-----CGGG-----CT--GGTGTCTGTGT 72
Db	57	TGGGTACCTGTTTCTGCCCTGGAAGTGCCTCGTGTCTCTCAGGCTG--CTGT-T 113
Qy	73	CTCTTT-----CCA-AGAGATGCCGTGCGCAGCGGAGATGCCACCTTCCCAAAGCTATGG 127
Db	114	C-CTTGTACCCACAGAGATGCCGTGCGCAGCGGAGATGCCACCTTCCCAAAGCTATGG 172
Qy	128	ACAACGTGACGATCCGGCAGGGGGAGAGCCACCTCAGGTGCATATTTGACAAACCGGG 187
Db	173	ACAACGTGACGATCCGGCAGGGGGAGAGCCACCTCAGGTGCATATTTGACAAACCGGG 232
Qy	188	TCACCGGGTGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGT 247
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Qy	248	GCTCGGATCCTCGCTGGTTCCTCTTGAGCAACACCCCAAACGAGATACAGATCGAGATCC 307
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Db |||||
QY 368 CAAAGACCTCTAGAGTCCACCTCATTTGTGCAAG-----T-----A 402
Db |||||
QY 413 CAAAGACCTCTAGAGTCCACCTCATTTGTGCAAGTAGGTGGGGGGCTTGGGGGGAGA 472
Db |||||
QY 403 TCT--C--CCA-----AAA---TT---GTAGAGATTTC--TCAGATATCTCCATTAA 443
Db |||||
QY 473 TCTGCTGGCCAGCCTCGAAGCCCTCAGGTAAAGTTTGTCTCTGAT--CCTC----- 525
Db |||||
QY 444 TGAAGGAACA---AT-A--TTAGCCTCACCTGCATNA--GCAACTGTTAGACAGAGCCTAC 497
Db |||||
QY 526 -----AACAGATGAGTTATCCTTA--TTC-TAGCATCTGG-GGTCCAG----- 567
Db |||||
QY 498 GGTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG-AGT--GAAGACGATA 554
Db |||||
QY 568 -----GG---CACATTCT-----GGTTGTCATTTGCAGTTAGAAG----- 601
Db |||||
QY 555 CTTGGAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCRA 614
Db |||||
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Db |||||
QY 615 TGAGTGGCCGCGCCCGTGTAC--GGAGAGTAAAGT-----CA-----CCGTG 657
Db |||||
QY 625 TGA-----GTGGAAGTACGA-ATT-----GTTTTTTTCATTTTGTTC-- 663
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Db |||||
QY 664 AA-TA-----ATATATTTCTCAGGA--AATTATCTTGA-ATTATGCTCTTCC--T 710
Db |||||
QY 705 GGGACAAAAGGGGACACTGCGTGTGAAGCTCAGCAGTCCCTCAGCAG-----AATTCC 760
Db |||||
QY 711 GG-----CT---TTT---TTC-----TCCCT-A--AGTTTAAAT-- 737
Db |||||
QY 761 A---GTGTACAGGATGACAAAGACTGATTGAAGGAAGAAAG---GGTGAAAGTGG 814
Db |||||
QY 738 ATTTTGGT--TTGGTG-----G--TTTTTG-----GTTGGGT---TTGG 772
Db |||||
QY 815 AAAACAGACCTTTCTCTCAAACTCATCTCTTCAATGCTCTGAACATGACTATG-GG 873
Db |||||
QY 773 -----TTTTGGTTTAAATTT--TCTTC--CAAT--TC-C---CAAGA--ATGTGG 811
Db |||||
QY 874 AACTACACTTGGTGGCCCTCCAAAGCTGGGCCACAC-----CAATGCCAGCATCATGCT 929
Db |||||
QY 812 --TTA---TG-GT---T-AA-AA-C---CCAGACTTTTAAAGGCC-----CT 843
Db |||||
QY 930 ATTTGCTCCAGCGCGCTCAGCGAGGTGAGCAACGCGAGCTCGAGAGGGCAGGCTGCGT 989
Db |||||
QY 844 TTTTGG-----A---A---AG-AAC-----AGGGA-----T 863
Db |||||
QY 990 CTGGC--TGCTGCCCTCTCTGCTCTTGACCTGCTCTCAAAATTTGA 1035
Db |||||
QY 864 -TGGCCATG-TCCCCCCCC-----CCCCAGC--C-C---TTAA 894
Db |||||
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Search completed: May 28, 2004, 21:07:59
Job time : 2999.63 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:14 ; Search time 4693 Seconds
(without alignments)
3177.073 Million cell updates/sec

Title: US-10-017-084a-523

Perfect score: 2408

Sequence: 1 MKTIQPMNSISWALFTGL.....RRAGCVMLPLVLVLLKLF 344

Scoring table: BLOSUM30
Xgapop 1.0 , Xgapext 0.1
Ygapop 1.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=GenEmbl -QFT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum30 -TRANS=human40.cdi -LIST=100
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-FGAPEXT=7 -YGAPOP=1 -YGAPEXT=0.1 -DELOP=6 -DELEXT=7

Database :

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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2408	100.0	1679	6	AX358872 Sequence
2	2408	100.0	1679	6	AX362365 Sequence
3	2408	100.0	1679	6	AX403748 Sequence
4	2408	100.0	1679	6	AX454470 Sequence
5	2408	100.0	1679	6	AX464242 Sequence
6	2408	100.0	1679	6	AX490948 Sequence
7	2408	100.0	1679	9	AX358331 Homo sapi
8	2316.6	96.2	1839	6	AX665342 Sequence
9	2316.6	96.2	1839	9	AF126426 Homo sapi
10	2303.7	95.7	2040	10	FNH8845
11	2274.5	94.5	1068	6	AX665344 Sequence
12	2273.3	94.4	1104	6	AX665346 Sequence
13	2272.1	94.4	1140	6	AX665348 Sequence
14	2262.1	93.9	1615	10	BC023307
15	2214.6	92.0	1410	10	AF282980
16	2167.7	90.0	1325	9	BC050716
17	2066.7	85.8	3216	5	GCCEPUI
18	2057.1	85.4	1257	5	GCCEPUI
19	2049.4	84.9	2935	12	AF271233
20	2045	84.9	2935	12	AF271618
21	1997.6	83.0	1035	5	AB011810
22	1969	81.8	1058	5	AF292935
23	1914.3	79.5	1013	5	AF292936
24	1902.1	79.0	3069	10	RATCALMA
25	1901.6	79.0	2593	4	BTBOCAM
26	1897.2	78.8	2337	10	RATCALMC
27	1888.7	78.4	2179	10	RATCALMB
28	1879.4	78.0	6380	9	HSM805672
29	1867.8	77.5	1533	5	PFNINH55A
30	1866	77.5	3110	6	AX665340
31	1860.7	77.3	1478	9	HUMOBAM
32	1856.4	77.1	1556	5	AF292934
33	1846.8	76.7	20731	9	AP004721
34	1846.8	76.7	43087	9	AP005155
35	1830.2	76.0	219249	2	AC102028
36	1792.5	74.4	186792	2	AC116523
37	1791.3	74.4	110000	2	AC110642
38	1780.6	73.9	123320	9	AP000863
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40	1777.8	73.8	93801	6	BD186121
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42	1776	73.8	251570	2	AC094463
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44	1772.9	73.6	116069	2	AP000784
45	1772	73.6	171102	2	AP002808
46	1766.3	73.4	184716	2	AC018368
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48	1764.3	73.3	15597	3	AF074901
49	1763.9	73.2	191071	9	AP004248
50	1763.2	73.2	186110	2	AC102204

51	1755.3	72.9	184716	2	AC018368	Human sapi
52	1753.9	72.8	18207	6	AX828384	Sequence
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54	1751.1	72.7	18848	4	OCV14852	Oryctolagus
55	1748.8	72.6	11673	6	AR262359	Sequence
56	1748.8	72.6	11673	6	AX305377	Sequence
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58	1746	72.5	92432	2	CNS08C9G	Sequence
59	1744.5	72.4	186110	2	AC102204	Oryza sat
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61	1743.6	72.4	11187	10	AB049473	Rattus no
62	1743.6	72.4	11453	10	AB062680	Rattus no
63	1743.5	72.4	16076	3	AB055862	Procamb
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65	1743.4	72.4	244055	8	AF469045	Hypocrea
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67	1740.4	72.3	10634	5	AF090441	Gallus ga
68	1739.9	72.3	225419	1	EC00W76	E. coli chr
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70	1738.8	72.2	15244	3	AB026845	Drosophil
71	1738.7	72.2	54502	9	AC092104	Homo sapi
72	1738.7	72.2	81940	9	HSTITIN2B	H. sapiens m
73	1738.6	72.2	12699	5	D83390	Gallus gall
74	1738.5	72.2	255090	2	AC073798	Mus muscu
75	1737.3	72.1	19160	8	AY223812	Emericell
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77	1737.1	72.1	11580	6	AX410790	Human reeli
78	1737.1	72.1	11580	9	HSU79716	Sequence
79	1737.1	72.1	11580	11	G30936	SWSS2926 Er
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82	1736.4	72.1	177855	9	AC013718	Homo sapi
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84	1735.7	72.1	102807	2	AP002773	Homo sapi
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86	1735.2	72.1	152731	10	AC144855	Mus muscu
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89	1734.4	72.0	141254	9	AF265342	Homo sapi
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91	1734.1	72.0	157235	3	AC009338	Drosophil
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93	1734	72.0	20628	4	OC0TITNR	O. cuniculus
94	1733.8	72.0	161147	10	AL672069	Mouse DNA
95	1733.8	72.0	194663	2	EX890578	Mouse DNA
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98	1733.6	72.0	220333	2	AC025886	Homo sapi
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FEATURES	Location/Qualifiers
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organism	"Homo sapiens"
mol_type	"unassigned DNA"
db_xref	"taxon:9606"

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Alignment Scores:
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Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
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US-10-017-084a-523 (1-344) x AX358872 (1-1679)

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QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	194	GCTGCTCTGTCTCTTCCAAGGAGTCCCGTGCAGCGGAGATGCCCTTCCCAAA	253
QY	41	AlaMetAspIleValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATGACCAACGTGACGGTCCGACAGGGGAGAGCGCCACCTCAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
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QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
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Db	674	AGTGAAGACCAATCTTGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG	733
QY	201	CysSerAlaSerAsnAspValAlaProValValArgValValValValValValVal	220
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QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys	260
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCCCTCAGCAGATTTCCAGTGTGTACAGGATGACAAA	913
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            /mol_type="unassigned DNA"
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Score:          2408.00      Matches:      344
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
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US-10-017-084A-523 (1-344) x AX403748 (1-1679)

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QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GTGCTCTGTGCTCTTCCAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGCAACAGTGCAGCTCCGCGAGGGGAGAGCGCCCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaThrIleLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTGTAACCGCAGCACCCTCTATGCTGGGATGAC 373
QY 81 LysTirCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTCCCTGGATCCCTCGGTGTGCTCTTCGACCAACCCCAACAGCAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACTGCTCGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGAGCTCTAGGGTCCACCTCATTTGCAAGTATCTCCCAAAATGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyValAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAATGAGGGAAACATATTAGCCTCAGCTGCATGCAACT 613
QY 161 GlyArgProGluProThrValThrTirArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAGAGCTACGGTTACTTTGAGACACATCTCTCCCAAGGGTTGGTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACGAATATCTTGGAAATTCAGGGGATCACCCGGGAGCAGTCCAGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValIleValThrValAsn 220
Db 734 TGCAGTGCCTCCATGACGTGGCGCCCGCTGGTACGGAGTAAGGTACCGGTGAAC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnThrIleAspAspLys 260
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Db 974 ATCTTCTCAATGTCCTCGAATGACTATGGAACTACACTTGGCTGCCCTCCACAG 1033
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ACCESSION AX454470
VERSION    AX454470.1
KEYWORDS   GI:21713859
SOURCE     Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS    Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Goddard,K.P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE      Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL    Patent: WO 0208284-A 55 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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US-10-017-084A-523 (1-344) x AX454470 (1-1679)

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RESULT 5
AX464242
LOCUS
DEFINITION Sequence 375 from Patent WO0140466.
ACCESSION AX464242
VERSION AX464242.1 GI:21899137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 375 07-JUN-2001;
Genentech Inc. (US)
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 Sequence 55 from Patent WO0200690.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 AUTHORS
 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
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 and Ye, W.
 TITLE
 Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
 JOURNAL
 Patent: WO 0200690-A 55 03-JAN-2002;
 Genentech, Inc. (US)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
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Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K.,
Xie, M.H., Yansua, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I., and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Alignment Scores:

Pred. No.: 8..9e-102 Length: 1679
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-10-017-084A-523 (1-344) x AY358331 (1-1679)

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RESULT 8

AX665342

LOCUS

DEFINITION

AX665342

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.:

Score:

Length:

Matches:

Conservative:

Mismatches:

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Db 625 AACCAACCAAGACCTCTAGGGTCCACTTATGCAAGTATCTCCCAAAATGTAGAG 684
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DEFINITION AF126426
ACCESSION AF126426
VERSION AF126426.1 GI:7158997
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Cloning and identification of human neurotrophin full length cDNA
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1839)
Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
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Best Local Similarity: 77.59% Mismatches: 2
Query Match: 96.20% Indels: 84
DB: 9 Gaps: 15

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 Db 97 TTAGACTCGGAGGAGTCTGCGCGCTTTTCCTCTCCCGCGCTCCCGGTCGCGCGGTT 156
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 Db 217 CGTGTGCGGTGCGCTGCGGAGTTCGGGAGATTGTGG-----CTGTCGAGATGGGG 270
 QY 19 -----GlyLeuAlaLeu-----Cys-----24
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 QY 25 ---Leuphe-----GlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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RESULT 10
 RNUI6845
 LOCUS Rattus norvegicus neurotrophin mRNA, complete cds.
 DEFINITION
 ACCESSION U16845
 VERSION U16845.1 GI:755184
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 2040)
 AUTHORS Struyk,A.F., Canoll,P.D., Wolfigang,M.J., Rosen,C.L., D'Eustachio,P.
 and Salzer,J.L.
 TITLE Cloning of neurotrophin defines a new subfamily of differentially
 expressed neural cell adhesion molecules
 JOURNAL J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
 MEDLINE 95198094
 PUBMED 7891157
 REFERENCE 2 (bases 1 to 2040)
 AUTHORS Salzer,J.L.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
 Center, 550 First Avenue, New York, NY 10016, USA
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ORIGIN

Alignment Scores:
 Pred. No.: 4,73e-95 Length: 2040
 Score: 2303.70 Matches: 326
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 Best Local Similarity: 68.49% Mismatches: 4
 Query Match: 95.67% Indels: 133
 DB: 10 Gaps: 19

US-10-017-084A-523 (1-344) x RNUI6845 (1-2040)


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Qy 116 SerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSer 135
Db 346 TCGGTGCAGACAGACACACCCAAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCT 405
Qy 136 ProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeu 155
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LOCUS AX665346 1104 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 104 from Patent WO03002765.
ACCESSION AX665346
VERSION AX665346.1 GI:29290466
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar, G.C. and Gabra, H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 104 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES
source 1..1104
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ORIGIN

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Score: 88.44% Conservative: 5
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Query Match: 94.41% Indels: 38
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RESULT 13
AX665348 1140 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 106 from Patent WO03002765.
ACCESSION AX665348
VERSION AX665348.1 GI:29290467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Sellar,G.C. and Gabra,H.
AUTHORS
TITLE Cancer
JOURNAL Patent: WO 03002765-A 106 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES
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Pred. No.: 3.54e-96 Length: 1140
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Best Local Similarity: 94.36% Mismatches: 6
Query Match: 50 Indels: 50
DB: 6 Gaps: 6

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QY      321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
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QY      341 LeuLeuLysPhe 344
Db      1126 CTTCTCAAAATTT 1137

RESULT 14
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LOCUS Mus musculus neurotrophin, mRNA (cdna clone MGC:30504
DEFINITION IMAGE:4480983), complete cds.
ACCESSION BC023307
VERSION BC023307.1 GI:23958300
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 1615)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

```

Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22389257
12477932
2 (bases 1 to 1615)
Strausberg,R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaevati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAP Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26986610.

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Alignment Scores:
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Percent Similarity: 90.16% Conservative: 10
Best Local Similarity: 87.43% Mismatches: 6
Query Match: 93.94% Indels: 30
DB: 10 Gaps: 9
US-10-017-084A-523 (1-344) x BC023307 (1-1615)

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Db 1 CGGACG---CGTGGCGCGAGTTCGGGAAGTTGTGGCTGCGAGATGGGGTCTG--- 54
QY 14 TrpAla-IlePheThrGlyLeuAlaLeu-----Cys----- 24
Db 55 TGGGTACCTGTTTC-----CTGCCCTGGAGTGCCTCGTGGTGTCTCT 99
QY 25 -----LeuPhe-----GlnGlyValProValArgSerGlyAspLarPhePr 39
Db 100 CAGGCTGCTATTCTCTTGTACCCACAGAGTGCCTGGTGGTAGCGGAGATGCCACCTTCC 159
QY 39 oLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrII 59
Db 160 CAAAGCTATCGACAACTGACGTACGTCAGGTCAGGCGGGGGAGAGCGCCACCTCAGGTGCAAT 219
QY 59 eAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuThrAlaGlyAs 79
Db 220 TGACACCGAGTACCCCGGTGGCTGGCTAAACCGCAGTACCATCTCTATGTGTA 279
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Db 280 TGACAAGTGGTGGCTAGATCTCTGTGGTCTCTCTGAGTAAACCCAGACCCAGTACAG 339
QY 39 rIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnTh 119
Db 340 CATTGAGATCCAGAAATGTGGATGTACGATGAGGGCCCTTATACCTCGGTACAGAC 399
QY 119 rAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleVa 139
Db 400 AGACAAACCCACTAAGACCTCCAGGGTCCACCTCATTTGTACAGTATCTCCAAATTTGT 459
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Db 520 CACAGGTAGACCGGAGCTTACAGTAACCTGGAGACATATTTCTCCAAAGGCGGTGGCTT 579
QY 179 eValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTy 199
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QY 199 rGluCysSerAlaSerAsnAspValAlaAlaProValValArgValValThrVa 219
Db 640 CGAGTGCAGCGCTCAACAGCAGTGGCGGACCACTGGTGTACGAAGTGAAGTCAAGTCCCGT 699
QY 219 lAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGI 239

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Db      760  GACTCTGCAGTGTGAAGCTTCCGAGTCCGCTTCAGCAGAAATTTCAATGTTCAAGGATGA 819
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Db      820  CAAAAGACTGGTGGAGAAAGAGGAGTCAAGTGGAAACAGACCTTCTCTTCAAA 879
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Db      940  CAACTGGGTGCACACCAAGCCAGCATCATGCTATTGTGTCGGGTGCTGTGAGTGGGT 999
Qy      319  lSerAenGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHi 339
Db      1000  CAAACATGGGACATCAAGGAGGCGCTGCAATTTGGCTTCTCCCTCTTCTGCTCTTACA 1059
Qy      339  sLeuLeuLeuLysPhe 344
Db      1060  CCTGCTCTCTCAAAATTT 1075

RESULT 15
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LOCUS      Mus musculus neurotrophin mRNA, complete cds.
DEFINITION
ACCESSION      AF282980
VERSION      AF282980.1 GI:12642539
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS      Kim.T.H., Choi.S.C., Kim.J., Jeon.J.W., Kim.K.D. and Lee.S.H.
TITLE      Cloning and expression of mouse neurotrophin gene in the developing
            nervous system
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1410)
AUTHORS      Kim.T.H., Choi.S.C., Kim.J., Jeon.J.W., Kim.K.D. and Lee.S.H.
TITLE      Direct Submission
JOURNAL      Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea
            University, 1,5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea

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CDS
            Alignment Scores:      5.98e-92      Length:      1410
            Pred. No.:      2214.60      Matches:      312
            Score:

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Percent Similarity: 92.26%      Conservative: 10
Best Local Similarity: 89.40%      Mismatches: 13
Query Match: 91.97%      Indels: 15
Db: 10      Gaps: 5

US-10-017-084A-523 (1-344) x AF282980 (1-1410)
Qy      3 Thrile-----Gln-----ProLysMetHisAsnSerIleSerTyrAlaIlePheThr 18
Db      8 TCTGTGGGTACTCTGTCTGGCCCT-----GGAAGTGCCTCGTGTCTGTCTCTCA 58
Qy      19 GlyLeuAlaAlaLeuCysLeuPhe-----GlnGlyValProValArgSerGlyAsp 35
Db      59 GGC-----TGCTA-TTCCTTTGATACCCACAGAGTGCCTGCGTAGCGAGAT 105
Qy      36 AlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeu 55
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Db      946  GTCAAGTGGGTCAACAATGGGACATCAAGGAGGCGAGGTGCTGATTTGGCTCTCCCTCTT 1005
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RESULT 16
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LOCUS   Homo sapiens neurotrimin, mRNA (cDNA clone MGC:60329
DEFINITION IMAGE:6166839), complete cds.
ACCESSION BC050716
VERSION   BC050716.1 GI:30047134
KEYWORDS MGC
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1325)
AUTHORS  Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klauener,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stachenko,M., Soares,M.B., Donald,M.F., Casavant,T.L.,
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          Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
          Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
          McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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          Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
          Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
          Generation and initial analysis of more than 15,000 full-length
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          Proc Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
          22388257
JOURNAL MEDLINE
PUBMED 12477932
REFERENCE 2 (bases 1 to 1325)
AUTHORS Strausberg,R.
TITLE   Submitted (08-APR-2003) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
REMARK  NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
          Email: gcaphe-remail.nih.gov
          Tissue Procurement: ATCC/DCTD/DTDP
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Center, Stanford University School of Medicine, Stanford, CA 94305
          Web site: http://www-sbpc.stanford.edu
          Contact: (Dickson, Mark) mcd@paxil.stanford.edu
          Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
          R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 110 Row: m Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7705412.
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115E-89 Length: 1325
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Score: 75.59%
Percent Similarity: 71.83%
Best Local Similarity: 90.02%
Query Match: 9
DB: 15

US-10-017-084A-523 (1-344) x BC050716 (1-1325)

QY 2 Lys-----ThrIle---Gln-----ProLysMetHisAsnSerIleSerTrpAla 15
Db 13 GAATGGGGGTCTGTGGGTACTCTTCTTCTGCCCT-----GGAAAGTGCCTCGTGTGCG 63
QY 16 IlePheThrGlyLeuAlaLeuAlaLeuCysLeuPhe-----GlnGlyValProValArg 32
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QY 33 SerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGluSer 52
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QY 53 AlaThrIleuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSer 72
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 QY 173 SerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyLeThr 192
 DB 531 TCTCCAAAGCGGTGGCTTGTGTAGTGAAGACGAATACTTTGGAAATTCAGGGCATCAC 590
 QY 193 ArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaProValVal 212
 DB 591 CGGAGCAGTACAGGGAGTACAGTGCAGTGCCTCCAAATGACGTGGCCGCCCGCTGGTA 650
 QY 213 ArgArgValIleValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGly 232
 DB 651 CGGAGGTAAAGTCAACCTGAACTATCCACCATATCTTCAAGCCAGGGTACAGGT 710
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 DB 1011 GGGAGGGCCCTCAAGGCCAGGG-TCAGAGGTTTAGCAGGTTATCAGTGGACATGGAGAGG 1069
 QY 321 -----Asn-----GlyThrSerArgAla 327
 DB 1070 GAGGAAAAAAGAGAGAGACACAGAAAGAAATGGAGAGAGAGGAGACAGAGAGAGGA 1129
 QY 328 Gly-----CysValTyrLeuLeuPro 334
 DB 1130 GAGGCGACAGAGAAAGAAAGAACAGACATACAGTTTACATGTATA-----CAA 1180
 QY 335 -----LeuLeuValLeuHis-----Leu----- 340
 DB 1181 AGTAGTATATGTATAGTATATAGTATATAAAGTAGATCTCAGAGTGGGAAAAAGAAATGA 1240
 QY 341 -----LeuLeuLysPhe 344
 DB 1241 AAAAGAAATGTTCAATGTT 1258
 RESULT 17
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 LOCUS 3216 bp DNA linear VRT 17-AUG-1999
 DEFINITION Gallus gallus CEPU gene.
 ACCESSION AJ225897
 VERSION AJ225897.1 GI:2897596
 KEYWORDS CEPU gene; neural secreted glycoprotein.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1
 Kim,D.S., Rhew,T.H., Moss,D.J. and Kim,J.Y.
 cDNA cloning of the CEPU, a secreted type of neural glycoprotein
 belonging to the immunoglobulin-like oploid binding cell adhesion

molecule (OBCAM) subfamily
 Mol. Cells 9 (3), 270-276 (1999)
 9347334
 10420985
 2 (bases 1 to 3216)
 Kim,D.
 Direct Submission
 Submitted (16-FEB-1998) Pukyong National University, Microbiology,
 599-1 Daeyeon-3dong, Nam-gu, Pusan 608-737, KOREA (ROK)
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 Alignment Scores:
 Pred. No.: 1,05e-79 Length: 3216
 Score: 2066.70 Matches: 297
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 Best Local Similarity: 31.46% Mismatches: 15
 Query Match: 85.83% Indels: 603
 DB: 5 Gaps: 42
 US-10-017-084a-523 (1-344) x GGCEPUS (1-3216)
 QY 3 Thr-----Ile----- 4
 DB 211 ACCTCTCCTCTTTTTCCTCGCGCTTCGTCGGGAAAGCTGGATTTTAAACCTCTCCTCGG 270
 QY 5 ---Gln-----Pro----- 6
 DB 271 CAGCAGCAGTGAAGTGGGGAAGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 330
 QY 7 LysMet---HisAsnSerIleSerTyrAlaIlePheThrGlyLeuAlaAlaLeuCysLeu 25
 DB 331 AAAATGCAGCAC---CCGCTCTCATGGGTGATCTTCGCGGGATGGCGGACTCCTCCTC 387
 QY 25 PheGlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnVal 45
 DB 388 TTCCAAGAGTGCCTGCGCAGGAGATGCCACCTCCCAAAAGCTATGGACACGTTG 447
 QY 46 ThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArg 65
 DB 448 ACTGTGCGCAAGGGAGAGTCCAGCTCAGTGTCTCGTGAGCAACCGCGTACCCCG 507
 QY 66 ValAlaTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAsp 85


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QY 331 ----- 331
Db 2728 ACCTGGGTTAATGAGCATCACAGTCACTCTGCAGGAAGAGTCGGTGTGAAGTG 2787
QY 332 -----LeuLeu-----Pro-----LeuLeu----- 336
Db 2788 ACAGACATTAGTTGTACCTGGCTGTGAAGCCTTCATTAGGTTGCTTAGAAAACGATCTC 2847
QY 337 -----Val----- 337
Db 2848 AGCTTCTTCCCATCGGCTTCTGTAATATGTTGGTGCACAAATGACCCCATTTTCAAGG 2907
QY 338 -----LeuHis----- 339
Db 2908 AGAGGACAGACACCTCGGGGCCACGCGCTCCATCCATGCTGGCTGCCCTGGGGACC 2967
QY 340 -----Leu-----Leu-----LeuLeu----- 343
Db 2968 CACATGGCTGGGATTGTAATCTCTGTATTGTTATGGATGAAAATCTCATGTATCCT 3027
QY 344 -----Phe 344
Db 3028 GGGACCCCATTC 3039

RESULT 18
LOCUS GCEPU1
DEFINITION G.gallus mRNA for CEPU-1.
ACCESSION 272437
VERSION 272497.1 GI:1325950
KEYWORDS Brain; CEPU-1; glycoprotein; GPI-anchor protein.
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Spaltmann, F. and Brummendorf, T.
TITLE CEPU-1, a novel immunoglobulin superfamily molecule, is expressed
by developing cerebellar Purkinje cells
J. Neurosci. 16 (5), 1770-1779 (1996)
JOURNAL 96370549
MEDLINE 877445
PUBMED 877445
REFERENCE 2 (bases 1 to 1257)
AUTHORS Brummendorf, T.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1996) Brummendorf T., Max-Planck-Institute for
Developmental Biology, Molecular Biology, Spemannstrasse 35,
Tuebingen, Germany, 72076
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1. 1257
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ORIGIN

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Alignment Scores:
Pred. No.: 8.2e-84 Length: 1257
Score: 2057.10 Matches: 284
Percent Similarity: 76.14% Conservative: 32
Best Local Similarity: 68.43% Mismatches: 20
Query Match: 85.43% Indels: 79
DB: 5 Gaps: 20

US-10-017-084A-523 (1-344) x GCEPU1 (1-1257)
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QY 5 -----Pro-----LysMet-----HisAsnSerIleSer 13
Db 64 AGGGGGAGGCACGACAGCTCCGAATATGCCCCAGGCGAAAATGCAGCAC---CCCCTCTCA 120
QY 14 TrpAlaIlePheThrGlyLeuAlaLeuCysLeuPheGlnGlyValProValArgSer 33
Db 121 TGGGTGATCTTCGCGGGATGCGCCACTCTCTCTTCCAAAGGAGTGGCCGTGGCAGC 180
QY 34 GlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAla 53
Db 181 GGAGATGCCACTTCCCCAAAGCTATGGACAAGTACTGTGCGGCAAGGGGAGAGTGCC 240
QY 54 ThrLeuArgCysThrIleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThr 73
Db 241 ACCCTCAGGTGCTCCGTGGACAACCGCGTCACCCCGCTGGCTGGCTGAACCGCAGCAGC 300
QY 74 IleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsn 93
Db 301 ATCCTCTATGTCGGGCAATGACAAGTGGTCTTGGACCCGAGGGTGGTCTCTCTGGCCAC 360
QY 94 ThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyr 113
Db 361 ACCAAACCCAGTACAGCATCCAGATCCAGACGTCGACGTGTACGATGAAGGCGCTAC 420
QY 114 ThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGln 133
Db 421 ACCGTGCTCGGCAGACAGACAATACCCCAAGACATCTCGGCTGCACCTCATTTGTGCAA 480
QY 134 ValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIle 153
Db 481 GTGTCCCGGAAATTTACCGAGACCTCTTCTGACANTCTCCATCATGAAGGTGGCAAGTC 540
QY 154 SerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSer 173
Db 541 AGCCTCACCTGTATAGCCAGCGGCGAGCCAGACCAATACCTTGGAGACACATCTCG 600
QY 174 ProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArg 193
Db 601 CCCAAAGCTGTGGGCTTCATCAGCGAGGACGAGTACTCTGGAGATCACAGGCAATCAGAGG 660
QY 194 GluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArg 213
Db 661 GAGCAGTCCGGGCGAGTACGAGTGCATGCTGCCACAGCGTGGCGGCTGTCTGCTCCAG 720
QY 214 ArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyVal 233
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QY 234 ProValGlnGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPhe 253
Db 781 CCGGTGGGGGAGAAAGGCGATCTCTGATGTGTGAAGCCCTCCGCTGTGCCCTCCGCTGACTTC 840
QY 254 GlnTTrpTyrLysAspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsn 273

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Db 841 CAGTGGTACAAAGACGACAGCGGTGGCTGAAGCAGACAGAAAGGCTGAAGTGGAAAC 900
Qy 274 ArgProPheLeuSerLysLeuLeuPhePheAsnValSerGluHisAspTyrGlyAsnTyr 293
Db 901 AAAGCGCTTCTTCCGCACTGACTTCTTCAACAGCTCTCCGAGCAGGACTACGGCAACTAC 960
Qy 294 ThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSer---IleMetLeu----- 310
Db 961 ACCTGGTGGCTCTCAACAGCTAGGAACACCAACAGCCAGCATGATCTTTATGNAGAG 1020
Qy 311 -----Phe-----GlyProGlyAlaValSerGluValSerAsn--- 321
Db 1021 ACAACAACCGCTCTGACACCTCGAAAGGCCCGGTGCGAGTGCACGAT---GGCAACAGC 1077
Qy 322 GlyThrSer---ArgArgAlaGly---CysValTrpLeu-----LeuProLeu----- 335
Db 1078 GGT---GCGTGGCGGCA---GSCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
Qy 336 Leu-----ValLeu-----HisLeuLeuLeuLys 343
Db 1132 CTCGCCCGCAGTCTGAGCCCGGCGGCCACGACCACGACAGAAAGGAGAGGAA 1191
Qy 337 -----ValLeu-----HisLeuLeuLeuLys 343
Db 1192 GAAGATGTATTCACTGTTTCTGAATAATATCAT-----AAG 1227

RESULT 19
AF271233
LOCUS
DEFINITION Synthetic construct secretory IgCEPUS-GFP fusion protein
(IgCEPUS-GFP) gene, complete cds.
ACCESSION AF271233
VERSION AF271233.1 GI:14161268
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL

1. (bases 1 to 1638)
Kim, D.-S. and Moss, D.J.
Direct Submission
Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea

FEATURES
source
gene
CDS

Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 4,43e-82 Length: 1638
Score: 2049.40 Matches: 286
Percent Similarity: 65.28% Conservative: 28
Best Local Similarity: 59.46% Mismatches: 21
Query Match: 85.11% Indels: 146
Gaps: 31
DB: 12

US-10-017-084A-523 (1-344) x AF271233 (1-1638)

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Qy 20 LeuAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPhePro 39
Db 52 ATGGCGCAGCTCTCTCTTCCAGGAGTGCCTGCGCAGGAGATGCCACCTTCCTCC 111
Qy 40 LysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIle 59
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Qy 60 AspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsn 79
Db 172 GACAAACCGCGTCAACCGCGTGGCTGGCTGAACCGCAGCAGCATCTCTATGCGGCAAT 231
Qy 80 AspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSer 99
Db 232 GACAAAGTGGTGTGGACCCGAGGGTGGTGTCTCTGCGCAACACCAACCCAGTACAGC 291
Qy 100 IleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThr 119
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Qy 120 AspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleVal 139
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Qy 140 GluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAla 159
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Qy 160 ThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPhe 179
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Qy 180 ValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlnGlnSerGlyAspTyr 199
Db 532 ATCAGCGAGGACGAGTACCTGGAGATCACAGGATCACAGGAGGAGCAGTGGGCGAGTAC 591
Qy 200 GluCysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrVal 219
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Qy 240 ThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAspAsp 259
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Qy 280 LeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsn 299
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QY 312---Gly-----Pro-----GlyAlaVal-----Ser 317
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QY 318 GluValSerAsn-----Gly-----ThrSerArgArgAlaGly----- 328
Db 1006---GTGTCGGCGAGGCGGAGGCGCATGCCACC-----TAC---GGCAGCTGACCCCTG 1053
QY 329-----Cys-----Val---Trp-----Leu-----Leu 333
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QY 333-----Leu-----ValLeu-----His---Leu----- 340
Db 1114 ACCTACGGGTGTCAGTGTCTTACGCGCTACCCCGACCATGAAGCAGCAGCACTTCTTC 1173
QY 334-----Pro-----Leu-----Leu----- 334
Db 1174 AAGTCGCGCATGCCCGAAGCTACGTCCAGGAGCGCACCATCTTCTTCAAGCAGCAGCGC 1233
QY 335-----Leu-----Leu----- 335
Db 1234 AACTACAGACCGCGCGCGAGGTGAAGTTTCAGGAGCGGACACCTGGTGAACCGCATCGAG 1293
QY 336 Leu-----ValLeu-----His---Leu----- 340
Db 1294 CTGAAGGCGATCGACTTCAAGGAGGAGCGGCAACATCTCGGGGCAAGCTGGAGTACAAC 1353
QY 341-----Leu-----Leu-----Leu----- 343
Db 1354 TACAAGCGCCACACCTATATATATGTCGCGCAGCAAGCAGAGACCGCATCAAGGTGAAC 1413
QY 344 Phe 344
Db 1414 TTC 1416

RESULT 20
AF271618 2935 bp DNA linear SYN 21-MAY-2001
LOCUS Synthetic construct secretory IgCEPUS-GFP fusion protein
DEFINITION (IgCEPUS-GFP) gene, complete cds.
ACCESSION AF271618
VERSION AF271618.1 GI:14161270
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 2935)
AUTHORS Kim,D.-S. and Moss,D.J.
TITLE Neuronal-specific secretory IgCEPUS-GFP fusion protein expression
in transfected cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2935)
AUTHORS Kim,D.-S. and Moss,D.J.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea
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Alignment Scores:
Pred. No.: 5,87e-79 Length: 2935
Score: 2045.00 Matches: 290
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Best Local Similarity: 37.28% Mismatches: 17
Query Match: 84.93% Indels: 440
DB: 12 Gaps: 46

US-10-017-084a-523 (1-344) x AF271618 (1-2935)
QY 1 Met-----Lys-----Thr-----Ile 4
Db 393 ATGCTAGCAGGGGGGAGGGGGAGAGATTACCTCATCATCGCTCGCTTGCACCAATC 457
QY 3-----Gln----- 5
Db 453 ACCACTCTCTGTCGCGGCTTCTCTGGGCGACAGGAGGGGTCTGGACCAACAGGAAGGCC 517
QY 5-----Prolys----- 7
Db 518 TTGGCCCATCCCATGTTGACCGAGCTGTATATAAGAGGCGCATCCGCCCAAGTGCAGC 577
QY 7----- 7
Db 578 TACCGGACTCAGATCTCGAGCTCAAGCTTCGAATTTCTGCAGTCGACGGTACCGCGGCGCC 637
QY 8 Met-----His-----Asn-----Ser----- 11
Db 638 CTGGCAGTCAGTGGGGGAGGAGGGGAGGACGACGAGCTCCGAATATGCCCGCAGCGAAA 697
QY 12-----IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGln 27
Db 698 ATGCAGCACCCCGTCTCATGGGTGATCTTCGCGGGATGGCGGCACCTCTCTCTCTCCAA 757
QY 28 GlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrVal 47
Db 758 GGAGTGCCCGTCGCGCAGCGAGATGCCACTTCCCAAGCTATGACACACGACTGTG 817
QY 48 ArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAla 67
Db 818 CGGCAAGGGGAGTCCACGCTCAGTGTCTCGGTGGACAAACCGGTACCCCGCGTGGCC 877
QY 68 TrpLeuAsnArgSerThrIleLeuTyraAlaGlyAsnAspLysTrpCysLeuAspProArg 87
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QY 88 ValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspVal 107
Db 938 GTGGTGTCTCTGGCCAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 997
QY 108 TyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArg 127
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Db      998  |||TACGATGAAGGCCCTTACACCTGCTCCGTGCAGACAGACAATCACCCCAAGACATCTCGC 1057
QY      128  ValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIle 147
Db      1058  |||GTGCACCTCATTTGTGAAGTGTGCGGAAATTTACCGAGATCTTCTGACATCTCCATC 1117
QY      148  AsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrVal 167
Db      1118  AATGAAGTGGCAACGTACGCTCCTCCTCATATGACCCAGCGGAGCCAGACCCCAATC 1177
QY      168  ThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTrpIleGlu 187
Db      1178  ACCTGAGACACATCTCGGCCCAAGCTGTGGCTTCATCAGCGAGACAGTACCTGGAG 1237
QY      188  IleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspVal 207
Db      1238  ATCAGGCAATCAGAGGAGCAGTCTGGCGGAGTACGAGTGCAGTGCCTCCCAACGAGGTG 1297
QY      208  AlaAlaProValValArgArgValLysValThrValAsn-----Tyr----- 221
Db      1298  GCGCGCTGCTGCTCCAGCGAGTCAAAAGTCAACGCTCAACTGTGAGTAGCTGTGGGTGTG 1357
QY      222  -----ProPro----- 223
Db      1358  GGGACAGCCCGAGGCCACATTTGTCACCCCGAGGGGATGCACCGTTACCTCCCTTTGG 1417
QY      223  ----- 223
Db      1418  TCCACACCCAGCCTGGCAGCAGCAGGTTTCCACGACAGTGTGTCTTGGCCCTTTATT 1477
QY      224  -----Tyr----- 224
Db      1478  CCCCTTTTGTGTGTTTCAAGTCTAGTCTTTTCCACCTCCTCCTCAGCTGTCTCTAT 1537
QY      224  ----- 224
Db      1538  CAACCTGAGTTTTTGCTGTGTGTGAGATGCTGTGTGATAAAGTCTCAGGGAGAGAGGG 1597
QY      224  ----- 224
Db      1598  AAGTGACGAGTAACAGGCATTCTTCGTTTGAATAAAGAGGAGAGAGAGAGAGAGAG 1657
QY      225  -----Ile-----SerGlu----- 227
Db      1658  AAAGCAGCACTGTTGTGCTCATAGACAGAAGTGAAGACCTCCAAACCCCCCGACACTC 1717
QY      228  -----AlaLys----- 229
Db      1718  CACTCTGGCCACCCCTGGAGCTTCGGGCGATCAGGGAGAGCCAAAGAGTGTGTCTCTTG 1777
QY      229  ----- 229
Db      1778  GAGGATCGAGGAGTGTGTTGGTTCGCCCATCTGCTCAGCCCTTCGGACAGAGAACA 1837
QY      230  -----Gly----- 230
Db      1838  AGAGCTGCGAGGCTGGGCATAGCTGGAGATGATTTTCTCCTCTTGGATGGGA 1897
QY      230  ----- 230
Db      1898  AAGAAAGGAGAGAGAGTGGAGGAGCCAAACCCCGAGCTCGTCTCCCAAGAGCCCA 1957
QY      231  -----ThrGlyValProValGlyGlnLysGlyThrLeuGln 242
Db      1958  CCGTACATCTCGGATCGCAAGAGCACCGTGTGCGGTGGGGAGAGAGGCGATCTGTATG 2017
QY      243  CysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspIleArgLeu 262
Db      2018  TGTGAAGCCTCGCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2077
QY      263  IleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysIlePhe 282

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Db      2078  GCTGAGGACAGAAAGGGCTGAAGTGGAAACAAAGCCCTTCTTCTCCGAGTGACTTTC 2137
QY      283  PheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGly 302
Db      2138  TTCACGCTCTCCGAGCAGGACTACGCGCAACTACACTGCTGGCTGCCAACCAG--GGG 2194
QY      303  ---His-----ThrAsnAlaSerIleMet-----LeuPhe---Gly--- 312
Db      2195  ATCCACCGCGCGGTGCGCCACCATGTGTGAGC--AAGGGGAGGAGCTGTTCAACGGGGTG 2251
QY      313  ---Pro-----GlyAlaVal-----SerGluValSer 320
Db      2252  GTGCCCATCTGTCGAGCTGGAGCGCGACGCTAAACGGCCACCAAGTTCAGC--GTGTCC 2308
QY      321  Asn-----Gly-----ThrSerArgArgAlaGly----- 328
Db      2309  GCGGAGGCGAGGGCGATGCCACC-----TAC-----GGCAAGCTGACCTGAAGTTCATC 2359
QY      323  Cys-----Val---Trp-----Leu----- 333
Db      2360  TGCACACCGCGCAAGCTGCCCGTGCCTGGCCGCCACCTCTGTGACCCACCTGACCTACGGC 2419
QY      333  ----- 333
Db      2420  GTGCAGTGTCTTCAGCGCTACCCCGACACATGAAGACGACGACGCTTCTTCAAGTCCGCG 2479
QY      334  ---Pro-----Leu----- 334
Db      2480  ATGCCCGAAGGCTACGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAG 2539
QY      335  -----Leu----- 336
Db      2540  ACCCGCGCGAGTGAAGTTCGAGGGCGACACCTCTGTGAACCGCATCGAGCTGAAGGCG 2599
QY      337  -----ValLeu---His---Leu----- 340
Db      2600  ATCGACTTCAAGGAGGAGCGCAACATCTCTGGGGCACAAAGCTGGAGTACAACTACACAGC 2659
QY      341  -----Leu-----LeuLys-----Phe 344
Db      2660  CACAACGTCTATATCATGCGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2713

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RESULT 21

AB011810 LOCUS 1035 bp mRNA linear VRT 09-JUL-1998
 Gallus gallus mRNA for CEPU-1, complete cds.

AB011810 DEFINITION

AB011810 ACCESSION

AB011810.1 GI:3298455

alternative splicing; CEPU-1.

Gallus gallus (chicken)

Gallus gallus

ORGANISM

1 (sites)

Kimura, Y., Shirabe, K., Fukushima, M., Takeshita, M. and Tanaka, H.

CEPU-1: an Immunoglobulin Superfamily Molecule, Has Cell Adhesion

Activity and Shows Dynamic Expression Patterns in Chick Embryonic

Spinal Cord

Unpublished

2 (bases 1 to 1035)

Kimura, Y., Shirabe, K. and Tanaka, H.

Direct Submission

Submitted (03-MAR-1998) Yoshihide Kimura, Kumamoto University

Graduate School of Medical Sciences, Division of Developmental

Neurobiology; 4-24-1 Kihonji, Kumamoto, Kumamoto 862-0976, Japan

(E-mail: ykimura@gpo.kumamoto-u.ac.jp, Tel: 81-96-373-5294,

Fax: 81-96-373-5292)

Location/Qualifiers

1. 1035

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

FEATURES

source

YPPYISDAKSTGVFVGQKILMCEASVPSADFOWYKDDRLAEGQKGLKVENKAFPS
RLTFFNVSEQDYGNYTCVASNQLGNTNASMILYGEQH"

ORIGIN

Alignment Scores:
Pred. No.: 8.56e-80 Length: 1058
Score: 1969.00 Matches: 273
Percent Similarity: 83.57% Conservative: 27
Best Local Similarity: 76.04% Mismatches: 19
Query Match: 81.77% Indels: 41
DB: 5 Gaps: 12

US-10-017-084A-523 (1-344) x AF292935 (1-1058)

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QY 5 Gln-----Pro-----Lys 7
Db 7 CAGCGAGTGTGGGGAAGAGGGGAGGAGCGAGCTCCGATATGCGCCAGCGGCAAA 66
QY 8 Met---HisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaLalaLeuCysLeuPhe 26
Db 67 ATGCAGCAC---CCCGTCTCATGGGTGATCTTCGCCGGGATGGCGCACTCCTCCTCTTC 123
QY 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
Db 124 CAAGGAGTGGCCGTGGCGAGGAGATGCCACCTTCCCAAAGCTATGGACAACGTGACT 183
QY 47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
Db 184 GTGGCGGAGGGGAGAGTCCACCGTCACTGAGTGCTCCGTGGCAACCGCGTCCACCGGGTG 243
QY 67 AlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspPro 86
Db 244 GCCTGGCTGAACCGCAGCAGCATCTCTATGCCGGCAATGACAAAGTGGTGTGGACCCG 303
QY 87 ArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIleGluIleGlnAsnValAsp 106
Db 304 AGGGTGTGTCTCTGGGCAACACCAACCCAGTACGATCCAGATCCAGAGCTGGAC 363
QY 107 ValTrpAspGluGlyProTyThrCysSerValGlnThrAspAsnHisProLysThrSer 126
Db 364 GTGATGATGAGGGCCCTACACTGTCTCGTGAGAGACATCATCCCAAGACATCT 423
QY 127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
Db 424 CGCGTGCACTCATTTGTCAAGTGTGCGGCAAAATTAACGAGATCTCTTCTGACATCTCC 483
QY 147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
Db 484 ATCAATGAAGTGGCAAGCTCAGCTTCACTGTGATAGTACCGGAGGAGGAGGAGTACCTG 543
QY 167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyIleu 186
Db 544 ATCACTTGAGACACATCTCGCCCAAGCTGTGGCTTCATCAGGAGGAGGAGTACCTG 603
QY 187 GluIleGlnGlyIleThrArgGluGlnSerGlyAspTyTrpGluCysSerAlaSerAsnAsp 206
Db 604 GAGATACAGGCATCACAGGAGGAGTGGCGGCGAGTACGAGTGCAGTGCCTCCAAACGAC 663
QY 207 ValAlaIleProValValArgValLysValThrValAsnTyTrpProTyTrpIleSer 226
Db 664 GTGGCGGCGCTGTCTGTCAGCGAGTCAAGTCAACCTCACTCCACCGCTCATCTCTG 723
QY 227 GluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSer 246
Db 724 GATGCGAGAGACACCGGTGTGCGGTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783
QY 247 AlaValProSerAlaGluPheGlnTrpTyTrpLysAspLysArgLeuIleGluGlyLys 266
Db 784 GCTGTGCGCTCTGCTGACTTCCAGTGTGTACAAAGACGACAAAGCGGCTGGCTGAAGGACAG 843
QY 267 LysGlyValLysValGluAsnArgProPheLeuSerLysLeuIlePheAsnValSer 286
Db 844 AAAGGGCTGAAGGTGAAACAAAGCCCTTCTTCTCCGACTGACTTTCTTCTCAACGCTCTCC 903

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QY 287 GluHisAspTyTrpGlyAsnTyThrCysValAlaSerAsnLysLeuGlyHisThrAsnAla 306
Db 904 GAGCAGGACTACGGCAACTACACCTCGCTGGCTCCACACGAGTAGGAACACCAACGCC 963
QY 307 Ser---IleMetLeuPheGlyPro-----GlyAlaValSerGluValSerAsnGly 322
Db 964 AGCATGATC---CTTATGTGTGAGCAGCAGCTGAGGG---TCT-----GGATGGGG 1008
QY 323 ThrSerArg-----ArgAlaGlyCysValTrp 331
Db 1009 ACC---CGCACAGCTTAACGGAGTGACCAACCACTGTGCAAGAGC---TGCAG-TGG 1058

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RESULT 23

AF292936 1013 bp mRNA linear VRT 24-AUG-2000
LOCUS
DEFINITION
Gallus gallus CEPU-Se alpha 1 isoform (CEPU-Se) mRNA, complete cds.

AF292936
ACCESSION
AF292936.1 GI:9887386

VERSION
AF292936.1
KEYWORDS
Gallus gallus (chicken)
SOURCE
Gallus gallus
ORGANISM
Gallus gallus

REFERENCE
1 (bases 1 to 1013)
Lodge, A.P., McNamee, C.J., Howard, M.R., Reed, J.E. and Moss, D.J.
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
2 (bases 1 to 1013)
Lodge, A.P. and Moss, D.J.
Direct Submission
Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK

FEATURES
source
1. .1013
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/tissue_type="brain"
/dev_stage="E18"
/gene="CEPU-Se"
/gene="CEPU-Se"
/gene="CEPU-Se"
/notes="IgION family protein; secreted isoform of CEPU-1"
/product="CEPU-Se alpha 1 isoform"
/protein_id="AAG01879.1"
/db_xref="GI:9887387"

ORIGIN
Alignment Scores:
Pred. No.: 5.51e-77 Length: 1013
Score: 1914.30 Matches: 264
Percent Similarity: 81.84% Conservative: 29
Best Local Similarity: 73.74% Mismatches: 18
Query Match: 79.50% Indels: 48
DB: 5 Gaps: 15

US-10-017-084A-523 (1-344) x AF292936 (1-1013)
QY 1 MetLysThr-----IleGln---ProLysMethisAsnSerIleSerTrp----- 14
Db 1 ATGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 39

QY 15 ---AlaIlePheThrGlyLeuAlaLeuCys-----LeuPhe-----Gln 27
 Db 40 CTAGTCGTC-----CTCTGCTCAGGCTCTCTCTCTGTCGCCGCA 81
 QY 28 GlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrVal 47
 Db 82 GGAGTGCCCGTGGCAGCGAGATGCCCTTCCCAAGCTATGACAACTGACTGTG 141
 QY 48 ArgGlnGlySerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAla 67
 Db 142 CGCAAGGGAGAGTGCACCGCTCAGGCTCTCGTGGCAACCGCGTACCCGCGTGGCC 201
 QY 68 TrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspProArg 87
 Db 202 TGCTGACCGCAGCAGATCTCTATGCGCAATGACAGTGTGTCTGGACCGAGG 261
 QY 88 ValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspVal 107
 Db 262 GTGGTGTCTCTGGCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 321
 QY 108 TyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArg 127
 Db 322 TACGATGAAGGGCCCTACACCTCTCGTGCACACAGCAATCACCCACAGCATCTCGC 381
 QY 128 ValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIle 147
 Db 382 GTGCACCTCATTTGTGCAAGTGTGCGCGAAATTAACGAGATCTCTTCTGACATCTCCATC 441
 QY 148 AsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrArgProGluProThrVal 167
 Db 442 AATGAAGGTGCCAAGCTCAGCTCCTCATGTCATGCCAGCGAGGAGCAGCCCAAC 501
 QY 168 ThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGlu 187
 Db 502 ACCTGGAGACACATCTCGCCCAAGCTGTGGCTTATCAGCAGCAGCAGTACTCGGAG 561
 QY 188 IleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAspVal 207
 Db 562 ATCAGAGCATCAGAGGAGCAGTGGCGGAGTACGAGTGCAGTGCCTCCACAGCAGTG 621
 QY 208 AlaAlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGlu 227
 Db 622 GCGCGCTCTGCTGCCAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 681
 QY 228 AlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAla 247
 Db 682 GCGAGAGCAGCCGCTGTCGCGTGGGCGAGAGGCGATCTGATGTGTGAGCCTCGCT 741
 QY 248 ValProSerAlaGluPheGlnTyrTyrLysAspAspLysArgLeuIleGluGlyLysLys 267
 Db 742 GTGCGCTCTGCTGACTTCCAGTGTGTACAAAGACACAGAGCGGCTGGCTGAAGGACAGAA 801
 QY 268 GlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGlu 287
 Db 802 GGGCTGAAGGTGGAACAAAGCCCTTCTTCCGACTGACTTCTTCAAGCTCTCCAG 861
 QY 288 HisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSer 307
 Db 862 CAGGACTACGGCACTACACTGTGGTGGCTCCCAACAGCTAGGAACACCAACCGCAGC 921
 QY 308 ---IleMetLeuPheGlyPro-----GlyAlaValSerGluValSerAsnGlyThr 323
 Db 922 ATGATC---CTTTATGGTGGACGACACTGAGG---TCT-----GGGATGGGAGCC 966
 QY 324 SerArg-----ArgAlaGlyCysValTyr 331
 Db 967 ---CGGACAGCTTAACGGAGTGACCACTGTGCAAGACG---TGCAG-TGG 1013

RESULT 24

RATCALMA

LOCUS

DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete CDS.

ACCESSION M88709
 VERSION M88709.1 GI:203245
 KEYWORDS cell adhesion-like molecule; opioid binding protein.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 3069)
 AUTHORS Lippman, D.A., Lee, N.M. and Loh, H.H.
 TITLE Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
 rat brain cDNA library
 JOURNAL Gene 117 (2), 249-254 (1992)
 MEDLINE 92347701
 PUBMED 1339369
 COMMENT Original source text: Rattus norvegicus (strain Simonsen ICR)
 (library: UZ) brain cDNA to mRNA.
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 /mol_type="mRNA"
 /strain="Simonsen ICR"
 /db_xref="taxon:10116"
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 /tissue_lib="UZ"
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 /rpt_unit="556..558"
 638..1654
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 /protein_id="AA40858.1"
 /db_xref="GI:203245"
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 TWRHLSVGGGFGVSEDEYLETSIDKQSGVECSALNDVAAPDVRVKIVTPYPPY
 ISKANTGVSGQKGLSCESASVPWAEFOMFKEDTRLATGLDGVRIENKGRISTLT
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 FIKF"

ORIGIN

Alignment Scores:
 Pred. No.: 7.7e-71 Length: 3069
 Score: 1902.10 Matches: 276
 Percent Similarity: 41.79% Conservative: 27
 Best Local Similarity: 38.07% Mismatches: 32
 Query Match: 78.99% Indels: 390
 DB: 10 Gaps: 43

US-10-017-084A-523 (1-344) x RATCALMA (1-3069)

QY 1 Met---Lys-----ThrIle-----GlnPro----- 6
 Db 47 ATGATAAGGCTTTGGCATGGGTATTAGTTAATTCTGCCAGGAAGCAGCTTTCTCTGTT 106
 QY 6 ----- 6
 Db 107 CTTTGTCTCTGAGACCTGCTAGGTTAGATTAGGGAAGGGCATTAGACCCCTCCCGCT 166
 QY 7 -----LysMet-----His----- 9
 Db 167 GCCACCCAGGAGCGGGTGTGCCCTCCGAGTCACACTGGCATACTCACACAAATCCAG 226
 QY 9 ----- 9
 Db 227 CAGTACTGTGCGGTGAGGGGTGCGCAAGGACGAGCTTCAACTCCCTTTGGAGTGG 286
 QY 10 -----Asn-----Ser-----IleSer 13
 Db 287 AGCCTTCCCAACAGGAAGTCTCCCGGTGTGCTCAGGAGAGTGGAGCCCAATGTGTGGCT 346
 QY 14 Trp-----Ala-----Ile-----Phe----- 17

Db	347	TTGAGGTGTGTCTGTCTGCTCCAGTGAAGATTGGTCTGATGATTTCTTACCACTTTGTGT	1409	ACTGGCCTGGATGGCTGAGAAATTGAGAAACAAGGCCGC	-----ATATCCACTTTGACT	1462
QY	18	-----Thr-----Gly-----LeuAla-----Ala 22	282	PhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeu		301
Db	407	GTATGTGCAAGGGGAAATAATCAGAGAGCGTGTCTGTCCCTGCTCCCATCTCGCGCGCT	1463	TTCTTCAATGTCTCAGAGAGGATTATGGAACTATATCTGTGTGGCCACAACAAGCTTT		1522
QY	23	Leu-----Cys-----24	302	GlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaVal	-----	316
Db	467	CTCTCTCTTCTGTCTCTCCCTCCCTTTCGAACATTGGATTAAACCTGCTCAGAAATTC	1523	GGGAACACCAATGCCAGCATCACCTGTATGGCCCTGGAGCAGTCATTGATCGGTGAAC		1582
QY	24	-----24	317	-----Ser-Glu-----ValSerAsn-----Gly-----ThrSer-----324		
Db	527	AGTACAGAGGAGCAGCTCGGTGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	1583	TCGGCCTCTAGAGCACTGGCTGTCTCTGGCTCTCAGGACCTTCTTGGCCACTTCTTC		1642
QY	24	-----24	324	-----324		
Db	587	GCACCAGCACCAGCAGGAGCTCGCGGCGCGCGCACCAAGCTCGAGATGTACCAT	1643	ATCAAGTTTGTATAGAAACCTTAGTCTCTCTGAGCATCGCTGCTTCTCCATATCACAG		1702
QY	25	-----LeuPhe-----GlnGlyValPro 30	325	-----ArgArgAlaGly-----328		
Db	647	CCGCGCTACTGGATCGTCTCTCGGCCACCACTGCCCTGCTCTTATCCAGGAGTCCG	1703	ACTTTAATCTACATGCGGAGG-----GGCAACACAGTTTGGGCTTCTTTGGTTATTTT		1759
QY	31	ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly	329	-Cys-----329		
Db	707	GTGCGCAGCGGAGATGCCCTTTCCCAAGCTATGGACAACGTGACGGTCCGCGCAGGA	1760	TTGTTCTTCTGACTGTTAGTTTTTGGTTGATTTCTGGGATTTTCAATTGATTGT		1819
QY	51	GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTyrLeuAsn	330	-----Val-----330		
Db	767	GAGAGCGCCACCTTCAGTGTACCATAGATGACGGGTCCACAGATGAGCTGGCTAAAC	1820	TTTTCTTTTTTCTGTAATGGACCGGGTTGGGGTTGGGATGGGCAGGTTTCTACCAC		1879
QY	71	ArgSerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspProArgValValLeu	331	-----Tyr-----LeuLeuPro-----334		
Db	827	CGCAGCAATCTCTACGCTGGGAATGACAAGTGTCTCATAGACCTTCGAGTGATCATC	1880	GAGTAGGATAATCAGGTATTTGGTGGGCCCCCAATGGAATATATTTCTGTCTTGGCC		1939
QY	91	LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu	335	-----LeuLeu-----336		
Db	887	TTGCTCAACACGCTACCCAGTACAGTATCATGATCCAGAAATGTGGATGTTATGACGA	1940	TTCTCTTTCTCTACTTCT		1999
QY	111	GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu	337	-----Val-----Leu-----338		
Db	947	GGTCCGTACACCTCTCTGTGACAGACAGACATCACCCCAAACTCCCGGTCCACTC	2000	TAAAGATGGCCTAAATAATGCTCCCATGACACGACCCCTGAAGGTACAACTTGGCCACAG		2059
QY	131	IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly	339	-----His-----Leu-----341		
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QY	151	AsnAsnIle-----SerLeuThr-----CysIleAlaThrGlyArgProGluProThrVal	342	-----LeuLys-----343		
Db	1064	-----ATAAGCAGTGTGACCTTGTATGTCTCGCAATTGGCAGACCAACCAACAGTG	2120	ATAAGACAGTTTAAAGAGACACATCTTATCTCTATGTTTGTATCATCTATCCATTAA		2179
QY	168	ThrTyrArgHisIleSerProLysAlaVal-----GlyPheValSerGluAsp	344	-----Phe 344		
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QY	184	GluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAla	RESULT 25			
Db	1169	GAATACCTGGAAATCTCAGACATCAACCGCAGCAATCTGGAGAGTATGAGTGCAGCGCC	BTBCHAM			
QY	204	SerAsnAspValAlaAlaProValValArgValValValValValValValValValVal	LOCUS			
Db	1229	TTGATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	DEFINITION			
QY	224	TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys	BTBCHAM			
Db	1289	TATATCTCAAGGCGAAGACACTGGCTTTCAGTAGGCGCAGAGGCGATCTTGAGCTGT	LOCUS			
QY	244	GluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLysArgLeuIle	DEFINITION			
Db	1349	GAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	BTBCHAM			
QY	264	GluGlyLysGlyValLysValGluAsn-----ArgProPheLeuSerLysLeuIle	LOCUS			

BTBCHAM 2593 bp mRNA linear MAM 31-MAR-1995
 LOCUS
 DEFINITION
 OBCAM.
 X12672.1 GI:585
 cell adhesion molecule; glycoprotein; immunoglobulin superfamily;
 membrane protein; opiod binding protein.

SOURCE
 ORGANISM
 Bos taurus (cow)

REFERENCE
 AUTHORS
 Schofield, P.R., McFarland, K.C., Hayflick, J.S., Wilcox, J.N.,
 Cho, T.M., Roy, S., Lee, N.M., Loh, H.H. and Seeburg, P.H.
 Molecular characterization of a new immunoglobulin superfamily
 protein with potential roles in opiod binding and cell contact

```

EMBO J. 8 (2), 489-495 (1989)
89251576
MEDLINE
PUBMED
2721489
REFERENCE
2 (bases 1 to 2593)
Schofield, P.R.
AUTHORS
Direct Submission
TITLE
Submitted (23-AUG-1988) Schofield P.R
JOURNAL
Data kindly reviewed (19-may-1989) by Schofield P.R.
COMMENT
Location/Qualifiers
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9913"
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            /tissue_type="brain"
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mat_peptide
polya_site

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Alignment Scores:
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Score:          1901.60      Matches:      270
Percent Similarity: 42.58%      Conservative: 34
Best Local Similarity: 37.82%      Mismatches: 35
Query Match:      78.97%      Indels:      375
DB:              4          Gaps:      43

US-10-017-084A-523 (1-344) x BTOBCAM (1-2593)

Qy      1 MetLysThr-----Ile--Gln-----5
      |||
      |||
Db      337 ATG---ACATCTCCTTTATGTGTCAGAGACACTGCTCGCTTCTTTGGGTATAAACTTTT 393
      |||
Qy      6 -----ProLys-----Met-----His-----9
      |||
      |||
      |||
Db      394 GATGCCAGACCTCGCAGGAGCTGCCCACTGAATGTTAAAGTAGCACTCGAAGAGAGG 453
      |||
Qy      10 -----Asn-Ser-----Ile-----12
      |||
      |||
      |||
Db      454 CAGAGAAAGAACACCGTGACCTTCACTCCCGCAGCTCTCTCTCTCTCTCTCTCTCCCGG 513
      |||
Qy      13 -----Ser-----Trp-----14
      |||
      |||
      |||
Db      514 CCGCTCTCTCTTCCCGAGGGAGATCGAAGAGGGCTTTTUGATGCAGGAGGGGGC 573
      |||
Qy      15 -----Ala-----Ile-----16
      |||
      |||
      |||
Db      574 ATCTGGTTGTCCAGGCTGGAAAGCTGAGGAGGATCTGAGGAAGAACAGTAGACTCCGG 633
      |||
Qy      17 -----PheThr-----Gly-----19
      |||
      |||
      |||
Db      634 AGAGCGTGGACTCCGCTTCTCTTACCCGCCCTCTCGGTTCTGGTGTGTCCAGCCCTTG 693
      |||
Qy      20 -----LeuAla-----21
      |||
      |||
      |||

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694	Db	CGCGCTCCCGCGCGCTGCCGAGACCCGCTCGCTGCGTGCGAGACCGAGCGCGCG	753
22	QY	-----Ala-----Leu-----Cys-----LeupheIn--	27
754	Db	COGAGTTCTTGGGAAGTTGGCTCTCGAGGAGGCGGTCTGTGGTCCCTGTTCAGCC	813
28	QY	-----GlyValPr	30
814	Db	CTGGAAGTCCTCGTGGTGTCTCTCAGGCTGTCTTCTTGTACCCACAGGAGTGC	873
30	QY	oValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnG	50
874	Db	CGTGGCGACGAGAGTGCACCTTTCCCAAGCGATGGCAACGTCACCGTCCGCGAGG	933
50	QY	yGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAs	70
934	Db	GAAGAGCGCCACCTCAGATGTACCATAGATCATCGGTCAACCGGTGGCTGGCTGA	993
70	QY	nArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValle	90
994	Db	COGACGACATCTCTACGCGCGGAATACAAAGTGTCTCCATAGACCCCTCGAGTGCAT	1053
90	QY	uLeuSerAsnThrGlnThrGlnTySerIleGluIleGlnAsnValAspValTyAspGl	110
1054	Db	CTGTGTGAACAGCCCAACCCAGTACAGCATCATGATCCAGAACGTGGAGTGTACGCG	1113
110	QY	uGlyProTyThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLe	130
1114	Db	GGSCCCTATACCTGTCTGTGCAGACGACACACCCAGACCTCCCGTGTCCACCT	1173
130	QY	uIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGl	150
1174	Db	CATCTGTGCAAGTCCCTCCCGAGATCATGAACATCTCTCAGATGTCCCGTGAATGAGG	1233
150	QY	yAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpAr	170
1234	Db	GAGCAGCGTGACCTGTCTGTCTCTGTCGACGACGACGACGACGACGACGAGTGAG	1293
170	QY	gHisIleSerProLysAlaVal-----GlyPheValSerGluAspGluTyIle	186
1294	Db	ACACCTGTCA-----GTCAAGGAAGCCAGGGCTTTGTGAGTGAGATGAATACCT	1344
186	QY	uGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyTrpGluCysSerAlaSerAsnAs	206
1345	Db	GGAAATCTTGACATCAACGTCACAGTCCGGGAGTATGAGTGCAGCGCCTGAATGA	1404
206	QY	pValAlaAlaProValValArgArgValLysValThrValAsnTyTrpProProTyIleSe	226
1405	Db	TGTTGTCTGCCCTGACGTCGCGGAAGTAAAGATCACTGTCAACTACCCCTATATCTC	1464
226	QY	rGluAlaIysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSe	246
1465	Db	CAAGCAAGAAACACAGGGGTCTCCGTGTGCCAGAGGGCATTTGAGTGTGAAAGCTC	1524
246	QY	rAlaValProSerAlaGluPheGlnTrpTyTrpLysAspAspLysArgLeuIleGluGlyLy	266
1525	Db	GGCAGTGCCCATGGCTGAGTTCAGTTCAGTGTTCAGGAAGACACAGGCTGGCCACCGCCT	1594
266	QY	sLysGlyValLysValGluAsnArg----PropheLeuSerLysIleullePhePheAsnVa	285
1595	Db	GGACGGCATGAGGATCGAGAACAAAGGCCAC--ATATCCACGCTGACCTTCTTCAACGT	1641
285	QY	lSerGluHiIAspTyTrpGlyAsnTyThrCysValAlaSerAsnLysLeuGlyHisThrAs	305
1642	Db	CTCAGAAAGAGATTATGGAACTATATCTTGTGTGCCCAACAAACAGCTTGGGATTACCA	1701
305	QY	nAlaSerIleMetLeuPheGlyProGlyAlaVal-----	316
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ORIGIN
Alignment Scores:
Pred. No.: 6,49e-72 Length: 2337
Score: 1897.20 Matches: 275
Percent Similarity: 45.48% Conservative: 27
Best Local Similarity: 41.42% Mismatches: 33
Query Match: 78.79% Indels: 329
DB: 10 Gaps: 44

US-10-017-084A-523 (1-344) x RATCALMC (1-2337)

QY 1 MetLys---Thr-----Ile---Gln-----Pro---LysMet 8
|||::: ||| ||| |||
DB 80 ATCCAGACCTCTGCAGAAATCGCCAACTGAATCTTAAAGTAGCTTACCGAGAGAGCA 139
|||::: ||| ||| |||

QY 9 HisAsn-----SerIle-----Trp----- 12
||| ||| ||| ||| |||
DB 140 GAGAAAGCAAACTGTGACCTCGTCCCTGCTCTCTTTTGTGTCTCCCTCTCCCGG 199
||| ||| ||| ||| |||

QY 13 -----Ser-----Trp----- 14
||| ||| ||| ||| |||
DB 200 GCTCCCTCCGCCAGGAGCGTTTGAGAAAGCTCTTTTGGATGACGAGGGGCATCT 259
||| ||| ||| ||| |||

QY 15 -----Ala-----Ile----- 16
||| ||| ||| ||| |||
DB 260 GGTCTTCGACGGCTGSAAGCTGAGGCTGGAGCAGAGGAGACTATTAGACTCGGAGA 319
||| ||| ||| ||| |||

QY 17 -----Phe 17
||| ||| ||| ||| |||
DB 320 GCCTGGACTCAGCCTTGCTCTCCCGCTCCAGCTCTGTGTTGCTCTCTGTGCTTT 379
||| ||| ||| ||| |||

QY 18 -----Thr-----Gly----- 19
||| ||| ||| ||| |||
DB 380 CGTCCCTCAACATTCCGGCTATTCTGAGAGCGAGGGACAAAGGACCGTGCAGCTCAAG 439
||| ||| ||| ||| |||

QY 20 -----LeuAla-----Ala-----Leu----- 23
|||::: ||| ||| ||| |||
DB 440 AGTTCTAGGAAGTGTGCTGTGAGATGCGGTCTGTGGTACCTGTTCTGTCCCTGG 499
||| ||| ||| ||| |||

QY 24 ---Cys-----LeuPhe-----GlnGlyValProVal 31
||| ||| ||| ||| |||
DB 500 AAGTGCTCGTGTGCTGTCTCTGAGGGTGTCTGTTCTTGTATCCACAGAGAGTGC 559
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QY 32 ArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGlu 51
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DB 560 GCGACGGAGATGCCACCTTTCCCAAGACTATGACACAGTACGCGTCCGCGAGGAGAG 619
||| ||| ||| ||| ||| |||

QY 52 SerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArg 71
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DB 620 AGCGCCACCCTCAGTGTATCCATAGATGACCGGGTCACCGAGTAGTACCTTGGCTAAAC 679
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QY 72 SerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
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DB 630 AGCACAATCTCTACGCTGGGAATGACAAAGTGGTCCATAGACCTCGAGTGATCACTTG 739
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QY 92 SerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGly 111
||| ||| ||| ||| ||| ||| ||| |||
DB 92 SerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGly 111
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QY 740 GTCACACGCCCTACCCAGTACAGTATCATGATCCAGAAATGTGGATGTTTATGACGAAGT 799
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DB 740 GTCACACGCCCTACCCAGTACAGTATCATGATCCAGAAATGTGGATGTTTATGACGAAGT 799
||| ||| ||| ||| ||| ||| ||| |||

QY 112 ProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuLeu 131
||| ||| ||| ||| ||| ||| ||| |||
DB 112 ProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuLeu 131
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Db      800  CCGTACACCTGCTCTGTGCAGACAGACATACCCCAAAACCTCCCGGCTGCACCTCAT 859
QY      132  ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db      860  GTGCAAGTTCTCCCCAGATAATGACATCTCTTTCAGACATTAAGTGTGAATGAG----- 913
QY      152  AsnIle-----SerLeuThr-----CysIleAlaThrGlyArgProGluProThrValThr 168
Db      914  ---ATAAGCAGTGTGACCTTGTATGTCGCAATTTGGCAGACCAACACAGTGACA 970
QY      169  TrpArgHisIleSerProLysAlaVal-----GlyPheValSerGluAspGlu 184
Db      971  TGGCGACACCTGTCA-----GTCAAGGAAGGCCAGGGCTTTTGTGAGTGAAGATGAA 1021
QY      185  TyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlnCysSerAlaSer 204
Db      1022  TACCTGGAATCTCAGACATCAAAACGCGACCAATCTGGAGAGTATGAGTGCAGCGCTTG 1081
QY      205  AsnAspValAlaAlaProValValArgArgValIleValThrValAsnTyrProProTyr 224
Db      1082  AATGATGTCTGCTGACCTGATGTTTCGGAAGTAATAATCACTGTAACTATCTCTCTAT 1141
QY      225  IleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGlu 244
Db      1142  ATCTCAAAGCGAAGAACACACTGGCGTTTCAGTAGGGCCAGAAAGGCATCTCTGAGCTGAA 1201
QY      245  AlaSerAlaValProSerAlaGluPheGlnTyrTyrIleAspAspLysArgLeuIleGlu 264
Db      1202  GCCTCTGCTGCTCCCATGCTGCTGAATTCAGTGTTCAGGAAGTAAACATCACTGTAACT 1261
QY      265  GlyLysLysGlyValLysValGluAsn-----ArgProPheLeuSerTyrLeuIlePhe 282
Db      1262  GGCTGTGTCGCTGAGATTGAGAACAAAGGCGC-----ATATCCACTTTGACTTTC 1315
QY      283  PheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGly 302
Db      1316  TTCAATGTCTCAGAGAAGGATTATGGAACTATACCTGTGTGGCCACAAACAAGCTTGGG 1375
QY      303  HisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaVal----- 316
Db      1376  AACACCAATCCAGCATCACCTGTATGGCCCTGGAGCAGTCAATGATGTGTAAACTCG 1435
QY      317  ---Ser-Glu-----ValSerAsn-----Gly-----ThrSer----- 324
Db      1436  GCCTCTAGACACTGGCTGTCTCTGCTCTCAGGGACCTTCTTGTGCCACTTCTTCATC 1495
QY      324  ----- 324
Db      1496  AAGTTTGTATAAGAAACCTTAGGTCCTCTGAGCATCGCTTCTCCATATCACAGACT 1555
QY      325  -----ArgArgAlaGly----- 329
Db      1556  TTAATCTACACTGGGAGG---GGCAACACAGTTGGGCTTCTTTGGTTATTTTITG 1612
QY      329  s----- 329
Db      1613  TTCTCTCTGACTGTTAGTTTGTGTTTGTGTTTCTGGGATTTTCAATTTGTTT 1672
QY      330  -----Val----- 330
Db      1673  TCCTTTTTCGTTGATGAGACCGGGGTTGGGGTTGGGATGGGCGAGGTCTACCCAGAG 1732
QY      331  -----Tip-----LeuLeuPro----- 334
Db      1733  TAGGTAATACAGGTATTGGTGGGCCCCCAATGGAATATATCTCTGTACTCTTGGCCTTC 1792
QY      336  -----LeuLeu----- 336
Db      1793  CTTTTCCTACTCTCTCTCTCTCCTACCACCATTAACACAAACACACACAGCACGCCCTAA 1852
QY      337  -----Val-----Leu----- 338

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Db      1853  AGATGGCCTAAAAAATGTCCATGACAGCAGCACCCCTGAAGGTACAACTTGGCCCAAGTGC 1912
QY      339  ---His-----Leu-----Leu----- 341
Db      1913  AGTACACAATAAGAGTTCATCTACATTTCTCTGTTCTTTCTTCTTTAAGTTTCAATA 1972
QY      342  -----LeuLys----- 343
Db      1973  AGACAGTTTAAAAAGAGCAGACATCTTATCCCTATGTTGTATCACCTATCCATTAAGCT 2032
QY      344  -----Phe 344
Db      2033  GCACACCTTT 2042

RESULT 27
RATCALMB
LOCUS      2179 bp mRNA linear ROD 27-APR-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
ACCESSION M88710
VERSION M88710.1 GI:203247
KEYWORDS cell adhesion-like molecule; opiod binding protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE 1 (bases 1 to 2179)
AUTHORS Lipman,D.A., Lee,N.M. and Loh,H.H.
TITLE Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
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JOURNAL Gene 117 (2), 249-254 (1992)
MEDLINE 92347701
PUBMED 1339369
COMMENT Original source text: Rattus norvegicus (strain Simonsen ICR) brain
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CDS
Alignment Scores:      8.64e-72      Length:      2179
Pred. No.:      1888.70      Matches:      271
Score:      47.69%      Conservative: 29
Percent Similarity: 43.08%      Mismatches: 35
Best Local Similarity: 78.43%      Indels: 294
Query Match: 10      Gaps: 41
DB:

US-10-017-084A-523 (1-344) x RATCALMB (1-2179)
QY      1 MetLys-----ThrIle-----Gln----- 5
Db      16 CTTAGAAGGCTTGTAGACAGCTGTGGGCTCAGTCTTCTCGCAGAAATGTTAAGTGGG 75
QY      6 -----ProLysMetHisAsnSer----- 11
Db      76 AGCAGGGGCTGTCTCTGACTCTCTGCTTTCCTGCGGCGAGTGGCAATGGTCTTTAGAAGACTT 135

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information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

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ORIGIN

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Alignment Scores:
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Score:          1879.40      Matches:      274
Percent Similarity: 27.36%      Conservative: 36
Best Local Similarity: 24.18%      Mismatches:  27
Query Match:      78.05%      Indels:      797
DB:               9          Gaps:         77

US-10-017-084A-523 (1-344) x HSM805672 (1-6380)

QY  1 Met---LysThr-----Ile-----4
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QY  5 -----Gln-----Pro-----LysMethIleAsn 10
Db  71 GGCAGCAGCGGTAGCAGCAGCAGCAGCAGTAGCAGCGCGGCGAGCTGAGAG---CACGCG 127
QY  11 SerIle-----Ser---TrpAlaIlePhe-----ThrGlyLeuAlaAla 22
Db  128 AGCGTCGAGATGTACCATCTCGCTACTGGGTCTCTTCGCGGACA-----ACTGCC 181
QY  23 LeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPheProLysAla 41
Db  182 CTG---CTCTTCATCCCGAGAGTGGCGGCGAGGAGATGCCACCTTCACCATAGATGAC 238
QY  42 MetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsn 61
Db  239 ATGGACACGTGACGCTCGGCGAGGGGAGAGCGCCACCCCTCAGGTGTACCATAGATGAC 298
QY  62 ArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLys 81
Db  299 CGGGTAAACCGGGGTGGCGCTAAACGCGACGACCATCTCTACGCTGGGAATGACAAAG 358
QY  82 TrpCysLeuAspProArgValValLeuLeuLeuSerAsnThrGlnThrGlnTyrSerIleGlu 101
Db  359 TGGTCCATAGACCCCTCGTGTGATCATCTCTGTGTCATATACACCAACCCAGTACAGCATCATG 418

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QY  102 IleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsn 121
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QY  122 HisProLysThrSerArgValHisLeulleValGlnValSerProLysIleValGluIle 141
Db  479 CATCCAAACGTCCTCCGGTTTCACCTAATAGTGAAGTTCCTCTCATGATCATGAAATATC 538
QY  142 SerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGly 161
Db  539 TCCTCAGACATACATGCTGAATGAGGAGACGATGTGACCCCTGCTGTCTGTCTATTGGC 598
QY  162 ArgProGluProThrValTrpArgHisIleSerProLysAlaVal-----177
Db  599 AGACCAGAGCCAACTGTGACATGGAGACACCTGTCTCA-----GTCAAGGAAGGCCAG 649
QY  173 GlyPheValSerGluAspGluTyrLeuGlnIleGlnGlyIleThrArgGlnSerGly 197
Db  650 GGCCTTGTAAAGTGAAGTGAAGTACCTGGAGATCTCTGACATCAAGCAGAGACGATCCGG 709
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QY  218 ThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGln 237
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QY  238 LysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLys 257
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QY  258 -----Asp-----258
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QY  259 -----Asp-----259
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QY  263 -----263
Db  1250 TTTTCTCTGTATTCTAGATTGTCTTTCTTTTGTCTTTTGTCTTTTGTCTTTTGTCTTT 1309
QY  264 -----Glu-----Gly-----265
Db  1310 TATTTCAGCTTGAATGAGTGGGGTTGGGGCGGGTGGGCGAGGGTCTACACAGGTGTAG 1369
QY  266 -----LysLysGlyVal-----269
Db  1370 GATATCATTTCAATGGTGTGTCCAAAAT---GGGGTCTGCTCTCTGCTACCTTGACCCCTTC 1428
QY  269 -----269
Db  1429 CTTTCCCTCTGCTCTCTCTCTCATCATCATCCCAACACATCCTCTCTGCCATACACAA 1488
QY  270 -----LysValGlu-----Asn-----273

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Db	1489	AACGTAAGTTTCATTTTGGGCAAAATAGGCTCACAATAAACAACCCCTGAAGACACAAC	1548	Db	2569	GAAAAACACATCTGTCTGTGCAATGCAAAAGTGAAGAGTCCACCCGCTGAGTGGGATGAC	2628
Qy	274	-----Arg-----Pro-----	275	Qy	314	-----	314
Db	1549	TGACTTATAACATAGTGCACAGCAAGAGTACATCCAAGTGTCTATTATCTGTGATTAT	1608	Db	2629	TTTCTAGTGTCTCTTTCTGTCTCAGTCTGGTTTAAATCTGTTTGAATACTATCCAGT	2688
Qy	276	PhelLeu-----SerLysLeuLeu-----	281	Qy	315	-----Ala-----ValSer	317
Db	1609	TTTCTTAATGACAATGACATATGCCCCCATCCATGTTAATATTATTAATCTAATTCATTAG	1668	Db	2689	AAAAAGCTGATGGAGGCCAATTACATGGGGGTGTATTGACAACTCTGGTATTGTTTCA	2748
Qy	282	-----Phe-----PheAsn	284	Qy	317	-----	317
Db	1669	GGTTCACGTCTTTCTTTCTGGGACATCTCTACTATATATCCATATCATATAGATTTCAT	1728	Db	2749	GGAAGCTCTTAAACTGAGGGCAGCTTGAGCAACTGACTTAATTTTCAAGCACTTGATTA	2808
Qy	285	Val-----Ser-----	286	Qy	318	-----Glu-----ValSer	320
Db	1729	ATAGATGATTGTGCCATCTCTGTAGCCCTCCGCTCTACTCTATCTCCATCCCATCTGC	1788	Db	2809	ACACAACACTGCAACAGAGGAGAAAGTGTCAGTGACACAGTTCCTCTGTATGACGCT	2868
Qy	287	-----Glu-----His-----	288	Qy	321	-----Asn-----Gly-----	322
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Qy	312	-----Gly-----Pro-----	314	ACCESSION	Y08170		
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					Phasianinae; Gallus.		
				REFERENCE	1		
				AUTHORS	Wilson,D.J., Kim,D.S., Clarke,G.A., Marshall-Clarke,S. and		
				TITLE	A family of glycoproteins (GP55), which inhibit neurite outgrowth,		
					are members of the Ig superfamily and are related to OBAM,		
					neurotrophin, LAMP and CEPU-1		
				JOURNAL	J. Cell. Sci. 109 (Pt 13), 3129-3138 (1996)		

97157768 MEDLINE
9004047 PUBMED
2 REFERENCE
Lodge, A.P., Kim, D.S., Howard, M.R., McNamee, C.J., Smith, N. and Moss, D.J.
TITLE Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from chick: structural diversity of IgLON family proteins
JOURNAL Unpublished
3 Wilson, D.J.A.
REFERENCE Direct Submission
AUTHORS Submitted (21-MAR-1996) D.J.A. Wilson, Liverpool University, Human
TITLE Anatomy and Cell Biology, Liverpool, L69 3BX, UK
JOURNAL
REMARK Revised by (3)
REFERENCE 4 (bases 1 to 1533)
AUTHORS Moss, D.J.
TITLE Direct Submission
JOURNAL Submitted (20-APR-1999) D.J. Moss, Liverpool University, Human
Anatomy and Cell Biology, Liverpool, L69 3BX, UK
COMMENT On Apr 26, 1999 this sequence version replaced gi:1617043.
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DEFINITION Sequence 98 from Patent WO03002765.
ACCESSION AX665340
VERSION AX665340.1 GI:29290463
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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2757.321 Million cell updates/sec

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Listing first 100 summaries

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and is derived by analysis of the total score distribution.

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 95 2408 100.0 1679 8 ADB22857 Human PRO
 96 2408 100.0 1679 8 ADB23630 Human PRO
 97 2408 100.0 1679 8 ADA92352 Novel hum
 98 2408 100.0 1679 8 ADB15415 Human PRO
 99 2408 100.0 1679 8 ADB83615 Novel hum
 100 2408 100.0 1679 8 ADB80721 Novel hum

ALIGNMENTS

RESULT 1
 AA247892
 ID AA247892 standard; cDNA; 1032 BP.

XX AC AA247892;
 XX
 DT 10-MAR-2000 (first entry)
 XX Human protein encoding cDNA SEQ ID NO:2.
 DE
 XX Human; haematopoietic cell regulation; tissue generation; reparation;
 KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
 KW receptor; ligand; autoimmune; infection-related immunodeficiency;
 KW inflammatory disorder; neurological disease; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1032
 FT /*tag= a
 FT /note= "no stop codon given"

XX W09958668-A1.
 XX 18-NOV-1999.
 XX 13-MAY-1999; 99WO-JP002485.
 XX 14-MAY-1998; 98JP-00131815.
 XX (ONCY) ONO PHARM CO LTD.
 XX Fukushima D, Shibayama S, Tada H;
 XX WPI; 2000-062298/05.
 XX P-PSDB; AAY57601.
 XX
 PT New polypeptides of human origin having cell regulatory, tissue
 PT generation, coagulant and other activities.
 XX
 PS Claim 4; Page 41; 84pp; Japanese.
 XX
 CC The present sequence encodes a specifically claimed novel human protein.
 CC The novel human protein can be used in therapeutic drugs for the
 CC prevention and treatment of a broad range of disorders including
 CC autoimmune and infection-related immunodeficiency, inflammatory
 CC disorders, and neurological diseases. The novel protein is expected of
 CC having haematopoietic cell regulatory activity, tissue generation/
 CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
 CC blood coagulation and thrombus activity, and receptor/ligand activity

XX SQ Sequence 1032 BP; 267 A; 281 C; 270 G; 214 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1032
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-017-084a-523 (1-344) x AA247892 (1-1032)
 QY 1 MetLysThrIleGlnProLysMethIleSerIleSerIlePheThrGlyLeu 20
 DB 1 ATGAAACCAATCCAGCCAAAATGCAATTCATCTCTTGGGCAATCTTACGGGGCTG 60
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 61 GCTGCTCTGTCTCTTCCAGGAGTGGCGGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 121 GCTATGGACACGTGACGGTCCGGGAGGGGAGGGCCACCTCAGGTGCACTATTGAC 180
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 181 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrClnTyrSerIle 100
 DB 241 AAGTGGTGCTGGATCTCGCTGGTCTTCTTGAGCAACACCCAAACGAGTACGATC 300
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 301 GAGATCCAGAACGTGATGTATGACGAGGGCCCTTACCTGCTCGTGGCAGACAGAC 360
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 361 AACCAACCAAGACCTCTAGGGTCCACCTCATGTGCAAGTATCTCCAAAATTTAGAG 420
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 421 ATTCTTCAGATATCTCCATTATGAAGGGAACATATTAGCTTACCTTGCATAGCACT 480
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 481 GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
 QY 181 SerGluAspGluTyrLeuGlnIleGlnGlyIleThrArgGlnSerGlyAspTyrGlu 200
 DB 541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCAGGGGAGCAGTCAGGGGACTAGGAG 600
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 DB 601 TGCAGTGCCTCCAATGACGTGGCCGCCCGCTGGTACGGAGAGTAAGGTCAACGTGAAC 660
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 661 TATCCACCATACATTTCAGAAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGGTACAGAGTACAAA 780
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 781 AGACTGATTGAAGAAAGAAGGGGTGAAGTGGAAAACAGACCTTCTCTCAAACTC 840
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 841 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCTGGGCTCCCAACAG 900

PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082700P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082804P.
PR	23-APR-1998;	98US-0082767P.
PR	23-APR-1998;	98US-0082796P.
PR	27-APR-1998;	98US-0083336P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083392P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083500P.
PR	29-APR-1998;	98US-0083545P.
PR	29-APR-1998;	98US-0083554P.
PR	29-APR-1998;	98US-0083558P.
PR	29-APR-1998;	98US-0083559P.
PR	30-APR-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	06-MAY-1998;	98US-0084441P.
PR	07-MAY-1998;	98US-0084598P.
PR	07-MAY-1998;	98US-0084600P.
PR	07-MAY-1998;	98US-0084627P.
PR	07-MAY-1998;	98US-0084637P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	13-MAY-1998;	98US-0085323P.
PR	13-MAY-1998;	98US-0085338P.
PR	13-MAY-1998;	98US-0085339P.
PR	15-MAY-1998;	98US-0085573P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085689P.
PR	15-MAY-1998;	98US-0085697P.
PR	15-MAY-1998;	98US-0085700P.
PR	15-MAY-1998;	98US-0085704P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086414P.
PR	22-MAY-1998;	98US-0086430P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087106P.
PR	28-MAY-1998;	98US-0087208P.
PR	30-JUL-1998;	98US-0094651P.
PR	11-SEP-1998;	98US-0100038P.
XX	(GETH) GENENTECH INC.	
XX	Wood WF, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
XX	WPI; 1999-551358/46.	
XX	P-PSDB; AAY41773.	
XX	New secreted and transmembrane polypeptides and their polynucleotides,	
PT	useful for treating blood coagulation disorders, cancers and cellular	
PT	adhesion disorders.	
XX	Claim 2; Fig 221; 530pp; English.	
XX	The present invention describes secreted and transmembrane polypeptides	
CC	and their polynucleotides. The nucleotide sequences are useful as sources	
CC	of probes, primers, for chromosome mapping, and for generation of	
CC	antisense sequences. They can also be used to create transgenic animals.	
CC	The proteins can be used to treat a variety of diseases and disorders,	
CC	depending on their function. Diseases that may be treated include blood	
CC	coagulation disorders, cancers and cellular adhesion disorders. They may	
CC	also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to	
CC	AAY41774 represent polynucleotide and polypeptide sequence given in the	
CC	exemplification of the present invention	

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 2

US-10-017-084A-523 (1-344) x AA234324 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAACCAACATCCAGCCAAATATCTCTCTTTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAGAGGTGCCGTGCGCAGCGAGATGCCACCTTCCCAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60
 DB 254 GCTATGACAACTGACGCTGCGGCGAGGGGAGAGCCACCTCAGGTGACATATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGTACACCGGGTGGCTGGCTGTAAACCGCAGCACCATCTCTATGCTGGGATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTGGCTGGATCTCGCTGGTCTCTCTGAGCAACACCCAAACGCGAGTACGATC 433
 QY 101 GluIleGlnAsnValAspValThrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTTGATGTATGACGAGGGGCTTTACACCTGCTCGGTGCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACACCCAAAGACCTTAGGTCCACTCATTTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerIleThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCCTCCTCAGCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGAGCCTACGTTTACTTTGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCCCGGAGAGCAGTACGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 DB 734 TGCAGTGTCTCCATGACGTGCGCGCGCGCTGGTACGAGAGTAAGGTACCGGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATATCATTTTCAAGACCCAGGGTACAGGTGTCCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGCAAGTGTGAAGCTCTACGAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTTGAGGAAGAAAGGGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAG 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTCTTCAATGTCTCTGAACATGACTATGGAATCTACACTTGGTGGCTCCCAACAG 1033

QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCGACACCAATGCGCAGCATCATCTATTGGTCCAGGCGCGTCAAGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCTGAGGAGGCGAGGCTGCTGGTCTGCTCTCTCTCTCTCTCTCTCT 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTTCTCAAAATTT 1165

RESULT 3

AACT78590
 ID AACT78590 standard; cDNA; 1679 BP.

XX AACT78590;

XX 08-FEB-2001 (first entry)

DE Human PRO337 nucleotide sequence SEQ ID NO:522.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer; ss.

XX Homo sapiens.

XX WO200053756-A2.

XX 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US004341.

XX 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.

PR 26-JUL-1999; 99US-0145698P.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 30-DEC-1999; 99WO-US031243.

PR 05-JAN-2000; 2000WO-US0031274.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

XX (GETH) GENENTECH INC.

XX Aehkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;

XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;

XX Stewart TA, Tumas D, Williams PM, Wood WI;

XX WPI: 2000-611443/58.

XX P-PSDB: AAB44329.

Novel PRO polypeptides and polynucleotides used in detection methods to target bioactive molecules to specific cells, and to modulate cellular activities.

Claim 2; Fig 221; 636pp; English.

AACT78458 to AACT78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytosolic activity. The polynucleotides and polypeptides can be used for detecting the presence

CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores: 6.72e-36 Length: 1679
 Pred. No.: 2408.00 Matches: 344
 Score: 2408.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-017-084a-523 (1-344) x AAC78590 (1-1679)

QY 1 MetIysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAAACCATCCAGCCAAATATCTATCTCTTGGGCAATCTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTGTCTCTTCCAAAGAGTGGTGGCGAGCGGAGATGCCACCTTCCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACAAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTTCAGGTGCATTTATGAC 313
 QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGAGCACCCTCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrInTyrSerIle 100
 DB 374 AAGTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAACGACGATCAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCAITTTGCAAGTATCTCCAAATTTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTCTCTCAGATATCTCCATTAAAGAGGGAACATATATAGCCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGACGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValArgValValThrValAsn 220
 DB 734 TGCAGTGGCTCCAAATGATGCGCGCGCGGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAAGACCAAGGTTACAGGTGTCCTCCGCGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIlysAspAspLys 260
 DB 854 CTGCACTGTGAGACCTCAGACGTCCTCCGCGCAATTTCCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280

DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGCTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCAAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTCAGAGAGGCGAGGCTGCGTCTGCTGCTCTTCTTCTTGTGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165
 RESULT 4
 AAC87037
 ID AAC87037 standard; cDNA; 1679 BP.
 XX
 AC AAC87037;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of human polypeptide PRO337.
 XX
 KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
 KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
 KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
 KW PRO1600; PRO9940; PRO9533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
 KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2650;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
 KW ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 134..1168
 FT sig_peptide 134..216
 FT /*tag= a
 FT /*tag= b
 XX WO200077037-A2.
 XX PD 21-DEC-2000.
 XX
 XX 22-MAY-2000; 2000WO-US014042.
 XX
 XX 15-JUN-1999; 99US-0139695P.
 XX 20-JUL-1999; 99US-0145070P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 17-AUG-1999; 99US-0149396P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 08-SEP-1999; 99WO-US020594.
 XX 15-SEP-1999; 99WO-US021090.
 XX 15-SEP-1999; 99WO-US021547.
 XX 30-NOV-1999; 99WO-US028313.
 XX 01-DEC-1999; 99WO-US028301.
 XX 02-DEC-1999; 99WO-US028565.
 XX 07-DEC-1999; 99US-0169495P.
 XX 05-JAN-2000; 2000WO-US000219.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 18-FEB-2000; 2000WO-US004342.
 XX 22-FEB-2000; 2000WO-US004414.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 20-MAR-2000; 2000WO-US007377.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 15-MAY-2000; 2000WO-US013358.
 XX 17-MAY-2000; 2000WO-US013705.

Db	1034	CTGGGCCACACCAATGCGAGCATCATGCTATTATTGGTCTCAGCGCCGCTCAGCGAGGTGAGC	1093
Qy	321	AsnGlyThrSerArgAlaGlyCyvalTrpLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGGACGTCGAGGAGGCGAGGCTGGCTGTGGCTGTGCTCTTTCGGTCTTGCACCTG	1153
Qy	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAAAATT	1165
RESULT 6			
ABK33598			
ID	ABK33598 standard; cDNA; 1679 BP.		
XX	ABK33598;		
XX			
XX			
DT	08-MAY-2002 (first entry)		
XX			
DE	cDNA encoding human PRO protein, Seq ID No 125.		
XX			
KW	Human; secreted protein; PRO; tumour; lung cancer; colon cancer;		
KW	breast cancer; prostate tumour; rectal tumour; liver tumour;		
KW	puricyte cell proliferation; chondrocyte cell proliferation;		
KW	tumour necrosis factor-alpha; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200208288-A2.		

Claim 2; Fig 125; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK3356-ABK33657 represent human PRO protein coding sequences of the invention

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:		
Pred. No.:	6,72e-36	Length:
Score:	2408.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DR:	6	Gaps:
XX		0
SQ		0

US-10-017-084A-523 (1-344) x ABK33598 (1-1679)

Qy	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
Db	134	ATGAAACCAATCAGGCAAAATGCAAAATCTATCTCTTGGGCAATCTTCACGGGGCTG	193
Qy	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	154	GCTGCTCTGHTCTCTTCCAAAGGAGTCCCGTGCAGCGGAGATGCCACCTTCCCCAAA	253
Qy	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATGACAACGTACGGTCCGCGACGGGGAGAGCGCCACCTCAGGTGCACATATTGAC	313
Qy	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
Db	314	AACCGGTGACCCGGGTGGCTGCTAAACGCGAGCACCATCTCTATGCTGGGAATGAC	373
Qy	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle	100
Db	374	AAGTGTGTCCTGGATCTCGCGTGGTCTCTTGAGCAACACCCAAACGAGTACAGCATC	433
Qy	101	GluIleGlnAsnValAspValTyAspGluGlyProTyThrCysSerValGlnThrAsp	120
Db	434	GAGATCCAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTCGTGCGACACAGC	493
Qy	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCAAAATTTGTAGAG	553
Qy	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTCTTCAGTATCTCCATTAAAGAGGAAACAATATTAGCTTCACTCGCATAGCAACT	613
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db	614	GGTAGACGAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	673
Qy	181	SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyGlu	200
Db	674	AGTGAAGACGAATATTCTGGAAATTCAGGGCATCACCCGGGAGCACTCAGGGGACTACGAG	733
Qy	201	CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn	220

PN	WO200208288-A2.	
XX		
PD		
XX		
XX	31-JAN-2002.	
PF		
XX	29-JUN-2001; 2001WO-US021066.	
XX		
PR	20-JUL-2000; 2000US-0219556P.	
PR	25-JUL-2000; 2000US-0220585P.	
PR	25-JUL-2000; 2000US-0220605P.	
PR	25-JUL-2000; 2000US-0220607P.	
PR	25-JUL-2000; 2000US-0220624P.	
PR	25-JUL-2000; 2000US-0220638P.	
PR	25-JUL-2000; 2000US-0220664P.	
PR	25-JUL-2000; 2000US-0220666P.	
PR	26-JUL-2000; 2000US-0220893P.	
PR	28-JUL-2000; 2000WO-US020710.	
PR	01-AUG-2000; 2000US-0222425P.	
PR	22-AUG-2000; 2000US-0227133P.	
PR	23-AUG-2000; 2000WO-US023522.	
PR	24-AUG-2000; 2000WO-US0233328.	
PR	10-NOV-2000; 2000WO-US030873.	
PR	28-NOV-2000; 2000US-0253646P.	
PR	01-DEC-2000; 2000WO-US032678.	
PR	20-DEC-2000; 2000US-00747259.	
PR	20-DEC-2000; 2000WO-US034956.	
PR	28-FEB-2001; 2001WO-US006520.	
PR	01-MAR-2001; 2001WO-US006666.	
PR	22-MAR-2001; 2001US-00816744.	
PR	10-MAY-2001; 2001US-00854208.	
PR	10-MAY-2001; 2001US-00854280.	
PR	25-MAY-2001; 2001WO-US017092.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
XX	Baker KP, Desnoyers L, Gehrtsen ME, Goddard A, Godowski PJ;	
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;	
XX		
XX	WPI: 2002-172001/22.	
DR	P-PSDB; AAU83654.	
DR		
XX		
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,	
PT	useful for treating a PRO related disorder and for diagnosing tumors such	
PT	as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor	
PT	or liver tumor.	
XX		
XX		

Db 734 TGCAGTGCCTCAATGACGTGGCCGCGCCGTGGTACGAGAGTAAGGTCCACCGTGAAC 793

Qy 221 TTTProProTyrTyrTyrSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240

Db 794 TATCCACCATACATTTTCAAGCAAGGGGTACAGGTGTCCCGTGGGCAAAAGGGGACA 853

Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrPheGlnTyrLysAspAspLys 260

Db 854 CTGACGTGTGAAGCCTCAGCAGTCCCTTCAGCAGAAATTCAGTGGGTACAGGATGACAA 913

Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280

Db 914 AGACTGATTGAGGAAGAAAGGGGTGAAGAGTGAAGAAACAGACCTTCTCTCAAAATC 973

Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300

Db 974 ATCTTCTTCAATGCTCTGAACATGACTATGGGAATACACTTGGCGGCTTCAACAG 1033

Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 1034 CTGGGCCACCAATGCGAGCATCATCTATTGTTCCAGGCGCGTCAGCGAGGTGAGC 1093

Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340

Db 1094 AACGGCAGTCCAGAGGAGCGAGCGTGGTCTGGCTGCTGCTCTCTCTGTGCTTGCACCTG 1153

Qy 341 LeuLeuLysPhe 344

Db 1154 CTTCTCAATTT 1165

RESULT 7

ABL88099

ID ABL88099 standard; cDNA; 1679 BP.

XX ABL88099;

DT 16-MAY-2002 (first entry)

DE Human PRO337 cDNA sequence SEQ ID NO:55.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

XX vunerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX age-related macular degeneration; arterial restenosis; angina;

XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

XX wound healing; chromosome mapping; Gene mapping; gene; ss.

OS Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

22-JAN-2001; 2001US-00767609.

28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006666.

09-MAR-2001; 2001US-00802706.

14-MAR-2001; 2001US-00808689.

22-MAR-2001; 2001US-00816744.

05-APR-2001; 2001US-00828366.

10-MAY-2001; 2001US-00854208.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

30-MAY-2001; 2001US-00870574.

30-MAY-2001; 2001WO-US017443.

01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

P-PSDB; ABB84844.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

Claim 2; Fig 55; 565pp; English.

ABL89072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vunerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-017-084A-523 (1-344) x ABL88099 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

Db 134 ATGAAACCATCCAGCCCAAAATGCACAAATTTCTATCTCTGGGCAATCTTCACGGGGCTG 193

Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40

Db 194 GCTGCTGTGTCTCTTCCAGGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

Db 254 GCTATGGACACGTGACGCTCCGTCGGCAGGGGAGAGCGCCACCTCAGGTGCATTATTGAC 313

PT infarction), endothelial or angiogenic disorders in a mammal.
 XX PS Claim 1; Fig 55; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x ABL95588 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAGAACATCCAGCCAAAATGACAAATCTATCTCTTGGGCAATCTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTGTGTCTCTTCCAGGAGTGCCCGTGGCAGCGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGCAACAGTACCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGTTCACCGGGTGCTGCTGCTAAACCGCAGCACCATCTCTAATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGTGCTGGATCCTCGGTGCTCTTCTAGCAACACCCAAACGACGATACGATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTATGACGAGGGGCCCTTACCTGCTCGTGACGACGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCCAAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGCCCTACGGTGTACTTGGAGACACAATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGGCATCCCGGGAGCAGTCAGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaIleProValValArgValIleValThrValAsn 220
 DB 734 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGTGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaIleGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAAGAGCCAAAGGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853

QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValIleValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGTGAAGACAGACCTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 AACTTCTCAATGTCTCTGACATGACTATGGAACTACACTTGGCTGCTCCCAACAAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTGCGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165
 RESULT 9
 ACD24040
 ID ACD24040 standard; cDNA; 1679 BP.
 XX AC ACD24040;
 XX AC ACD24040;
 DT 26-AUG-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing; gene; ss.
 XX Homo sapiens.
 OS US2003032156-A1.
 PN 13-FEB-2003.
 PD 06-MAY-2002; 2002US-00140474.
 PF 31-MAR-1997; 97WO-US005230.
 XX 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.

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PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 15-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341980/32.
DR P-PSDB; ABO17803.
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury.
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX Claim 2; Fig 375; 660pp; English.
XX The invention describes an isolated nucleic acid (i) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (i) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the binding of A-peptide
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD24040 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAATAACCATCCAGCCAAATATGACATCTATCTCTTGGGCAATCTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCCCAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGACAACTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGTGCACATTATGAC 313
Qy 61 AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGGTCCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTTATGTGTGGGATGAC 373
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QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGGTGGATCTCGCGTGGTCTTCTGAGCAACACCAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTTAGGTGCTACCTCATTTGCAAGTATCTCCCAAAATGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTCTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAGACCAATATTGGAATTCAGGGCATCACCGGAGCAGTCCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaIleProValValArgArgValLysValThrValAsn 220
DB 734 TGCAAGTCCCTCCATGATGCGGCGCGCGGTGATCGGAGAGTAAGGTTCACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTCAGAAAGCAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnThrTyrLysAspAspLys 260
DB 854 CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGATTCAGTGTGTACAAAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTCATGTCTCTGAACATGACATGATGGAACATACACTTGGTGGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTGTGTCAGCGCGCGTCCAGCGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCAGCTCGAGAGGGCAGGTGGCTGTGGCTGTGGCTGTCTCTCTGTCTTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTCTCAAAATT 1165
RESULT 10
ID ACA66903 standard; cDNA; 1679 BP.
XX AC ACA66903;
XX AC ACA66903;
DT 23-JUN-2003 (first entry)
XX cDNA encoding human PRO polypeptide #63.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
KW gene; ss.
XX Homo sapiens.
OS

US2003036635-A1.
20-FEB-2003.
28-AUG-2002; 2002US-00230163.
25-JUL-2000; 2000US-0220638P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
(GETH) GENENTECH INC.
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
WPI; 2003-342045/32.
P-PSDB; AB080801.
One hundred and twenty two nucleic acids encoding PRO polypeptides,
useful for the manufacture of a medicament for diagnosing or treating
tumor.
Claim 2; Fig 125; 314pp; English.
The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides and polynucleotides are useful for preparing a medicament
useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
useful in diagnostic assays for PRO, by detecting its expression in
specific cells, tissues or serum, and for affinity purification of PRO
from recombinant cell culture or natural sources. ACA66841-ACA66962
represent cDNA sequences encoding the human PRO polypeptides of the
invention. Note: The sequence data for this patent was obtained in
electronic format directly from the USPTO web site at
seqdata.uspto.gov/psipdb/entry.html
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-017-084A-523 (1-344) x ACA66903 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAATAATGCAATCTCTCTGGGCAATCTTCCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAAACGTGACGGTCCCGCAGGGGAGAGAGCCACCTCAGTGCATATTGAC 313
QY 51 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrTyrSerIle 100
DB 374 AAGTGGTGGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 493


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QY 121 AsnHisProLysThrSerArgValHisLeuValGlnValSerProLysLeuValGlu 140
DB 494 AACCCACCAAGACCTCTAGGGTCCACCTCATGTGCAAGTATCTCCAAATTTGAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTCAGATATCTCCATTATGAAGGAACAATATTAGCCTCACCCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACACAGGCTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGCTTTTGG 673
QY 181 SerGluAspGluTrpLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTrpGlu 200
DB 674 AGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTACGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaProValValArgValLysValThrValAsn 220
DB 734 TGCACTGCTCCATGACGTGGCGCGCGTGTACGGAGAGTAAAGGTACCGTGAAC 793
QY 221 TyrProTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACATACATTTTCAAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTrpIleLysAspLys 260
DB 854 CTGCAGTGTGAGCTCAGCAGTCCCTCAGCAGATTCAGTGTGTACAGGATGACAA 913
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGAAAGAGGGGTGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 973
QY 281 IlePhePheAsnValSerGluHisAspTrpGlyAsnTrpTrpCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGCTCTGAACATGATGAGTATGAGTATGAGTATGAGTATGAGTAT 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACCAATGCCAGCATATGCTATTGTTCCAGGGCGGTCCAGGAGTGCAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCAGCTCGAGAGGCGAGGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTTCTCAAAATTT 1165
RESULT 11
ACD42387
ID ACD42387 standard; cDNA; 1679 BP.
XX AC ACD42387;
XX AC ACD42387;
XX DT 05-SEP-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX KW Human; secreted and transmembrane protein; PRO; antidiabetic;
XX KW ophthalmological; cytostatic; immunostimulant; gene therapy;
XX KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
XX KW protein secretion disorder; pancreas disorder; diabetes;
XX KW vascular permeability; retinal neuron cell survival; retinal disorder;
XX KW immune response; inflammation; mononuclear cell infiltration;
XX KW eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
XX OS Homo sapiens.
XX PN US2003040014-A1.
XX PD 27-FEB-2003.
XX XX
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PR 01-FEB-2002; 2002US-00066269.
XX 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-009598P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 25-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 98WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
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PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JF, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
 PI Wood WI, Zhang Z;

XX WPI; 2003-503396/47.
 DR P-PSDB; ABO251175.

XX New secreted and transmembrane PRO polypeptides, useful for treating
 PT diabetes, retinal disorders and stimulating an immune response.

PS Claim 2; Fig 51; 254pp; English.

XX The invention describes an isolated polypeptide (I) having at least 80 %
 CC amino acid sequence identity to 30 secreted and transmembrane
 CC polypeptides. PRO polypeptides are also useful for stimulating
 CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
 CC factor stimulated proliferation of endothelial cells, stimulating
 CC proliferation of stimulated T-lymphocytes and for inducing proliferation
 CC of PB12 pancreatic ductal cells and are thus useful in the treatment of
 CC disorders which involve protein secretion by the pancreas, including
 CC diabetes. PRO polypeptides are useful for inducing vascular permeability
 CC and in enhancing survival of retinal neurons cells and are thus useful
 CC for the treatment of retinal disorders. PRO polypeptides are also useful
 CC for stimulating an immune response and inducing inflammation by inducing
 CC mononuclear cell and eosinophil infiltration at the site of infection of
 CC an animal. The PRO polypeptides are further useful for inducing apoptosis
 CC in endothelial cells for inhibiting neoplastic growth. This sequence
 CC encodes a novel human secreted and transmembrane PRO polypeptide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD42387 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAATAACATCCAGCCAAATGACAAATCTATCTCTGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGGCGCAGCGGAGATGCCACCTCTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACAACGTCACCGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGACATATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrrAlaGlyAsnAsp 80
 Db 314 AACCGGTGTCACCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGTGTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 374 AAGTGGTGGCTGGATCTCTCGCGTGTCTCTTCTGAGCAACACCAACCGCAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGACAGACGAC 493

QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCCAAAGAGCCTTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluCysAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCACCCTGCATCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACCAAGACCTTACGGTACTTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAspAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 Db 734 TGCAGTGGCTCCATGACGTGGCGCCCGCGGTGTACGGAGGTAAAGGTACCGGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTCAAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAAGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTCAATGCTCTGAAATGACTATGGAACTACACTTGCCTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACACCAATGCCAGCATCATTGCTATTGCTCCAGCGCCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 AACGGCACGTCGAGAGGGGAGGCTGGCTGCTGGCTGCTGCTCTTCTGCTTGTGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 Db 1154 CTTCTCAAAATTT 1165

RESULT 12

ACD42857
 ID ACD42857 standard; cDNA; 1679 BP.

XX AC ACD42857;

XX 09-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
 KW cell death; growth induction cascade; blood coagulation cascade;
 KW viral infection; gene; ss.

XX Homo sapiens.

XX OS US2003050239-A1.

XX PN 13-MAR-2003.

XX PD 15-OCT-2001; 2001US-00978191.

XX PF 17-OCT-1997; 97US-0062250P.

XX PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0065364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
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PR 12-MAR-1998; 98US-0077791P.
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PR 17-MAR-1998; 98US-0004022P.
PR 20-MAR-1998; 98US-0078866P.
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PR 01-APR-1998; 98US-0080327P.
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PR 08-APR-1998; 98US-0081049P.
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PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
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PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
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PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
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PR 22-MAY-1998; 98US-0086486P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
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PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-00168978.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
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PR 22-DEC-1998; 98US-00202054.
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PR 05-JAN-1999; 99WO-US000108.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
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PR 12-MAR-1999; 99US-00267213.
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PR 12-APR-1999; 99US-00284291.
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PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000US-00709238.
 PR 27-NOV-2000; 2000US-00723749.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-FEB-2001; 2001WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00816920.
 PR 10-MAY-2001; 2001WO-US009552.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUN-2001; 2001US-00918585.
 XX PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrata N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Alignment Scores: 6.72e-36 Length: 1679
 Pred. No.: 2408.00 Matches: 344
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 7 Gaps: 0
 DB:

US-10-017-084A-523 (1-344) x ACD42857 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCAATCCAGCCAAATGCAATATCTCTCTGGGCAATCTTCAAGGGGCTG 193

QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTCTCCAGAGTGCCTGCGCGAGGGAGATGCCACCTTCCCAAA 253

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACACGTGACGGTCCGGACGGGGGAGAGCCACCTCAGGTGCATATTGAC 313

QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCAACCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 373

QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGTGCTGGATCTCTCGCTGCTTCTTCTGAGCAACCAACCGAGTACAGATC 433

QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGATGTATGACGAGGGCCCTTACCTGCTCGTGCAGACAGAC 493

QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTTAGGGTCCACCTCATTTGCAAGTATCTCCCAAAATTTAGAG 553

QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160

DB 554 ATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACACAGACCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATACTTTGGAATTCAGGGCATCCCGGGAGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCATGACGTGGCGCGCGCGGTGCTACGGAGACTAAAGGTCAACGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATATCTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGCACAAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAGGAAGAAGAGGGTGAAGTGGAAACAGACCTTCTCTCAAAATC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGTCTGAACATGACTATGGAACTACACTTGCCTGGCGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCGCACCAATGCCAGCATCATCTATTGGTCCAGGCGCCGTCAGGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValHisLeu 340
 DB 1094 AACGGCACGTGAGGAGGGGAGGGTGGCTGGCTGGCTCTCTCTCTCTCTCTCTCTCT 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165

RESULT 13
 ACD68655 standard; cDNA; 1679 BP.
 ID ACD68655;
 AC ACD68655;
 XX 17-SEP-2003 (first entry)
 DT
 XX Novel human secreted and transmembrane protein PRO337 cDNA.
 DE Human; secreted and transmembrane protein; PRO; cytostatic;
 KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
 KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
 KW pharmaceutical; diagnostic; biosensor; bioeffector; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; bone disorder; cartilage disorder; sports injury;
 KW arthritis; wound; gene; ss.
 XX Homo sapiens.
 OS
 XX US2003045687-Al.
 FN
 XX 06-MAR-2003.
 PD
 XX 12-AUG-2002; 2002US-00218631.
 PF
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.

XX Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WL;
 XX P-PSDB; ABO33767.
 DR WPI; 2003-512315/48.
 DR P-PSDB; ABO33767.
 XX New genes, and its encoded secreted and transmembrane polypeptides,
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 PT pericyte proliferation, especially for treating lung tumors, arthritis or
 PT wounds in a mammal.
 XX Claim 2; Fig 125; 314pp; English.
 XX The invention describes an isolated nucleic acid molecule comprising a
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any these 122
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating proliferation of pericyte cells, or for modulating
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This sequence encodes a novel human secreted and transmembrane PRO
 CC polypeptide
 XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD68655 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAACCAATCCAGCCAAATAATGCAATCTATCTCTGGGCAATCTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAAGGAGTGCCTGGCGAGCGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleasp 60
 DB 254 GCTATGGACAACGTGACCGTCCGGCAGGGGAGAGCGCCATCTCAGGTGACATTTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
 DB 314 AACCGGGTCAACCGGGTGGCTGGCTGCTAAACCGCAGCACCAATCTATGCTGGGATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle 100
 DB 374 AAGTGGTGGCTGGATCTCTCGGTGCTCTCTGTAGCAACACCAACGACGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAsp 120

DB 434 GAGATCCAGAACGTTGGATGTGTATGACGAGGGCCCTTACACCTCTCGTGCACACGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCACCCTGCATGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGACCTTACGTTACTTGGAGACACATCTCTCCCAAGCGTTGGCTTTGTG 673
 QY 181 SerGluAspGluTyTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCCAGGGGACTTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValThrValAsn 220
 DB 734 TGCAGTGGCTTCCAATGACGTGGCGCGCGGTGGTACGAGAGTAAAGTCAACCTTGAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCAAGACCAAGGTACAGGTGTCCTCGTGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyriyAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGAACAGACCTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACATATGGAACTACACITGGCTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGACACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGGCGCGTCCAGGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGACAGTCCGAGGAGGAGGCTGCTGCTGGCTGCTGCTCTTCTGCTCTTGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCTCAAAATTT 1165
 RESULT 14
 ACA67181
 ID ACA67181 standard; cDNA; 1679 BP.
 XX AC
 AC ACA67181;
 XX XX
 DT 23-JUN-2003 (first entry)
 XX DE cDNA encoding human PRO polypeptide #188.
 XX KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
 KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
 XX OS Homo sapiens.
 XX PN US2003004311-A1.
 XX FN

PD 02-JAN-2003.
 XX 19-DEC-2001; 2001US-00028072.
 XX 18-JUN-1997; 97US-0049911P.
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 18-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059352P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 24-SEP-1997; 97US-0059836P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 17-OCT-1997; 97US-0063755P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 24-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063551P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 11-DEC-1997; 97US-0069212P.
 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 23-JAN-1998; 98US-0072320P.
 PR 04-FEB-1998; 98US-0073612P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 12-MAR-1998; 98US-0077919P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, DeForge L, Denoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-352836/33.
 DR P-PSDB; ABU81057.
 XX
 DR
 XX
 PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
 PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
 PT heart attack.
 XX
 XX
 PS Claim 2; Fig 3/5; 643pp; English.
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the treatment of diabetes, bone and/or cartilage disorders
 CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
 CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
 CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
 CC assays for PRO, by detecting its expression in specific cells, tissues or
 CC serum, and for affinity purification of PRO from recombinant cell culture
 CC or natural sources. ACA65994-ACA67268 represent cDNA sequences encoding
 CC the human PRO polypeptides of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from the USPTO web
 CC site at seqdata.uspto.gov/psipsDIDEntry.html
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-10-017-084A-523 (1-344) x ACA67181 (1-1679)

[illegible]

22-APR-1998; 98US-0082797P.
 23-APR-1998; 98US-0082804P.
 23-APR-1998; 98US-0082796P.
 07-OCT-1998; 98WO-US021141.
 20-NOV-1998; 98WO-US024855.
 05-JAN-1999; 99WO-US000106.
 08-MAR-1999; 99WO-US005028.
 10-MAR-1999; 99WO-US005190.
 14-MAY-1999; 99WO-US010733.
 02-JUN-1999; 99WO-US012252.
 02-NOV-1999; 99WO-US028313.
 02-DEC-1999; 99WO-US028511.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 02-DEC-1999; 99WO-US031243.
 02-DEC-1999; 99WO-US031274.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000277.
 06-JAN-2000; 2000WO-US000376.
 11-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004341.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000WO-US006319.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US000520.
 22-MAR-2001; 2001WO-US009552.
 25-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 28-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Goddard A, Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ;
 Kijavini Iu, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 WPI; 2003-328860/31.
 P-PSDB; ABU72281.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 2; Fig 221; 453pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence of, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-017-084A-523 (1-344) x ACA63892 (1-1679)

QY	1	MetLysThrIleGlnProIlyMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATCCAGCCAAAATGCAAAATCTATCTTGGGCAATCTTACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys	40
DB	194	GCTGCTCTGTGTCTCTTCCAGAGTGCCTGCGGAGGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACACAGTCAGCTCCGGGAGGAGGAGGAGATGCCACCTTCCCAAA	313
QY	61	AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AACCGGGTCAACCGGGTGGCTGGCTAAACCGAGCACCATCTCTATGCTGGGATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AGTGGTGGCTGGATCTCGGTGGTCTCTTGAGCAACACCCAAACGAGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGAACGTCGATGTATGACGAGGAGGAGGAGTACCTCTCCCAAAATGTAGAG	493
QY	121	AsnHisProIlyThrSerArgValHisLeuIleValGlnValSerProIlyIleValGlu	140
DB	494	AACCAACCAAGACCTCTAGGTCACCTCATCTGTGCAAGATCTCTCCCAAAATGTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTCTTCAGATATCTCCATTAATGAAGGAGCAATATAGCTCACCTCAGTACAGCACT	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProIlyAlaValGlyPheVal	180
DB	614	GGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG	673
QY	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
DB	674	AGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGGAGTACAGGAGTACAGAG	733
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
DB	734	TGCAGTGCCTCCAATGACGTGGCGCGCTGGTGGTGGAGAGTAAAGGTCAACGTGAAC	793
QY	221	TyrProTyrIleSerGluAlaLeuGlyThrGlyValProValGlnGlyGlyThr	240
DB	794	TATCACCACATCAATTCAGAAAGGAGGAGTGTCCCGTGGGACCAAGAGGAGCA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys	260
DB	854	CTGAGTGTGAGGCTCAGCAGTCCCTTCAGCAGAAATCCAGTGTGTAAGAGTACAAA	913
QY	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysIleu	280
DB	914	AGACTGATTGAAGCAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC	973
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
DB	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGTGGCTTCCAAACAG	1033

QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheCysValProGlyAlaValSerGluValSer	320
Db	1034	CTGGGCCACACCAATGCCAGCATCATGCTATTTTGGTCCAGCGCGGTCAAGGAGTGAGC	1093
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGCAGTCGAGGAGGCGGTGGCTCTGGCTGTGGCTCTTCTGGTCTTGCACCTG	1153
QY	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAAAATTT	1165

RESULT 16

ACA03790
IN ACA03790 standard: cDNA: 1679 BP.

AC 203790.

XX
DT 23-MAY-2003 (first entry)

XX DE cDNA encoding human PRO polypeptide #188.

XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
 KW ss.
 KW

OS Homo sapiens.

PN US2003036180-A1.

20-FEB-2003.

09-MAY-2002: 2002US-00143114.

XX	31-MAR-1997;	97WO-US005230.
PR	12-JUN-1998;	98WO-US012456.
PR	14-JUL-1998;	98WO-US014552.
PR	28-AUG-1998;	98WO-US017888.
PR	20-SEP-1998;	98WO-US018824.
PR	14-SEP-1998;	98WO-US019093.
PR	14-SEP-1998;	98WO-US019094.
PR	14-SEP-1998;	98WO-US019177.
PR	16-SEP-1998;	98WO-US019430.
PR	17-SEP-1998;	98WO-US019437.
PR	07-OCT-1998;	98WO-US021141.
PR	29-OCT-1998;	98WO-US022991.
PR	29-OCT-1998;	98WO-US022992.
PR	20-NOV-1998;	98WO-US024855.
PR	01-DEC-1998;	98WO-US025108.
PR	05-JAN-1999;	99WO-US000106.
PR	08-MAR-1999;	99WO-US005028.
PR	10-MAR-1999;	99WO-US005190.
PR	20-APR-1999;	99WO-US008615.
PR	14-MAY-1999;	99WO-US010733.
PR	02-JUN-1999;	99WO-US012252.
PR	01-SEP-1999;	99WO-US020111.
PR	08-SEP-1999;	99WO-US020594.
PR	13-SEP-1999;	99WO-US020944.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	05-OCT-1999;	99WO-US023089.
PR	29-NOV-1999;	99WO-US028214.
PR	30-NOV-1999;	99WO-US028313.
PR	30-NOV-1999;	99WO-US028409.
PR	01-DEC-1999;	99WO-US028301.
PR	01-DEC-1999;	99WO-US028634.
PR	02-DEC-1999;	99WO-US028551.
PR	02-DEC-1999;	99WO-US028564.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	20-DEC-1999;	99WO-US030999.

PR	22-DEC-1999;	99WO-US030720.
PR	30-DEC-1999;	99WO-US031243.
PR	30-DEC-1999;	99WO-US031274.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000277.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US0003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	18-FEB-2000;	2000WO-US004342.
PR	22-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	01-MAR-2000;	2000WO-US005601.
PR	02-MAR-2000;	2000WO-US005746.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	21-MAR-2000;	2000WO-US007532.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	11-AUG-2000;	2000WO-US022031.
PR	23-AUG-2000;	2000WO-US023522.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000WO-US030952.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032678.
PR	20-DEC-2000;	2000US-00747259.
PR	20-DEC-2000;	2000WO-US043956.
PR	05-APR-2001;	2001US-00796498.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-MAR-2001;	2001WO-US006666.
PR	09-MAR-2001;	2001US-00802706.
PR	14-MAR-2001;	2001US-00808869.
PR	20-MAR-2001;	2001US-00816744.
PR	22-APR-2001;	2001US-00828366.
PR	10-MAY-2001;	2001US-00854208.
PR	10-MAY-2001;	2001US-00854280.
PR	18-MAY-2001;	2001US-00860216.
PR	25-MAY-2001;	2001US-00866028.
PR	25-MAY-2001;	2001US-00866034.
PR	01-JUN-2001;	2001WO-US017092.
PR	21-JUN-2001;	2001US-00872035.
PR	01-JUN-2001;	2001WO-US017800.
PR	05-JUN-2001;	2001US-00874503.
PR	14-JUN-2001;	2001US-00882636.
PR	19-JUN-2001;	2001US-00886192.
PR	20-JUN-2001;	2001WO-US019692.
PR	21-JUN-2001;	2001US-00887879.
PR	22-JUN-2001;	2001WO-US020116.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	18-JUL-2001;	2001US-00908827.
PR	06-AUG-2001;	2001US-00924419.
PR	09-AUG-2001;	2001US-00927796.
PR	16-AUG-2001;	2001US-00931836.
PR	19-DEC-2001;	2001US-0098072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-332040/31.

P-PSDB: ABU66757.

New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue

PT typing, and in chromosome identification.

PS Claim 2; Fig 375; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsIDEntry.html
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6,72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA03790 (1-1679)

Qy 1 MetLysThrLeuGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCACTCCAGCCAAATAATGACAAATCTATCTCTTGGGCAATCTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTCTTCCAGGAGTGGCCGTGGCGAGGAGTGCACCTTCCCAAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGACCAACGTGACGCTCCGCGAGGGGAGAGCGCACCTTCAGTGCTACATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpIleuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle 100
Db 374 AAGTGGTCCCTGGATCTCTCGGTGGTCTTCTTGACCAACACCCAAACGCGATCAGCATC 433
Qy 101 GluIleGlnAsnValAspValTrpAspGluGlyProTyThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTGGTGCAGACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisIleuLeuValGlnValSerProLysIleValGlu 140
Db 494 NACCACCCAAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCCAAAATTTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTTCAGATATCTCCATTATGAGGGAACAATATATTAGCTTACCTGCATACCACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACACGAGCCTACGGTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
Qy 181 SerGluAspGluTyIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyIle 200

Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCAGGAGCAGTACGGGAGCTACGAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValVal 220
Db 734 TGCATGTGCTCAATGACGTGGCCGCCGCTGGTACGAGAGTAAAGGTCAACGTGAAC 793
Qy 221 TyrProTyroTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCACATATTCAGAACCAAGGATACAGGTGTCCTGGGACAAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyTrpLysAspAspLys 260
Db 854 CTGCACTGTGAAGCTTCAGCACTCCCTCAGCAGAAATTCACGTGGTACAGGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGTGAAGAAACAGACCTTTCCTCAAACTC 973
Qy 281 IlePhePheAsnValSerGluHisAspTyGlyAsnTyThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGCCTGGCTCCCAACAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCAACACCAATGCCAGCATCATCTATTGTTGGTCCAGGCGCCCTCAGCGAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1054 AACGGCACGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 17
ACA04996
ID ACA04996 standard; cDNA; 1679 BP.
XX
AC ACA04996;
XX
XX
DT 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW obesity; diabetes; insulinemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003032063-A1.
XX
XX 13-FEB-2003.
XX
XX 01-FEB-2002; 2002US-00066494.
XX
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
XX 27-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063329P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0066364P.
XX 25-NOV-1997; 97US-0066840P.


```
Db 554 ATTTCTTCAGATATCTCCATTAAATGAAGGAACAATATTAGCCTCACCTGCATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTTPAqHiaIleSerProIysAlaValGlyPheVal 180
Db 614 GGTAGACACAGAGCTACGGTTACTTGGAGACATCTCTCCCAAGCGGTGGCTTTGIG 673
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyLeuThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACCAATACTTGGAAATTCAGGGCATCACCGGAGCAGTACGGGACTACGAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValIArgArgValIysValThrValAsn 220
Db 734 TGCAGTGCCTCCAATGACGTGGCGCCCGTGTGTACGAGAGTAAGGTCAACCGTGAAC 793
Qy 221 TyrProTyrIleSerGluAlaIleValGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTTCAGAACCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTTCAGCAGAAATTCAGTGTGTACAAAGGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysLysGlyValIysValGluAsnArgProPheLeuSerIleLeu 280
Db 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGTGAAGTGTGTTCTCTCAAAACTC 973
Qy 281 IlePhePheAsnValSerGluHieAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGCTCTGAACATGACTATGGGAACCTACACTTCGGTGGCTCCCAACAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGCGCGCTCAGCAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValThrLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTGAGGAGGCGAGGTGCGTCTGGCTGCTGCTCTTCTGTGCTTGCACCTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTTCAAAATTT 1165

RESULT 18
ACA72056
ID ACA72056 standard; cDNA; 1679 BP.
XX
AC ACA72056;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted and transmembrane PRO polypeptide #37 cDNA.
XX
KW Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; pre-eclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
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PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00854280.
 PR 01-JUN-2001; 2001US-008717092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001US-008717800.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001US-0019692.
 PR 29-JUN-2001; 2001US-0021066.
 PR 09-JUL-2001; 2001US-0021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-328499/31.
 DR P-PSDB; AB084961.
 XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
 XX pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
 PT modulators of receptor-ligand interactions.
 PT
 XX Claim 2; SEQ ID NO 522; 55pp; English.
 PS The invention relates to an isolated secreted and transmembrane
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an
 CC antibody against it is useful for modulating a biological activity of a
 CC cell. The PRO polypeptide is useful in industrial applications including
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
 CC polypeptide is also useful as a thrombolytic agent, interferon,
 CC interleukin, erythropoietin, colony stimulating factor and other
 CC cytokines. The PRO polypeptide is useful for treating disease such as
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and
 CC myocardial ischemia; kidney disease e.g. renal failure and
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
 CC bowel disease; reproductive disorders e.g. premature labour and
 CC pre-eclampsia; carcinogenesis. The present sequence represents a cDNA
 CC encoding a PRO polypeptide of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20020177553
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Alignment Scores:
 Pred No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA72056 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAACCATTCAGCCAAAATGACAAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTCAAGAGAGTCCCGGCGCAGCGAGATGCCACCTTCCCCAAA 253

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACACAGTGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
 Db 314 AACCGGGTCAACCGGGTGGCTGTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrLysSerIle 100
 Db 374 AAGTGGTCCCTGGATCTTCGGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyAspGluGlyProTyThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGTGCAGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCCAAAGACCTTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTCTTCAGATATCTCCATTAATGAAGGGAACATATATTAGCCTCACCTGCATCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACACAGACCTTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTG 673
 QY 181 SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyGlu 200
 Db 674 AGTGAAGACGAATCTTGGAAATTCAGGACATCACCCGGGAGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
 Db 734 TGCAGTGCCTCCATGACGTGSCCGGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 QY 221 TyrProTyThrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTCAAGAACCAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAspAspLys 260
 Db 854 CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyGlyAsnTyThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTCAATGCTCTGAACATGACTATGGGAACCTACACTTGCCTGCCCTCCAAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACACCAATGCCAGCATCTATTGTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTGTGCTGCTGCTCTTCTGCTTGTGCACCTG 1153
 QY 341 LeuLeuLysPhe 344
 Db 1154 CTTCTCAAAATTT 1165

RESULT 19
 ABX89328
 ID ABX89328 standard; cDNA; 1679 BP.
 XX
 AC ABX89328;
 XX
 DT 13-MAY-2003 (first entry)
 XX

DE DNA encoding novel secreted and transmembrane protein PRO337.
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW chondrocyte; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003017563-A1.
XX
XX 23-JAN-2003.
XX
XX 07-MAY-2002; 2002US-00140808.
XX
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 27-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 29-OCT-1998; 98WO-US022992.
XX 01-DEC-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 22-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 20-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 20-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
XX P-PSDB; ABUS9838.
XX
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX Claim 2; Fig 375; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This sequence
 CC encodes a novel human PRO protein
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ABX89328 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCACTCCAGCCAAATGCAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTCCAGAGAGTCCCTGGCGAGGGAGATGCCACTTCCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACACGCTGACGGTCCGGCAGGGGAGAGCCACCTTCAGTGCGACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
 DB 314 AACCGGTTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
 DB 374 AAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCCCAACGCAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTTGGATGTATGACAGGGGCCCTTACCTCTCGTGGTGCAGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCCAAAGACCTCTAGSGTCCACCTCATTTGCAAGTATCTCCCAAAATGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGAGCCCTTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGTGGTGTG 673
 QY 181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCCCGGGAGCAGTCCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220

DB 734 TGCAGTGCCTCAATGACGTGGCGCGCCCGTGTGTACGGAGTAAAGGTCAACGTGAAC 793
 QY 221 TyrProProTrpIleSerGluAlaIleGlyThrGlyValProValGlyGlyLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAAGACCCAGAGGTACAGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTrpLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValIleValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAATCTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTrpGlyAsnTrpCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGCTCTGAAACATGACTATGGAACTACACTTGGGTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTTCAGGAGGGGAGGCTGGCTGTGGCTGTGGCTCTTCTGTGTGTGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165
 RESULT 20
 ABX92696
 ID ABX92696 standard; cDNA; 1679 BP.
 XX
 AC ABX92696;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE cDNA encoding human PRO337 polypeptide.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
 KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
 KW cardiant; gene; ss.
 OS Homo sapiens.
 XX
 PN US2002169284-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 16-OCT-2001; 2001US-00978697.
 XX
 PR 26-MAY-1981; 81US-00267213.
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
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 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
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PR 27-MAR-1998; 98US-0079668P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-0000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99US-0005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99US-00050190.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00311832.
PR 02-JUN-1999; 99US-00311832.
PR 28-AUG-1999; 99US-00380137.
PR 28-AUG-1999; 99US-00380137.
PR 28-AUG-1999; 99US-00380138.
PR 28-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-0028313.
PR 02-DEC-1999; 99US-0028551.
PR 02-DEC-1999; 99US-0028565.
PR 16-DEC-1999; 99US-0030095.
PR 30-DEC-1999; 99US-0031243.
PR 30-DEC-1999; 99US-0031243.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000277.
PR 06-JAN-2000; 2000US-0000376.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 24-FEB-2000; 2000US-0005004.
PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
PR 21-MAR-2000; 2000US-0007532.
PR 30-MAR-2000; 2000US-0008439.
PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014042.
PR 30-MAY-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-0072678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-0074956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-00809552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-0017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-0017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 30-JUL-2001; 2001US-00918585.
PR 30-JUL-2001; 2001US-00918585.
XX

PA (GETH) GENENTECH INC.
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IU, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR P-PSDB; ABU61159.
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX Claim 2; Fig 221; 459pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC polypeptides are useful for detecting other PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule may be a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. The present sequence encodes a human PRO polypeptide
CC of the invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsdIDEntry.html
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-017-084A-523 (1-344) x ABX92696 (1-1679)
Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAAACCATCCAGCCAAAATGCAATCTCTTTGGGCAATCTTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCCTCTTCCAGGAGTCCCGTGGGAGAGATGCGAGATGCACTTCCCAAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60
Db 254 GCTATGGACAACTGACGGTCCGGCAGGGGAGAGCCACCTCAGGTGCTATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleuArgAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
Qy 31 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100
Db 374 AAGTGGTCCCTGGATCTCTCGGTGCTCTCTTCTAGGACACACCCAAACGAGTACAGCATC 433
Qy 131 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACCTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

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QY 121 AenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAACACCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAenAenIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTCTCATATCTCCATTTAATGAGGACATATATGCTTACCTGCTCATGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGACCTACGGTTACTTTGGAGACATCTCTCCCAAGCGGTTGGCTTTGTG 673
QY 181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 ACTGAAGACGAATCTTGGAAATTCAGGCACTACCCGGGAGCAGTACGGGACATACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCATGACGTGCGCGGCCGCGGTACGGAGAGTAAGGTACCCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnIysGlyThr 240
DB 794 TATCCACCATACATTTCAAGACCAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleLysAspAspLys 260
DB 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCGAATTCAGTGTGTCAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerIysLeu 280
DB 914 AGACTGATTGAGGAAAGAAAGGGGTGAAGTGAAGACAGACCTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerIleLys 300
DB 974 ATCTTCTCAATGCTCTGAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCAACCAATGCCAGCATATGCTATTTGGTCCAGGCGCCGTACGGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
DB 1094 AACGGCACGTCGAGGAGGCGAGGTGCGTGTGCTGTGCTCTTCTGTGCTTGTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTTCTCAAAATTT 1165
RESULT 21
ACD41982
ID ACD41982 standard; cDNA; 1679 BP.
XX
AC ACD41982;
XX
DT 05-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #188.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour;
KW cytosolic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
KW PMBC; glucose uptake; PFA; skeletal muscle cell; adipocyte cell;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell; A-peptide; factor VIIa.
XX
OS Homo sapiens.
XX
PN US2003036179-A1.
XX
PD 20-FEB-2003.
XX
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PF 10-MAY-2002; 2002US-00142431.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
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PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028401.
PR 01-DEC-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 10-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US008439.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US007532.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
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PR 01-DEC-2000; 2000WO-US032678.
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PR 20-DEC-2000; 2000WO-US034956.
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PR 28-FEB-2001; 2001WO-US008520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
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PR 09-JUL-2001; 2001WO-US021735.
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PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
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PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-466355/44.

P-PSDB; ABO25028.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PRO4978, useful in molecular biology, chromosome and gene mapping, in
generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 375; 659pp; English.

The invention relates to an isolated nucleic acid comprising at least 80%
sequence identity to a PRO (secreted and transmembrane protein) cDNA
comprising a nucleic acid (a) encoding a PRO polypeptide, or its
extracellular domain (with or without its associated signal peptide),
which comprises any of the 275 120-850 residue amino acid sequences,
given in the specification; (b) comprising any of the 275 300-3500
nucleotide sequences, given in the specification; or (c) comprising the
full-length coding sequence of the nucleotide sequences given in the
specification, or of the DNA deposited under any of the American Type
Culture Collection (ATCC) Accession Numbers listed in the specification.
Also included are a vector comprising the novel nucleic acid, a host cell
comprising the vector, producing a PRO polypeptide, the isolated PRO
polypeptides detailed above, a chimeric molecule comprising the PRO
polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
antibody, detecting a PRO polypeptide in a sample suspected of containing
the PRO polypeptide, linking a bioactive molecule to a cell expressing a
PRO polypeptide, modulating at least one biological activity of a cell
expressing a PRO polypeptide, stimulating the release of tumour necrosis
factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
modulating the uptake of glucose or FFA by skeletal muscle cells or
adipocyte cells, stimulating the proliferation or differentiation of
chondrocyte cells (or proliferation of or gene expression in pericyte
cells), stimulating the proliferation of inner ear utricular supporting
cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
binding of A-peptide to factor VIIA, or differentiation of adipocyte
cells, detecting the presence of a tumour in a mammal and an
oligonucleotide probe derived from any of the nucleotide sequences given
in the specification. The polynucleotide is useful in molecular biology,

CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence encodes a PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores: 6.72e-36 Length: 1679
Pred. No.: 2408.00 Matches: 344
Score: 2408.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD41982 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTIPAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCAATCCAGCCAAATATGCACAAATCTATCTCTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCGCGCAGCGAGATGCCACTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyCysSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACTGACGGTCCGGCAGGGGAGCGCCACCCCTCAGGTGACATTTGAC 313
QY 61 AsnArgValThrArgValAlaTTPLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGTTCACCGGGTGGCTGGCTTAAACGAGCACCATCTCTATGTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGCCTGGATCTCTCGGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTTGATGATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGAGCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
QY 151 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTGTG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValValThrValAsn 220
DB 734 TGCAGTGCCTCCAAATGACGTGGCGCGCCCGCTGGGTAGCGAGAGTAAGGTCACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaIleGlyThrGlyValProValGlyGlnIleGlyThr 240
DB 794 TATCCACCATATCTTCAAGAGCCCAAGGGTACAGGTGTCCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
DB 854 CTGCAGTGTGAAGCCTTCAGCAGTCCCTCAGCAGNATTTCCAGTGTGTACAGGATGACAAA 913

QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrTyrLeuSerAspAspLys	260
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAA	913
QY	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
Db	914	AGACTGATTGAAGGAAGAAGGGGTGAAGTGAAGAAACAGACCTTTCCCTCTCAAAACTC	973
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
Db	974	ATCTTCTTCAATGTCTCTGAACATGATCATATGGGAATACACTTTCGCTGGCTCCAAACAG	1033
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
Db	1034	CTGGGGCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCGCGAGGTGAGC	1093
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGCAGCTCGAGGAGGAGGAGGCTGGTCTGGCTGCTGCTCTTCTGCTCTTGACCTG	1153
QY	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAAAATTT	1165
RESULT	23		
ID	ACAA04516		
XX	ACAA04516 standard; cDNA; 1679 BP.		
AC	ACAA04516;		
XX			
DT	28-MAY-2003 (first entry)		
XX			
DE	Novel human secreted and transmembrane protein PRO337 DNA.		
XX			
KW	Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;		
KW	PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;		
KW	PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;		
KW	fibroblast growth factor receptor; cell death; chromosome mapping;		
KW	gene mapping; transgenic animal; knockout animal; gene therapy; tumour;		
KW	obesity; diabetes; insulinemia; vascular permeability;		
KW	cardiac insufficiency disorder; immune response; hearing loss;		
KW	auditory hair cell regeneration; bone disorder; cartilage disorder;		
KW	sports injury; arthritis; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
XX	US2003032062-A1.		
XX			
PD	13-FEB-2003.		
XX			
PF	01-FEB-2002; 2002US-00066273.		
XX			
PR	26-AUG-1997; 97US-0056974P.		
PR	17-SEP-1997; 97US-0059115P.		
PR	18-SEP-1997; 97US-0059263P.		
PR	19-SEP-1997; 97US-0059588P.		
PR	17-OCT-1997; 97US-0062285P.		
PR	24-OCT-1997; 97US-0062816P.		
PR	24-OCT-1997; 97US-0063082P.		
PR	27-OCT-1997; 97US-0063329P.		
PR	29-OCT-1997; 97US-0063733P.		
PR	21-NOV-1997; 97US-0066364P.		
PR	25-NOV-1997; 97US-0066840P.		
PR	16-DEC-1997; 97US-0069694P.		
PR	09-FEB-1998; 98US-0074086P.		
PR	09-FEB-1998; 98US-0074092P.		
PR	25-MAR-1998; 98US-0079294P.		
PR	08-APR-1998; 98US-0081049P.		
PR	14-JUL-1998; 98WO-US014552.		
PR	10-AUG-1998; 98US-0095998P.		
PR	18-AUG-1998; 98US-0097000P.		
PR	09-SEP-1998; 98US-0099601P.		
PR	10-SEP-1998; 98US-0099803P.		


```
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValValValThrValAsn 220
Db 734 TGCAGTGGCTCCAAATGAGTGGCCGCGCGGTGACGAGAGTAAAGGTACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaIysGlyThrGlyValProValGlyGlnIysGlyThr 240
Db 794 TATCCACCATACTATTTCAGAACCAAGGTACAGGTGTCCTCCGCGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrIysAspAspIys 260
Db 854 CTGCACTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyIysGlyValIysValGluAsnArgProPheLeuSerIysLeu 280
Db 914 AGACTGATTGAAGAAAGAGGGGGAAGTGGAAAACAGACCTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTCAATGCTCTGAACATGACTATGGCACTACACTTGGTGGCTCCCAACAAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTACAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGACACGTCGAGAGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY 341 LeuLeuIysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT 24
ACAG66437
ID ACAG66437 standard; cdna; 1679 BP.
XX AC
AC ACAG66437;
XX AC
DT 24-JUN-2003 (first entry)
DE Human cDNA encoding secreted/transmembrane protein PRO337.
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
XX malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
XX leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
XX infertility; premature aging; psoriasis; inflammatory disease;
XX renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
XX hepatitis; multiple sclerosis; gene therapy.
XX Homo sapiens.
XX US2003004102-A1.
XX PD
XX 02-JAN-2003.
XX PF
XX 15-OCT-2001; 2001US-00978189.
XX XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078866P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 20-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 26-JUN-1998; 98US-00105413.
XX 07-OCT-1998; 98US-00168978.
XX 07-OCT-1998; 98WO-US021141.
XX 02-NOV-1998; 98US-00184216.
XX 06-NOV-1998; 98US-00187368.
XX 20-NOV-1998; 98WO-US024855.
XX 07-DEC-1998; 98US-00202054.
XX 22-DEC-1998; 98US-00218517.
XX 05-JAN-1999; 98WO-US000106.
XX 08-MAR-1999; 98US-00254465.
XX 10-MAR-1999; 98WO-US005028.
XX 10-MAR-1999; 98US-00265686.
XX 12-MAR-1999; 98WO-US005130.
XX 12-APR-1999; 98US-00267213.
XX 14-MAY-1999; 98US-00284291.
XX 14-MAY-1999; 98US-00311832.
XX 14-MAY-1999; 98WO-US010733.
XX 02-JUN-1999; 98WO-US012252.
XX 25-AUG-1999; 98US-00380137.
XX 25-AUG-1999; 98US-00380138.
XX 25-AUG-1999; 98US-00380142.
XX 30-NOV-1999; 98WO-US028313.
XX 02-DEC-1999; 98WO-US028551.
XX 16-DEC-1999; 98WO-US030095.
XX 30-DEC-1999; 98WO-US031243.
XX 30-DEC-1999; 98WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 10-MAR-2000; 2000WO-US006319.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 28-JUL-2000; 2000WO-US020710.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000US-00709238.
XX 10-NOV-2000; 2000WO-US030873.
XX 27-NOV-2000; 2000US-00723749.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 28-FEB-2001; 2000WO-US034956.
XX 22-MAR-2001; 2001US-00816744.
XX 22-MAR-2001; 2001US-00816920.
XX 22-MAR-2001; 2001WO-US009552.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001WO-US017092.
XX 01-JUN-2001; 2001US-00872035.
XX 05-JUN-2001; 2001WO-US017800.
XX 14-JUN-2001; 2001US-00874503.
XX 19-JUN-2001; 2001US-00886346.
XX 20-JUN-2001; 2001US-00886342.
XX 29-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
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PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;

XX WPI: 2003-341189/32.
 DR P-PSDB; ABUS0428.

XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
 PT PRO1559), useful for treating or diagnosing e.g. cancers,
 PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
 PT sclerosis in mammals.

XX Claim 2; Fig 221; 460pp; English.

XX The invention relates to a new isolated nucleic acid molecule comprising a
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 94 PRO polypeptides whose sequences are fully defined in the
 CC specification; or (b) any of 94 nucleotide sequences fully defined in the
 CC specification; or the full length coding sequence of any these 94
 CC nucleotide sequences. Also included are an isolated PRO polypeptide
 CC scoring at least 80% positives when compared to any of the PRO
 CC polypeptide sequences cited above (or an isolated PRO polypeptide having
 CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
 CC encoded by the nucleotide deposited with ATCC numbers listed in the
 CC specification; (b) the PRO polypeptide, lacking its associated signal
 CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
 CC lacking its associated signal peptide), a vector comprising the nucleic
 CC acid molecule, a host cell comprising the vector (and producing a PRO
 CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
 CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
 CC polypeptides or polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. These are particularly useful for
 CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
 CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
 CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
 CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
 CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. The present sequence encodes a PRO polypeptide

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA66437 (1-1679)

Qy 1 MetlysthrileGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAAGAACCAATCCAGCCCAAAATGCAAAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
 Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGCACAACTGACGGTCCGGCAGGGGAGAGCGCCCTCAGGTGCACTATTGAC 313
 Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
 Db 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCAATCTCTATGCTGGGAATGAC 373
 Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 374 AAGTGTGGCTGGATCTCTCGCTGCTCTCTCTGAGCAACACCCAAACGCACTACAGCATC 433
 Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAAACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCTGGTGCAGACAC 493
 Qy 121 AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCCAAAGACCTCTAGGGTCCACTCAATGTCGCAAGTATCTCCCAAAATGTAGAG 553
 Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTTCACCTGCATAGCAACT 613
 Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACAGAGCCCTACCGTTACTTGGAGACACATCTCTCCAAAGCCGGTGGCTTTGTG 673
 Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCAGGGGAGCAGTACGGGAGTACCGAG 733
 Qy 201 CysSerAlaSerAsnAspValAlaIleProValValArgValValThrValAsn 220
 Db 734 TGCAGTGGCTCCATGACGTGGCGCCGCGGTGTACGAGAGTAAAGGTCAACCGTGAAC 793
 Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTCCAGAGCCCAAGGGTACAGGTGCCCGTGGGACAAAGGGGACA 853
 Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 Db 854 CAGCAGTGTGAAGCTCAGCAGTCCCTCCAGCAGAAATCCAGTGGTACAGGATGACAAA 913
 Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 973
 Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTTCAATGTCTCTGAAATGAGAACTACACTTGGTGGCTTCCACACAG 1033
 Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACCAATGCCAGCATCATGTATTGTTGGTCCAGGCGCGGTACAGGAGGTGAGC 1093
 Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisIleLeu 340
 Db 1094 AACGGCACGCTCGAGGAGGGGAGGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 Qy 341 LeuLeuLysPhe 344
 Db 1154 CTCTCTCAAAATTT 1165

RESULT 25

ACA68559 standard; cDNA; 1679 BP.

XX ACA68559;

AC ACA68559;

XX 25-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

DE

XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping; gene;
 KW ss.
 XX Homo sapiens.
 OS
 XX
 XX US2003088063-A1.
 PN
 XX
 XX 08-MAY-2003.
 PD
 XX
 XX 12-AUG-2002; 2002US-00219003.
 PF
 XX
 XX 25-JUL-2000; 2000US-0220664P.
 PR
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 PR
 XX
 XX 29-JUN-2001; 2001WO-US021066.
 PR
 XX
 XX 09-APR-2002; 2002US-00119480.
 PR
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 FI P-PSDB; ABU82110.
 DR
 XX
 XX WPI; 2003-393229/37.
 DR
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 XX Claim 2; Fig 125; 314pp; English.
 PS
 XX
 CC The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This sequence encodes a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA68559 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAACACCATCCAGCAAAATGACAAATCTATCTTTGGGCAATCTTACGGGGGTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTGCTCTTCCAGAGTGCCTGGCGCAGCGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyLeuSerAlaThrLeuArgCysThrIleAsp 60

DB 254 GCTATGGACAAACGTCACCGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGTGCTCGATCTCTCGCTGGTCTCTTCGAGCAACACCCAAACGCGAGTACGATC 433
 QY 101 GlnIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCCACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCAATGACGTGGCGCGCCGCTGTGTACGGAGAGTAAAGGTCAACGTAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCCAGAACCCAGGGTACAGGTGTCCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGTATTGAAGAAAGAAAGGGGTGAAAGTGAAGAACAGACCTTTCTCTCAAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGNACTACACTTGGCTGGCTTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGTTTGGTCCAGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCTGAGGAGGAGGCGTGGCTGTGGCTGTGCTCTTCTGGTCTTGCACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTTCTCAAAATTT 1165

RESULT 26
 ACA04211
 ID ACA04211 standard; cDNA; 1679 BP.
 XX
 AC ACA04211;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;

inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 infertility; birth defects; premature aging; AIDS; biosensor;
 acquired immunodeficiency syndrome; cancer; diabetic complication;
 bioreactor; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-00137865.
 XX
 PR 31-MAR-1997; 97WO-US0005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US0005028.
 PR 10-MAR-1999; 99WO-US0005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 08-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 03-OCT-1999; 99WO-US023089.
 PR 23-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 18-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen WE, Goddard A, Godowski PU, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-331925/31.
 DR P-PSDB; ABU67033.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX
 PS Claim 2; Fig 375; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
 CC comprises the full-length coding sequence of the DNA deposited under
 CC American Type Culture Collection (ATCC) accession number in a list given
 CC in the specification. Also included are vectors and host cells for
 CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
 CC extracellular domains and mature sequences, methods of detecting PRO
 CC proteins, methods for stimulating the release of TNF-alpha (tumour
 CC necrosis factor alpha) from human blood, (and the proliferation of
 CC differentiation of chondrocyte cells, the proliferation of, or gene
 CC expression in pericyte cells, the release or proteoglycans from
 CC cartilage, proliferation of inner ear articular supporting cells, the
 CC proliferation of T-lymphocyte cells, the release of a cytokine from
 CC peripheral blood mononuclear cells (PBMC), or the proliferation of
 CC endothelial cells), a method for modulating the uptake of glucose or free

PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0133695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0143698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 03-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
 PI Paoi NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-341960/32.
 DR P-PSDB; ABU79804.

XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying biological
 PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 51; 255pp; English.

XX The invention relates to an isolated, secreted/transmembrane polypeptide,
 CC termed PRO polypeptide, having at least 80% sequence identity to a
 CC sequence selected from any one of the 37 sequences appearing as ABU79779
 CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 CC under any one of the ATCC numbers given in the specification. Also
 CC included are an isolated nucleic acid molecule having at least 80%
 CC sequence identity to a sequence selected from any one of the 37 cDNA
 CC sequences defined in the specification (or encoding the mature PRO

CC protein or a PRO protein extracellular domain), a PRO expression vector,
 CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
 CC antibodies and a method for linking a bioactive molecule to a cell
 CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
 CC radiolabel or an antibody and causes the death of the cell. PRO or the
 CC antibody is useful for modulating at least one biological activity of
 CC cell expressing the above polypeptides. PRO is useful for identifying
 CC agonists or antagonists of PRO, for preparing a variant of PRO, as
 CC molecular weight markers for protein electrophoresis purpose and PRO
 CC nucleic acid is useful for recombinantly expressing those markers. PRO is
 CC also useful as therapeutic agent. PRO is useful in assays to identify
 CC other proteins or molecules involved in binding interaction. PRO nucleic
 CC acid is useful as hybridisation probes, in chromosome and gene mapping,
 CC in generation of antisense RNA and DNA, in the preparation of PRO
 CC polypeptide, in gene therapy, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, to construct hybridisation
 CC probes for mapping the gene which encodes the PRO and for the genetic
 CC analysis of individuals with genetic disorders, for chromosome
 CC identification, as a chromosome marker, and for generating probes for
 CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
 CC Western analysis. The antibody is useful in diagnostic assays for PRO,
 CC e-g detecting its expression in specific cells, tissues or serum, for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. PRO or Ab is useful for the preparation of medicament for
 CC treating conditions which is responsive to the PRO polypeptide or anti-
 CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
 CC present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-017-084A-523 (1-344) x ACA65657 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ALGRAAACATCCAGCCAAAATGACAAATCTTCTCTTGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCCGTGCAGCGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACAACGTGACGTCGCGGAGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
 QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGTCACCGCGTGCCTTAAACCGCAGCACCACCTCTCTATCTGGATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTGCTGGATCCTCGCGTGTCTTCTTGAGCAACACCCAAACGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACGACGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTCAGATATCTCCATTAATGAAGGAGACAAATATTAGCTCCTCAGTCATGCAACT 613

QY 161 GIVArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
Db 614 GGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
QY 181 SerGluAspGluTyrLeuGluLeuGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
Db 674 AGTGAAGAGCAATACTTGGAAATTCAGGGCATCCACCGGAGCAGTCAGGGGACTACGAG 733
PR 29-OCT-1998; 98WO-US022992.
PR 29-OCT-1998; 98WO-US024855.
QY 201 CysSerAlaSerAsnAspValAlaProValValArgArgValLysValThrValAsn 220
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
Db 734 TGCAGTGCCTCCCAATACGTGGCGCGCCGCTGTACGGAGATAAGGTACCCGTGAAC 793
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
Db 794 TATCCACCATACATTCAGAGCAAGGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 913
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028403.
Db 914 AGACTGATTCAGAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 973
PR 30-NOV-1999; 99WO-US028403.
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaLysSerAsnLys 300
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
Db 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGGTGGCTCCAAAG 1033
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
Db 1034 CTGGGCCACACCAATGCACGATCATCTATTTGGTCCAGGCGCCGTCAGGAGGTGAGC 1093
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
QY 321 AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
PR 30-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
Db 1094 AACGGCAGTCGAGGAGGAGGCTGCTGGCTGTGCTCTTCTTGGCTTGGCACTG 1153
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
QY 341 LeuLeuLysPhe 344
PR 06-JAN-2000; 2000WO-US000376.
Db 1154 CTTCCTCAAAATTT 1165
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.

RESULT 28

ADA45894

ID ADA45894 standard; cDNA; 1679 BP.

XX AC ADA45894;

XX DE 20-NOV-2003 (first entry)

XX DT Novel human secreted and transmembrane protein PRO337 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; gene; ss;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW Glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokine release stimulator; tumour;
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.

XX OS Homo sapiens.

XX FN US2003022328-A1.

XX PD 30-JAN-2003.

XX PF 16-APR-2002; 2002US-00123904.

XX PR 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00860208.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00874636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 28-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00909827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2003-584997/55.
 DR P-PSDB; ADA45895.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 2; Fig 375; 659pp; English.
 XX
 CC The invention describes 305 nucleic acids encoding PRO (secreted and
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the
 CC release of TNF-alpha from human blood, for modulating the uptake of
 CC glucose or PFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating the proliferation or differentiation of chondrocyte cells,
 CC for stimulating the proliferation of or gene expression in pericyte
 CC cells, for stimulating the release of proteoglycans from cartilage, for
 CC stimulating the proliferation of inner ear utricular supporting cells,
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
 CC the release of a cytokine from BMC cells, for inhibiting the binding of
 CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
 CC cells, for stimulating proliferation of endothelial cells, for detecting
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 CC are useful for isolating genomic and cDNA nucleotide sequences or
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 CC in assays to identify other proteins or molecules involved in binding
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 CC and gene mapping, in generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptide, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, in gene therapy, for
 CC chromosome identification, as chromosome marker, and for generating
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
 XX a novel human secreted and transmembrane PRO polypeptide.
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0
 US-10-017-084a-523 (1-344) x ADA45894 (1-1679)
 QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACAACGTCACGCTCCGGCAGGGGAGAGCGCCCTCAGGTGCACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AGTGGTGTCTGGATCTTCGGTGTCTTCTTGAGCAACACCCCAACGCGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 ACCACCCCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTCTCTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCCTACCTGCGATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGACCTTAGGGTCTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGATATCTTGGAAATTCAGGGCATCATCCCGGAGCAGTCAGGGAGTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaProValValArgArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCAATGACGTCGGCGCGCGTGTACGGAGAGTAAAGSTCACCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCAAGCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
 DB 854 CTSCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGAAAGAAAGGGGTGAAAGTGAAGAACAGACCTTTCTCTCAAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGCTCTGACATGACTATGGAACTACACTTGGCTGGCTTCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATTTGGTCCAGGCCCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCGTCAGAGGGGCGAGCTCGTCTGGCTCTTCTTGGTCTTGGACCTG 1153
 QY 341 LeuLeuLysPhe 344

Db 1154 CTCTCAATT 1165
 RESULT 29
 ADA76325
 ID ADA76325 standard; cDNA; 1679 BP.
 XX
 AC ADA76325;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human PRO polynucleotide #188.
 XX
 KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
 KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
 KW liver; microvascular endothelial cell; glucose; RFA;
 KW skeletal muscle cell; adipocyte cell; pericyte cell;
 KW inner ear utricular supporting cell; T-lymphocyte cell;
 KW endothelial cell tube formation; bone disorder; cartilage disorder;
 KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
 KW immune system cell infiltration.
 XX
 OS Homo sapiens.
 XX
 XX US2003073212-A1.
 XX
 PD 17-APR-2003.
 XX
 XX 16-APR-2002; 2002US-00123903.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028584.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00818744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-687639/65.
 P-PSDB; ADA76326.

New isolated nucleic acid encoding a secreted and transmembrane
 polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
 gene mapping, in generating antisense RNA and DNA, and in gene therapy.
 Claim 2; Fig 375; 659pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor- α (TNF- α) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating differentiation of adipocyte cells, for stimulating
 CC proliferation of or gene expression in pericyte cells, for stimulating
 CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
 CC cells, for inducing endothelial cell tube formation and for treating
 CC various bone and/or cartilage disorders such as sports injuries and
 CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
 CC from cartilage are useful for treating sports-related joint problems. PRO
 CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
 CC polypeptides are also useful for treating various mammalian haemoglobin-
 CC associated disorders such as various thalassemias and conditions which
 CC may benefit from enhanced local immune system cell infiltration. This
 CC sequence represents a human PRO polynucleotide of the invention. Note:
 CC The sequence data for this patent is also available in electronic format
 CC from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-017-084A-523 (1-344) x ADA76325 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACACCATCCAGCCAAATGCAATCTATCTCTGGCAATCTTACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCTGGCGAGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACAACTGACGCTCGCGAGGGGAGAGCGCCACCTCAGTGCCTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrrAlaGlyAsnAsp 80
 DB 314 AACCGGTCCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrIleSerIle 100
 DB 374 AAGTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAACGCGAGTACGATC 433
 QY 101 GluIleGlnAsnValAspValTyrrAspGluGlyProTyrrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGCTGGATGTTATGACGAGGGCCCTTACACCTGCTGCTGCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140

DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATCTGTGCAAGTATCTCCCAAAATTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCCTGATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTriArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGAGCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrrGlu 200
 DB 674 AGTGAAGACGAATCTTGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValThrValAsn 220
 DB 734 TGCAGTGGCTCTCAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACGTGAAC 793
 QY 221 TyrProProTyrrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCAAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrrLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgIleIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerIleLysLeu 280
 DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAATC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrrGlyAsnTyrrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGTGGCTCCCAACAAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGTCTTGTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGCGACGTCAGAGGGGCGAGGCTGCGTCTGGCTGGCTCTTCTGTCTTGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165
 RESULT 30
 ABT44288
 ID ABT44288 standard; cDNA; 1679 BP.
 XX
 AC ABT44288;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO337 cDNA.
 XX
 KW PRO; proliferation; pericyte cell; TNF- α ; blood; chondrocyte; ss;
 KW differentiation; dermal fibroblast; tumour; gene therapy; gene;
 KW cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003050448-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 28-AUG-2002; 2002US-00230414.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.

XX Baker XP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 FI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX P-PSDB; ABJ72290.
 DR WPI: 2003-521818/49.
 XX P-PSDB; ABJ72290.
 XX
 XX New nucleic acid encoding for a PRO protein, useful for the manufacture
 PT of a medicament for diagnosing or treating tumors or for measuring or
 PT detecting expression of an associated gene.
 XX
 XX Claim 2; Fig 125; 315pp; English.
 XX
 XX The invention relates to a novel isolated nucleic acid encoding a fully
 CC defined PRO polypeptide. The molecules of the invention may be useful for
 CC stimulating proliferation or gene expression in pericyte cells or the
 CC release of TNF-alpha from human blood. Other possible uses include the
 CC stimulation or inhibition of chondrocyte proliferation or
 CC differentiation, the stimulation of human dermal fibroblast cell
 CC proliferation and the detection of the presence of a tumour within a
 CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
 CC of a medicament for diagnosing or treating a tumour within a mammal or
 CC for measuring or detecting the expression of an associated gene, as well
 CC as during gene therapy. The current sequence is that of the human PRO
 CC cDNA of the invention
 XX
 XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-017-084A-523 (1-344) x APT44288 (1-1679)

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 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrProLys 40
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 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60
 DB 254 GCTATGGACACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACCTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuIleuValAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCCGGGTGGCCCTGGCTAAACCGCAGCACCACCTCTATGTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTGGCTGGATCCTCGCGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluClyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTGTATGACAGGGGCCCTTACACCTGCTGGTGCACACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTCTAGGGTCACCTCATTTGGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACGACGCTTACCTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673

QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGACTTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheIleuSerLysLeu 280
 DB 914 AGACTGATTTGAAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATGACTTGGTGGCTTCCAAACAG 1033
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 DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGGCGCGTCCAGCGAGGTGAGC 1093
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 DB 1094 AACGGCACGTCGAGGAGGGCGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
 QY 341 LeuLeuLysPhe 344
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Search completed: May 28, 2004, 13:09:00
 Job time : 575 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:15 ; Search time 114 Seconds

(without alignment)
1674.589 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 2408

Sequence: 1 MKTIQPKMHSISWAFTGL.....RRAGCVWLPLVLLHLLKF 344

Scoring table: BLOSUM30

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Ygapop 1.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-LIST=100 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
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-FGAPEXT=7 -YGAPOP=1 -YGAPEXT=0.1 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	100.0	1032	4	US-09-700-397-1
2	2408	100.0	1693	4	US-09-700-397-2
3	2185	90.7	939	4	US-09-700-397-5
4	1748.8	72.6	11673	4	US-09-334-220-3
5	1737.1	72.1	11580	4	US-09-334-220-4
6	1727.6	71.7	35100	2	US-08-770-379-17
7	1727.6	71.7	35100	3	US-08-757-669A-17
8	1727.6	71.7	124884	4	US-09-230-371A-17
9	1725.9	71.7	124884	4	US-09-661-596A-76
10	1725.9	71.7	124884	4	US-09-913-514-1
11	1725.3	71.6	124884	4	US-09-661-596A-76
12	1725.3	71.6	124884	4	US-09-913-514-1

13	1722.9	71.5	125157	4	US-09-913-514-2	Sequence 2, Appli
14	1721.1	71.5	21126	1	US-08-008-216-19	Sequence 19, Appl
15	1721.1	71.5	21126	1	US-08-459-569-19	Sequence 19, Appl
16	1721.1	71.5	21126	1	US-08-458-831-19	Sequence 19, Appl
c 17	1719.8	71.4	125157	4	US-09-913-514-2	Sequence 2, Appli
c 18	1718.9	71.4	12752	2	US-08-459-146-1	Sequence 1, Appli
c 19	1718.9	71.4	12752	2	US-08-459-085-1	Sequence 1, Appli
20	1718.2	71.4	11444	2	US-08-222-617A-26	Sequence 26, Appl
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22	1717.5	71.3	14578	3	US-08-859-694-1	Sequence 1, Appli
23	1717.2	71.3	11272	4	US-09-341-461-1	Sequence 1, Appli
c 24	1717.2	71.3	63588	4	US-09-873-404-3	Sequence 3, Appli
c 25	1714.9	71.2	31880	4	US-09-453-702B-242	Sequence 242, App
26	1714.7	71.2	38584	4	US-09-453-702B-50	Sequence 50, Appl
c 27	1713.2	71.1	11580	4	US-09-334-220-4	Sequence 4, Appli
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c 29	1712.2	71.1	14311	3	US-08-646-695-1	Sequence 1, Appli
c 30	1712.2	71.1	14311	3	US-08-646-695-7	Sequence 7, Appli
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33	1712.2	71.1	38155	4	US-09-453-702B-79	Sequence 79, Appl
34	1712	71.1	12492	6	5206163-2	Patent No. 5206163
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36	1712	71.1	14078	4	US-08-702-330-1	Sequence 1, Appli
37	1711.3	71.1	10970	3	US-08-716-351A-5	Sequence 5, Appli
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39	1710.3	71.0	31328	4	US-09-215-694-19	Sequence 19, Appl
c 40	1710.1	71.0	786431	4	US-09-751-389-3	Sequence 3, Appli
c 41	1709.8	71.0	24595	6	5428147-1	Patent No. 5428147
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c 44	1708.5	71.0	21126	1	US-08-008-216-19	Sequence 19, Appl
c 45	1708.5	71.0	21126	1	US-08-459-569-19	Sequence 19, Appl
c 46	1708.5	71.0	21126	1	US-08-458-831-19	Sequence 19, Appl
47	1708.5	71.0	24595	6	5428147-1	Patent No. 5428147
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49	1708.1	70.9	12734	4	US-09-344-456-1	Sequence 1, Appli
50	1707.1	70.9	246240	2	US-08-724-394A-20	Sequence 20, Appl
51	1707.1	70.9	246240	2	US-08-724-394A-21	Sequence 21, Appl
52	1707.1	70.9	246240	2	US-08-724-394A-22	Sequence 22, Appl
53	1707	70.9	10878	4	US-09-911-842A-1	Sequence 1, Appli
c 54	1706.8	70.9	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 55	1706.8	70.9	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 56	1706.8	70.9	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 57	1706.5	70.9	1830421	4	US-09-557-884-1	Sequence 1, Appli
c 58	1706.5	70.9	1830421	4	US-09-643-990A-1	Sequence 1, Appli
c 59	1706.4	70.9	31328	4	US-09-215-694-19	Sequence 19, Appl
60	1706.4	70.9	63563	4	US-09-596-002-33	Sequence 33, Appl
61	1705.7	70.8	40429	4	US-08-311-731A-125	Sequence 125, App
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63	1705.4	70.8	7926	3	US-09-500-554-1	Sequence 1, Appli
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66	1705.4	70.8	36651	4	US-09-738-894A-3	Sequence 3, Appli
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68	1704.5	70.8	9848	4	US-09-385-222A-3	Sequence 3, Appli
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70	1703.9	70.8	59065	4	US-09-813-817-3	Sequence 3, Appli
71	1703.9	70.8	59065	4	US-09-978-197-3	Sequence 3, Appli
72	1703.8	70.8	9416	4	US-08-823-895A-26	Sequence 26, Appl
73	1703.8	70.8	9416	4	US-10-104-966-13	Sequence 13, Appl
74	1703.8	70.8	9599	3	US-09-014-416-2	Sequence 2, Appli
c 75	1703.8	70.8	87563	4	US-09-453-702B-57	Sequence 57, Appl
c 76	1703.7	70.8	11703	3	US-08-801-263A-8	Sequence 8, Appli
c 77	1703.7	70.8	11703	3	US-09-102-248-8	Sequence 8, Appli
c 78	1703.7	70.8	11703	3	US-09-367-764-8	Sequence 8, Appli
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80	1703.6	70.7	14042	3	US-08-652-877-85	Sequence 85, Appl
81	1703.6	70.7	14044	3	US-08-652-877-89	Sequence 89, Appl
82	1703.6	70.7	14080	3	US-08-652-877-87	Sequence 87, Appl
83	1703.6	70.7	14080	3	US-08-652-877-83	Sequence 83, Appl
84	1703.6	70.7	100848	4	US-09-596-002-39	Sequence 39, Appl
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 LOCATION: (214)...

US-09-700-397-2

Alignment Scores:

Pred. No.: 8,18e-46 Length: 1693
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
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US-10-017-084a-523 (1-344) x US-09-700-397-2 (1-1693)

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 Qy 21 AlaIleuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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 Db 250 GCTATGGACACGTCACGGTCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 309
 Qy 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
 Db 310 AACCGGGTCACCGGGTGCGCTGGTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 369
 Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnTrpSerIle 100
 Db 370 AAGTGGTGCTGGATCTCTCGCTGGTGTCTTCTGAGCAACCCAAACCGATGACAGCTC 429
 Qy 101 GluIleGlnAsnValAspValTrpAspGluGlyProTyThrCysSerValGlnThrAsp 120
 Db 430 GAGATCCAGAACGTGGATGTGTATCGCAGGGGCCCTTACACCTGCTCGTGCGAGACAG 489
 Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 Db 490 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCCAAATTTAGAG 549
 Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 Db 550 ATTCTTTCAGATATCTCCATTTATGAGGAGAACATATTAGCTCAGCTGATAGCACT 609
 Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 610 GGTAGACACAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 669
 Qy 181 SerGluAspGluTyrlLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrglu 200
 Db 670 AGTGAAGACGAATACTTGGAAATTCAGGGGCATCACCCTGGAGCAGTCAGGGACATACGAG 729
 Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 Db 730 TGCAGTGCCTCCATGACGTGGCGCGCGCTGGTACGGAGAGTAAGGTCCACCGTGAAC 789
 Qy 221 TyrProProTyrlIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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 Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrlLysAspAspLys 260
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 Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Qy 281 IlePhePheAsnValSerGluHisAspTyrlGlyAsnTyrlThrCysValAlaSerAsnLys 300
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 Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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RESULT 3

US-09-700-397-5
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 ; Patent No. 6664383
 ; GENERAL INFORMATION:
 ; APPLICANT: Onco Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
 ; FILE REFERENCE: Q61459
 ; CURRENT APPLICATION NUMBER: US/09/700,397
 ; CURRENT FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: JP 10-131815
 ; PRIOR FILING DATE: 1998-05-14
 ; PRIOR APPLICATION NUMBER: PCT/JP99/02485
 ; PRIOR FILING DATE: 1999-05-13
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 939
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-700-397-5

Alignment Scores:

Pred. No.: 2,33e-41 Length: 939
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 90.74% Indels: 0
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US-10-017-084a-523 (1-344) x US-09-700-397-5 (1-939)

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 Db 61 AGCGCCACCTCAGGTGCACTATTGCAACCGGGTCACCCGGGTGGCTGGCTAAACCGC 120
 Qy 72 SerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
 Db 121 AGCACCATCTCTATGCTGGGAATGCAAGTGTGCTGGATCTCGGTGCTCTTCG 180
 Qy 92 SerAsnThrGlnThrGlnTrpSerIleGluIleGlnAsnValAspValTrpAspGluGly 111
 Db 181 AGCAACCCCAACGAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGGGGC 240
 Qy 112 ProTyThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIle 131
 Db 241 CTTACACCTGCTCGGTGCGAGACACACCAACACCTCTAGGGTCCACCTCAT 300
 Qy 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
 Db 301 GTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAAC 360

QY 138 ---IleVal-----Glu---Ile 141
Db 3580 GGAGTCGTCTCTGGATCTTCTGTACTTCAGCAAGGCTGGGAAGGCGCTGGTG 3639
QY 142 Ser-----Ser-----Aap-----IleSerIle----- 147
Db 3640 AGCTGGACCTGGACACATCTCTGGTGGACTTTGTCCAGTTCTACATCCAGATAGAGGA 3699
QY 148 ---Asn-----GluGly----- 150
Db 3700 GAGAGTGTGCTGCTGCAACAGCTTCAGCAGCAGAGAGGAGGCATTTCTGCTCCAGTATAGC 3759
QY 151 AsnAsn-----Ile-----Ser--- 154
Db 3760 AACAAACGGGGCATCCAGTGGCACTCTGGCAGAGATGTACTTCTCAGACTTCAGCAAA 3819
QY 155 ---Leu-----Thr---Cys----- 157
Db 3820 CCCAGATTGTCTACTCTGGAGCTCCAGCTGTGTGGAAAGACCCCTTTGACCAGGTTCGCG 3879
QY 157 ----- 157
Db 3880 TGGTGAAGCCTGTGTTCTCGGGGAGGACTATGACCAAGTGGGCGGTGGTATGATATATC 3939
QY 158 -----Ile----- 158
Db 3940 ATTCTGTGAGAGAAGCAGAGCAGGTATCCAGTTGTCAACCCAACTTTGCCCCAGAAC 3999
QY 158 ----- 158
Db 4000 TTCTATGAAAGCCAGCTTTGATACCTATGAAACCAATGAGTGTGTGCTAATGTTG 4059
QY 159 -----AlaThr----- 160
Db 4060 GCCAATGAAGCANGCTTAABAAACGACAGCTTCTGTGCAACACGCCGTGAGCATGGTG 4119
QY 161 ---Gly-----Arg----- 162
Db 4120 TTTGAAAGTCAGATGGAGACCGGTTTGCAGTAACTCGAGATCTGACCTGAAACCTGGA 4179
QY 162 ----- 162
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QY 162 ----- 162
Db 4240 GTTCTCTGCTGAGTATTCATGATGTCGGGCTGCTGCTGTTCTGTTGAAGGAGGATGC 4299
QY 163 ---Pro-----GluProThr 166
Db 4300 TTCCAGGCTCAGCGCAAGAGGATGTGAAGGGAATCCAGGAAATTGAGTGAAGCTTACT 4359
QY 167 Val-----Tip---ArgHisIleSer-----Pro--- 174
Db 4360 GTCTATTATCTGGGACTTCGAGATGAGTACTAGA---ATCACCATTGCCATTTCCAAG 4416
QY 175 -----LysAla----- 176
Db 4417 TCCCTTGATCCAGCAAGACCAAGATTCGATGATCCAGAGAGCAGCTCTCAGAGAAT 4476
QY 177 -----Val----- 177
Db 4477 GTGCCCCGGTTTGCTTAGATGGGGTGTACATATCTGAGCCTTTGTCCAGTTACTGCAGT 4536
QY 178 -----Gly-----Phe----- 179
Db 4537 GGCCATGGAGACTGCATCTCGGGGGTGTGTTTTTGTGACCTGGGGTACACAGCTGCACAA 4596
QY 180 ---Val-----SerGlu-----Aap-----Glu----- 184
Db 4597 GGAACCTGTGTGTCAACACCCCTTAACACAGTGTGATGTCGACAGCTTTGAGGGGAAG 4656
QY 184 ----- 184

Db 4657 CTAAGCCCACTGTGGTACAAAATCACCGGGGGTTCAGGTTGGCAGGGCTGTGGCAACCTC 4716
QY 185 ---Tyr-----Leu-----Glu----- 187
Db 4717 AATGACGCGAGGTCCTCTACTTTAATGGCTTGGGAAAGGGAAGCCAGGACAGTCCCA 4776
QY 188 -----IleGln----- 189
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RESULT 5

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US-09-334-220-4
; Sequence 4, Application US/09334220
; Patent No. 6323177
; GENERAL INFORMATION:
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; APPLICANT: St. Judes Children's Research Hospital
; APPLICANT: Curran, Thomas
; APPLICANT: D'Arcangelo, Gabriella
; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND
; TITLE OF INVENTION: THERAPIES
; FILE REFERENCE: 2427/0F704
; CURRENT APPLICATION NUMBER: US/09/334,220
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11580
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-334-220-4
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Alignment Scores:

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Pred. No.: 1,47e-25 Length: 11580
Score: 1737.10 Matches: 296
Percent Similarity: 11.27% Conservative: 41
Best Local Similarity: 9.90% Mismatches: 4
Query Match: 72.14% Indels: 2649
DB: 4 Gaps: 249
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US-10-017-084a-523 (1-344) x US-09-334-220-4 (1-11580)

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QY 4 -----Ile-----Gln---Pro----- 6
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QY 7 -----Lys----- 7
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Qy ----- 213
7664 GTCTGTGATGAACAGTGGGTGGCTGTACTGTGATGACCCCGAGACCTCTCTTCCCAACC 7723
Qy -----Arg-----Val----- 215
7724 CAACTCAAGACAACTTCAATCGAGCTCCATCCAGTCAGACTGGCTGACTGTGAACCGA 7783

Qy -----Lys----- 216
Db GGGAAATTTGAGTACAGTGTGTGGAGCCGTGGCGTGGGAATGGCTCTCCATTTCAAGTGG 7843
Qy -----ValThrVal----- 219
7844 GGTGTAGTCTGATTTATTTAGTACACTGTGTGATCTAAACCTCAATAATGCTGATTCATCAA 7903
Qy ----- 219
7904 TTTTACTTATGATGGTGGCTGATTACACCAACCAACCGTACCAAGGTGTTCTCTTG 7963
Qy -----Asn----- 220
7964 GAATATTTCTCAATGAGGACATTTACCTGGAACCTGCTCATGGAGATTTTCTATGACCAG 8023
Qy Tyr-----ProPro----- 223
8024 TACAGTAAGCCCGATTTGTGAATATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8083
Qy -----Tyr----- 224
8084 CGCTTCGCTGTGGCAGCCAGACATGACGGCTGGATCAGAACGACTGGGCCATTGAC 8143
Qy -----IleSer----- 226
8144 AATGTCCTCATCTCAGGCTCTGCTGACCAAGAGCCGTTATGCTGGACACCTTCAGCAGC 8203
Qy -----Glu-----Ala 228
8204 GCCCAGTACCCAGCAGAGCGCTCCCTGTCAGATGCGCGCCCTGTCGGGAGATCGCC 8263
Qy -----Lys----- 229
8264 TTGACATGTTTATGGAAGACAAAATTCTCAGTCAATGAGCAGCTGGCTATTTCCATGATGAT 8323
Qy -----GlyThr----- 231
8324 TGACAGTAGAAGATTTCTGTGACTCCCTGATGTTGTGATGCTCTGTGGCAGTCTGAT 8383
Qy Gly-----Val-----ProVal-----Gly-----Gln 237
8384 GGACGGAGGTGTATGACAGTGACCCATGACCTCAGTCTCCCACTGAAGCTGGATTTGCAA 8443
Qy -----Lys-----Gly----- 239
8444 TTCAAGATCTCAGTTGGATGTAAGGTGTCTGAAAAAATTGCCCAAGATCAAAATTCATGTG 8503
Qy -----Thr-----Leu-----GlnCys-----GluAla 245
8504 CAGTATTTCTACTGACTTGGTGTGAGTTGGAATTTATCTGGTCCCTCAGTCTTGCCTGCT 8563
Qy -----Ser-----AlaVal-----ProSerAla----- 251
8564 GACCCAAATGCTCTGGAAGTGTCTTCAGCCATCTGTATCTTTCCAACTAAAGGTGG 8623
Qy -----Glu----- 253
8624 AAAAGGATCACCTACCCACTTCTCTGAAAGCTTAGTGGGAAATCCGGTAAGGTTTAGGTTC 8683
Qy -----GlnTyr----- 256
8684 TATCAGAGTACTCAGACATGTCAGTGGCAATCGATAATTTCTTACCTGGGCCCTGGATGC 8743
Qy -----Lys-----Asp----- 259
8744 TTGACACATGTCAGGGGCCATGGAGATTTGTTAAGGAACAGTGCATCTGTGATCCGGGA 8803
Qy -----Lys-----Arg----- 261
8804 TACTCAGGGCCAACTGCTACTTGTACCCACACTCTGAGACTTTCTCTGAAGGAACGCTTT 8863

QY 262 -----Leu----- 262
Db 8864 GACAGTGAAGAAATCAAACTGACTTATGATGCTTATGAGGTGGAGTACTTGCACT 8923
QY 263 -----Glu----- 264
Db 8924 GAGTGTGAATCTTGGCGAGGACACTGCACTCTAATTTGGGGGATCCACTGTGAGACAA 8983
QY 264 ----- 264
Db 8984 GCGGTTACAAAGATTGGATCTTCGAGGTGCAAGTTCCTGCAATACTGGGGCGGCATC 9043
QY 265 Gly-----LysLysGlyVal--- 269
Db 9044 GGTAGTGAGAACAAATGACCTCTTGCCATCGTCCCATCTGCCGGAAGGAGGCTGCTG 9103
QY 269 ----- 269
Db 9104 TTGGACTACTCTACCGATGGAGGAATTAACCTGGACTTTGCTCCATGAGATGGAATACCAG 9163
QY 270 Lys-----Val-----Glu-----Asn--- 273
Db 9164 AATATACATTTCTGTAGACAGCACTACATCTTCTCTGAAGATGCCCTCACCAACACA 9223
QY 274 -----Arg-----ProPhe---LeuSer--- 278
Db 9224 ACTCGACTTCTGCTGGTGGCAGCCTTTTGTGATCAGCAATGGAATTTGTGTCTCTGGGGTG 9283
QY 279 Lys-----LeuLeu----- 281
Db 9284 GAGGTGCTCAGTGGGCACTGGACACATTTTGAATGGTGGAGCAGAAATCAATCCAGC 9343
QY 282 -----Phe----- 283
Db 9344 CAATGTGTGACACTTTTGTATGATGAAGCACTTCCATGAAGAAACTGAGTTTTTAC 9403
QY 284 ---Asn---Val---Ser-----Glu-----His--- 288
Db 9404 CCTAATGCTGTAGGACAGCAGGATTTGTGGCAATCCATCTTTCACCTCTATTGGCCA 9463
QY 289 -----Asp----- 289
Db 9464 AATAAAGAGAGCAAGCACTCACAATGCTCTCTCTCCGAGAACTCATATACAGCCA 9523
QY 290 ---Tyr----- 292
Db 9524 GGATACATGATGAGTTAAATTTGGTGGTGTGTGAAGCCACTCTTGTGTGACCTT 9583
QY 293 -----TyrThr----- 294
Db 9584 CATTCCGTAATGCTGGAAATACATAAGGATGCAAGATCGGATTCCTGGCGAGCTCGTACAG 9643
QY 295 ---CysVal-----AlaSerAsnLysLeuGly-----His--- 303
Db 9644 ACCAGTGGCTTCTCTCTCTCTTAACAGCATTGGTGTCTCCCTTTCAGTTCATGAA 9703
QY 304 ---Thr-----AsnAlaSer-----IleMetLeu----- 310
Db 9704 GCACCATCTACAACTCTGTCAACAGCTCAAGTGGAAAAAGATCACCATCCAGCTGCCT 9763
QY 311 -----Phe----- 311
Db 9764 GACCATGCTCTCTCTAGTGCACACAGTTCCGCTGGATCCAGNAGGAGAGAACTGAG 9823
QY 312 -----Gly-----Pro----- 313
Db 9824 AAGCAAGCTGGGCAATTGACACAGCTGTATATTGGAGAGGCTTGCCCAAGCTCTGCAC 9883
QY 314 -----GlyAla----- 315
Db 9884 GGCACGGATATGTCACAGCCGGTGCATCTGATCTGGCAGGAGCTTCCAAGTGAT 9943
QY 316 -----Val-----Ser-----Glu----- 318

Db 9944 GACTGCTCTGTTTTCAGTCAGACCTTCCCGTGTATATTAAGATAATTTTGAGTCGCA 10003
QY 319 ---ValSer-----Asn-----GlyThr----- 323
Db 10004 AGAGTCACCGAGGCAAACTGGGAGACCAITTCAGAGTGGAGTCATAGGAGTGGCTGTGG 10063
QY 324 ---Ser-----Arg--- 325
Db 10064 CAGCTGGCCCCCTACGCCCATGGAGACTCACTGTACTTTAATGGCTGTCTCAGATCAGGCAA 10123
QY 326 ---ArgAla----- 327
Db 10124 GCAGCTACCAAGCCTCTGGATCTCACTCGAGCAAGCAAAATCATGTTTGTGTCAAAT 10183
QY 328 Gly-----Cys----- 329
Db 10184 GGGAGCATGTGCGAGACGGACAGCTGCAACAGTGAACCTGAGTGGCCCCCAGCTGTGGAC 10243
QY 330 ---Val-----Tyr----- 331
Db 10244 AAGCGGTGCTGTGCAATACAGCGTCAACAGCGGATCACCTGGCATGTCTATCGCCAG 10303
QY 331 ----- 331
Db 10304 CACCAGCAAAGGACTTTCACAAAGCTCAGAGTGTCTTACAATGTCCCCCTGGAGGCA 10363
QY 332 ---LeuLeu-----Pro----- 334
Db 10364 CGATGAAAGGAGTCTTACTGTGGCTGGTGGCAACACGCGCAATGGAACAGTCTATGAT 10423
QY 335 ---Leu-----LeuVal----- 337
Db 10424 CAATGGCTTTGGACCATGTGGAGTGTGCTCTAGTAAGCACTCGCAAAACAAATTACATG 10483
QY 338 ---Leu-----HisLeuLeu----- 342
Db 10484 ATGAATTTTCAGCAACATGGCTCAGACATTTCTACACAGAGAGCAAGTCACTT 10543
QY 343 ---LysPhe 344
Db 10544 AGCGATACCCATGAAGATCAAAAGTTT 10573

RESULT 6
US-08-770-379-17
; Sequence 17, Application US/08770379
; Patent No 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; SOFTWARE: Patent In Release #1.0, Version #1.30
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-17

Alignment Scores:
Pred. No.: 2,898-23 Length: 35100
Score: 1727.60 Matches: 302
Percent Similarity: 10.41% Conservative: 35
Best Local Similarity: 9.33% Mismatches: 5
Query Match: 71.74% Indels: 2895
DB: 2 Gaps: 250

US-10-017-084A-523 (1-344) x US-08-770-379-17 (1-35100)

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QY	3	-----	ThrIle	-----	4						
Db	6688	CTTCTTAGTTAGCGAGACCCGCGCAACACTGGGACACTAAAAGTCTGGCCCTCACTACAGG	6747								
QY	5	-----	Gln	-----	6						
Db	6748	AAGTTTCAGAGCCTTCACGGCACACTACTCCGCCCTCTCAGACGACAAAACGACACGAA	6807								
QY	7	-----	LysMet	---	His	-----	9				
Db	6808	TGCTCAGTCTGTCACTAGATTTGAGGACACTTTTGGAAAACGTGGCTGATGCTCTGGCCA	6867								
QY	10	-----	Asn	-----	SerIle	-----	12				
Db	6868	CGTTGGGAGTGTCACTAGCAGAAAACCTGTCTCCAGAGAGCAATTTTCCCTCTGTCATT	6927								
QY	13	-----	Ser	-----	TrpAla	15					
Db	6928	TGGACAAACATGCMAAAGCAACCGGAGCGTTAGTTTAATTTTACGSAATTTGGGCC	6987								
QY	16	-----	IlePhe	-----	17						
Db	6988	TTGGAGTTAAAGCTGTCACTAATAACGACGTGAAATTTTCTTTAAACGTCTTAGTAGC	7047								
QY	17	-----	17								
Db	7048	GTTTTATTATAGGATCGGCGAGTCTCTGGAGGGTTTGGGAGGATTCGGTTTC	7107								
QY	17	-----	17								
Db	7108	GTTCGGAAGCTGAGGGGTATCTCACCCGTA CTTGGGCGGACCTATATGTCTCAAAATGTG	7167								
QY	18	-----	Thr	-----	Gly	-----	20				
Db	7168	CCCTGCTTAGAATGCTTTCAGGAGTGTCTGACTCCCAACACGAGGACACGCTGTCAG	7227								
QY	21	AlaAlaLeu	-----	Cys	-----	24					
Db	7228	GCCATGCTCCCGACACGSCCTGCAGTCACATATGTATACCCCGCATGGGTGAGCCTGTC	7287								
QY	25	-----	LeuPhe	-----	Gln	-----	Gly	-----	ValPro	30	
Db	7288	CGGGCCCTCTTTGAGACGAGCTAAACAGCTCGGGCTTCAAAACCCCTGAGTCCATACCT	7347								

QY	31	-----	ValArg	-----	32			
Db	7348	ACTACCCCTGTCTAGTCCCGGTAAAGCAAGATGATGAATCAGACAGAGCTCTCTAATG	7407					
QY	32	-----	32					
Db	7408	GGGTAGGAGATCACCACATTTTCGGAGAGGTGACCAGATCTGTCTTGGAAATCTCAAA	7467					
QY	33	-----	SerGly	-----	AspAlaThr	-----	37	
Db	7468	CTGATCTATTGGAGCTCTGGCCACTTCGATGCCACCTCGAGCGGAGACAGAGACTGTCT	7527					
QY	38	-----	Phe	-----	38			
Db	7528	CACCTGGCCTCGCTGTTTACTCAGAGGCTGACATGATATAAAGCGCGCTGACCTGCC	7587					
QY	39	-----	ProLys	-----	40			
Db	7588	GGATGCTTGGCGGAACGGCGCACGCCCAACACTTTTGTGACTGCTTTCGCCGACACTCC	7647					
QY	40	-----	40					
Db	7648	CTAGAAACCTTTTCTGTGTGTGTTCTTTTAGCTCCGTGGAGGACACCATAGAAAGTCTC	7707					
QY	41	AlaMetAsp	-----	AsnValThr	-----	46		
Db	7708	CAAAAGGACTGCTCTTCTGCTTCTTACCAACAGGTAAACTACACTACTGCACTGCAAAA	7767					
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Db	7768	CAGAACGAGTTTACGTCGACTCAGCAAACTGCTGGCAGCTGCTGCTGCTAAATTTGGGC	7827					
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Db	7828	AAATGTTCCACTGAAAGTTGCAATCCGAGGCCGCTAGCAGCTGTTAGTGGGGGCAAA	7887					
QY	54	-----	ThrLeuArg	-----	56			
Db	7888	CCAGAGGAGTGTGAGGGATGCAAAACACGGCAAGAACTATATCTTCAGAAAGTGCA	7947					
QY	57	-----	Cys	-----	57			
Db	7948	CGGACGCTTTTAAAAACCTCTGTGATTGTATAGACACACGAGGCCACATCTCTCTCAG	8007					
QY	58	Thr	-----	Ile	-----	59		
Db	8008	ACCCTGGTCTAAGACTGTGGGGTCTGTCTATCAACAGGAGCATCTGCCCTACAAAAC	8067					
QY	60	-----	Asp	-----	60			
Db	8068	CATTTTTCACAGACACAGTTCATATCCCTCCCTGGCAGGACCTGACGGTCTGCTGT	8127					
QY	61	-----	Asn	-----	61			
Db	8128	CCACGCGTTTGAATTTCTAAATATATCAAAATTTCTGTGACTCCAGCGTCTGGG	8187					
QY	62	Arg	-----	ValThr	-----	64		
Db	8188	CGGGAACACGTAGAGATCTGACACTGGAGTTCTTACAAACTTATCACGGGCGCGCTGCA	8247					
QY	65	-----	Val	-----	66			
Db	8248	AAGGACATCTTTTATTTCCAGTCTCCAAATGTGACGCTGCTGCTGCTGAGGCT	8307					
QY	67	Ala	-----	67				
Db	8308	CGGGCATGCTTCCCATCAAAAGATGATGTATCAGAGATGATCTGCGCCGACATAGAG	8367					
QY	68	-----	Trp	-----	Leu	69		
Db	8368	CCGAGGACTGGATAGAGCCCAACTTCAACAGTTCTTATAGCTTTGAGAATCAAGACATA	8427					
QY	70	Asn	-----	Arg	-----	Ser	72	

8428 AACCATCTGCAAGAGAGCTTGGGAATATATCAGAGAGCTGGTATTATTCGGTTTCTCTG 8487
73 ---Thr---
8488 TACAACGAACCTTGGGAGGAGGCTAAATACTTCTCAGCCTCAGGGCTCACCAGGG 8547
75 ---LeuTyr---
8548 TTTGAGNACGAAACCGGAGGACTCAACAGGGGCTGTACCTAACATTGTGACATCT 8607
77 Ala---Gly---
8608 GCGCCCTTGGTGTGGTGAATAAATAATATGCTGATATTAAAGACCTGTACGCCCT 8667
79 ---AsnAsp---
8668 CTGTACCAACCACTGCAACTGAGCAACCAATGACTCCAGGTCTAGATTGGCCACCT 8727
81 ---Lys---
8728 GGGGACTGTATCTCTGTGTCTCTTTTGGCAGGCGGCGGCACTCGAGGGTGACAC 8787
81 ---
8788 CTTTCAGAGCTCCAGTTCGCCCAACCCAGGATCTTCTCTAAGGCCCCCAACCAACC 8847
82 ---Trp---Cys---Leu---
8848 TGGTGAAGATCTGTGCTTAAGAGTGTGGACTTTTACAGTTACAGAGTGTGTAGTGC 8907
85 ---Asp---ProArg---
8908 ATCGATCACCAGGAGCTTTTGGTTCAACCTGGACGACAGCTGCCCAACCAACCAAGA 8967
88 ---Val---ValLeuLeu---
8968 CAAGTACCACCAAGAGGAATTTTACTGGTGTACAAAAAACAATAGTGCCTCATATCTT 9027
91 ---
9028 TAAGTGGCGGCTATAGGAATTTGCCACTCTGTCAACGGTCTACAGGGGCTTGACAGA 9087
91 ---
9088 GTCCGCATCACCAAGATGAATCCCGAGACCGTGCCTCTATGAGATAGCCA 9147
92 ---Ser---
9148 CATGGACAGCACTATCAGTGTCTTGTAGTCCATGAAGGTAAATGTCAACGGGTAGAAA 9207
93 ---AsnThr---Gln---
9208 CACATTACTGACAGACGATGTTAACACCAAGTATTCTCCACCACTAGAGGGCT 9267
96 Thr---Gln---Tyr---Ser---Ile---Glu---
9268 TACGGATAACATTCAAGGTACTTTAGCCAGCGGTCTATACCGGAACCCCGCTGGTT 9327
102 ---Ile---Gln---Asn---ValAsp---Val---
9328 TCCGGCATATACAGATTAGGACCACTGTCAATTGGAGATAGTGACATGATAGCCAG 9387
108 ---Tyr---Asp---
9388 GTCTGCTGAACATACATTTACTTTGTCAAGTCACTGGGTGACACGGTGAAGTCTCCCC 9447
110 ---Glu---
9448 TTTTGTATAGGAATCTCTATGACAGCAACCCCGCAACAAAAATGGCTTAGCT 9507
111 ---Gly---
111 ---Pr 112

9508 CCAAGTAGTTTCTCAACCACTGTGTGCTACGTACTCTGACAGAGAACCACTGCCACTCC 9567
112 O---TyrThr---
9568 CCAAAACAGGATCTTTGTGAAACGGGAGGCTACACGCTTTCGTGGCTCCAGAGCAA 9627
115 ---Cys---SerValGlnThr---
9628 GACCACGGCGGTGTGCTCGCTGCACTGTGAAACCTTCCCGCTTCCATCCAGACTAC 9687
119 ---
9688 CCAGAGGACAGCTTCCACTTTGTGGCCAAACAGATACAGGCCCACTTACGGCTCTCT 9747
120 ---Asp---
9748 AAGCCAGTGGCCAACTTTTACGACAGTACTCTTGTCTGACCTCGGATATCAACACCAC 9807
121 ---Asn---His---ProLys---
9808 GTAAACGCCAGCAAGGCCAAACTGGCAGACTACAGTCCCTTAACGGGAGCGTCCAGTA 9867
125 ---ThrSer---Arg---Val---
9868 CTTCCACACACAGCGGAGTCTATTGTGTGGCAGCCCATGTCCGCGATTAACCTGAC 9927
129 His---
9928 TCACGCTCAGGGCGACAGGGGAAACCCACGTCATCGCCGCCCTCCGATCCCCCAT 9987
129 ---
9988 GACCACCTCTGCCAGCGCGAGAGAGACGTCACCGTACCGTGTGTCGGCGGGCG 10047
130 ---Leu---
10048 GGGGTCCACGGACAACCTGTCTTACAGCAGCTGCAGTTTGGCTACGACAAACTGGCGA 10107
131 ---Ile---Val---GlnVal---
10108 TGGCATTAACTAGGTGTTAGAGAACTCTCAGGGCATGTTGTCGGAGCAGTCAAGGA 10167
135 ---Ser---
10168 CAACCTAATGTGTAGAGCTCAGTAAATCAACCCACGCTTATGACAGCCATCTA 10227
136 ---Pro---Lys---Ile---Val---Glu---
10228 CGTCCGACCTGTATCCGCCAGTTCGTAGGAGACGCCATTTCCGTGACCGGTGATTAA 10287
141 ---Ile---
10288 COTGGACAGAGCTCCGTAACATCCACAGAGCTCAGAACAATAGTAGAGCGTGTG 10347
142 ---SerSer---
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143 ---
10408 GCTGGCGCGCGCAATGAGATAATACTGACCAACAACAGGTGGAAACCTGCAAGACAC 10467
143 ---
10468 CTGGAACTACTTCTATCAACCCGCAACGAGACTCTGGTGTATAGGACTACGCTACT 10527
144 ---AspIleSer---
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147 ---Ile---Asn---
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QY 149 -----Glu----- 149
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QY 150 -----Gly----- 152
Db 10708 TCTCGCGGTTTTCGCGAGGATCTGGACAACACCATAGATATGAACAAGGAGCGTTCT 10767
QY 153 -----Ile----- 153
Db 10768 AAGGACCTTGTGGAGATAGTGGCGACCTGGGTGGCATCGAAAAACGGTGTGAACGT 10827
QY 154 -----Ser-----LeuThr-----Cys----- 157
Db 10828 GGCCAGCAGCGTGGTCACTCTAATGTTGGCTCATTTGTTACCGGATTCATAAATTTTATTA 10887
QY 157 ----- 157
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QY 158 -----IleAla----- 159
Db 10948 TATGCTCAGTCCCGCACCAATACCATAGCCAGGCGCGGTGAAGATGATCTACCCGGA 11007
QY 160 -----Thr----- 160
Db 11008 CGTAGATCGAGGCACCTCTCTAGCGGGAGCCCAACACGGGAGGAATCAAAAAAT 11067
QY 161 -----Gly-----Arg----- 162
Db 11068 CCTGTGGAATGCAACAGCTACAAAGAGGAGGAGGAGGCGGATGATCTGAAAAA 11127
QY 163 -----Pro----- 163
Db 11128 AAGTACACCTCGTGTTCACGCTACCGAAGCGCCTTGTCTAGCGTCTGAGAGGATA 11187
QY 164 -GluPro--Thr-----Val-----Thr----- 169
Db 11188 TAAACCTCTGACTCAATCGTAGACATCAGTCCGGAACGGGGAGTGCAGATGATCG 11247
QY 170 -----Arg----- 170
Db 11248 AGGTTATGTTGATGTAATTTAGAAACACGCGCCCTCTGAAGCACCACATACAGA 11307
QY 171 -----His----- 171
Db 11308 CTGCAGTTATCAACCTACTCGTTGCACACAGACACAATTTACCGTCCGCGATCATGGA 11367
QY 172 -----Ile----- 172
Db 11368 TTTTTCATCCATTTATTCGACCACTCGCGAGGCGCCGAGAAACACTGTGAGGCAACC 11427
QY 173 -----SerPro-----Lys----- 175
Db 11428 CACGCGTCAAGTCGCCAATGTCCTCGGAGACAAGATATGACGGCTTATACCGGC 11487
QY 176 -----AlaVal----- 177
Db 11488 CTGTTTCCAAACCCGGGGGACCGGGGTGCGTGGAGACCACTATTCACCCAC 11547
QY 178 -----Gly-----PheValSerGlu----- 182
Db 11548 CTACTTCAGGCGCCCAAGCGGGAGAGATATTGCGGGAGAGACTGGGTCTATCTGGAA 11607
QY 183 ----- 183
Db 11608 AACAGGCGCGACAGGACGCAATGCTCTCTATGTCGACCTCATATTTCCACGTATACGA 11667
QY 183 p-----Glu-----Tyr-----LeuGlu----- 187
Db 11668 CATCGTGAGACCACTTACACGGCGCGCTGCGAGGACGTGCCATTTAGCTTCCAGAC 11727

QY 188 -----Ile----- 188
Db 11728 TGATATCATTCACAGGCAACGCTCTCAAGCTGCTCGSAGACACTAGATGGGCGCAG 11787
QY 189 -----GlnGlyL 191
Db 11788 TGTCTGCGTGAACGTTTTCAGGCAGCGTGTCTACTTCTACACACTAGACACCCAGGGGT 11847
QY 191 e-----Thr-----Arg----- 193
Db 11848 AAACCTGACCCACGTCCTCCAGCAGGCCCTCCAGGCTGGCTTCGGTCCGCGCATCTCGGG 11907
QY 194 -----Glu----- 194
Db 11908 CTTCTCCACCGAGCGGTTCAGAAAAAATTTTGGCGCGTACGACACACAACAATATGC 11967
QY 195 -----Gln-----Ser----- 196
Db 11968 TGTGCAAAAAATAACCTGTCTATCCAGTCCGATGATGCGAAGCTTAGCGCCGCTAAC 12027
QY 197 -----Gly-----As 198
Db 12028 AACCTGTGGTGGTGGAGTGTGAGTCCAAATGTGGACGCCATTAGCGCTTCGTCTGGA 12087
QY 198 p-----TyrGluCysSer----- 202
Db 12088 CCAGGGTTCTCGACATTCGGGTGTTAGAGTGCAGCAATCCGGCCCCCGCACCCAGGC 12147
QY 202 ----- 202
Db 12148 CAGAGACTCTTGGACGGAATGGAGTTTGACTGCGAGCTGGGAGGACCTAAGTTTATCCC 12207
QY 202 ----- 202
Db 12208 GGAGAGGACGAGTGGCCCCCATCTCAATCCTATCTTCTGATATAGAATGTATGGCGA 12267
QY 203 -----Ala-----Ser----- 204
Db 12268 GAAGGGTTTCCCAACCGGACTCAAGACGAGGACATGATTATACAAATCTCGTGTGTTT 12327
QY 205 -----AsnAsp----- 206
Db 12328 ACACAGATCGGCAACGATAAACCGTACACCCGCGATCTACTGGGCTTGGGACATGCGA 12387
QY 207 -----Val-----AlaAla-- 209
Db 12388 CCCCCTTCTGGGTGGAGTCTTTGAGTTTCTTTCGAGTACGACATGCTGGCGGCTT 12447
QY 209 ----- 209
Db 12448 CCTCAGCATGCTCCGCGATTACATGTGGAGTTTATAACGGGGTACACATAGCAAACTT 12507
QY 210 -----Pro----- 210
Db 12508 TGACCTTCCATACATCATAGCCCGGCAACTCAGGTGTAGCTTCAAGCTGCGAGGACTT 12567
QY 211 -----Val-----Val-----Arg----- 213
Db 12568 CACCAAAATAAAACTGGTTCGGTTCGGTTTGGAGTTCACCAACCCAGAGGCGGTTCGATGG 12627
QY 214 -----Arg-----ValLys----- 216
Db 12628 GGGCACTTCATGAGGTCCCGAGTCAAAAGTCAAAATATCGGGATCGTCCCATAGACAT 12687
QY 217 -----Val-----ThrVal----- 219
Db 12688 GTACAGGTTTGCAGGAAAAAGTGTGTCTGTCTGACTACAGCTGACACAGTGGGTAA 12747
QY 220 -----AsnTyr-----ProPro----- 223
Db 12748 GCATGCTCGTGCAGAAAAAGATGACATCTCATACAGGACATACCCCGCTTTTAA 12807
QY 224 -----Tyr----- 224

Db 12808 ATCTGGGCTGATGTCGCGCAAGGTGGGAACTACTGTGTTATTGACTCGGTCTGGT 12867
 QY 225 ----Tyr-----Lys----- 257
 Db 12868 TATGAGATCTTCTGCTACGGTTTCAGACCCATGTTGAGATCTCGGAAATAGCCAGCTGGC 12927
 QY 228 aLys----- 230
 Db 12928 CAAGATCCCAACCGTAGGTACTGACGGACGGCCAAACAGATCAGGGTATTTCTCTGCCT 12987
 QY 231 ----Thr-----Gly-----ValPro----- 234
 Db 12988 CTTGGAGGCTGCTGCCACGGAAGGTATCAATCTCCCGTCCCAAGAGGACGGGTAG 13047
 QY 235 ----Val-----Gly----- 236
 Db 13048 CGGTATCAGGGGCCACTGTAAATAGACCCCTCTCCGGGATTTCTATGACGACCCGCTACT 13107
 QY 237 ----Gln----- 237
 Db 13108 CGTGTGATTTTGCCAGCTTGATCCCAAGTATCATCCAGCGCAACTGTGTACTC 13167
 QY 238 ----Lys----- 238
 Db 13168 CACACTGATACCGGGGATTCGCTCCACCTGCACCCACACTCTCCCGGACGACTAGCA 13227
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 Db 13228 AACCTTGTCTCAGCGGAGGTTCGGTCCACTTTGTTAAAAAAACACAAAAGGAGTCCCT 13287
 QY 240 ----ThrLeu----- 241
 Db 13288 TCTTGCCAGCTTCTGACGGTATGGCTCGGAGAGAGAAAGAAATAGAAAGACCTGGC 13347
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 Db 13348 ATCATGACGGACCCGCACTGAAACTATTCTAGACAAACAACACTGCGCATCAAGT 13407
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 QY 243 ---- 243
 Db 13468 CATAGCGGACCGTGACACTACAGGGCGAAAGATGCTGGAGAGATCTCAGGCTTTGT 13527
 QY 244 -GluAla---Ser-----Ala-----Val---Pr 249
 Db 13528 AGAGGCCATCTCCCGAACCGCTAGGGGTCTCCTGCGAGGCCAATAGACGTCTCACC 13587
 QY 249 o----- 249
 Db 13588 CGAGCGCCGATTCAGGTGATATACGGGACACTGACTCTCTTTTCAATATGCTGATGG 13647
 QY 249 ---- 249
 Db 13648 TTTCAATGACAGCGGTGTACAGACTTCGCGAGGAGTAGCGTCAATCACCACCAACAC 13707
 QY 250 ----Ser-----AlaGlu----- 252
 Db 13708 GCTGTTTCTAGCCCATCAGCTGGAGGCTGAAAGATCTTCAAGTGCCCTTCTGCTCCT 13767
 QY 252 ---- 252
 Db 13768 GACTAAAGAGATACGTGGGGTACTCAGTGACGACAAAGTTCTGATGAAGGGCGTAGA 13827
 QY 253 ----Phe----- 253
 Db 13828 CCTCATTAGGAAACACGCTGTGTTTGTTCAGGAAAGAGCAGTCAAGTCTCTGACCT 13887
 QY 254 ----Gln----- 254

Db 13888 CATACTCGGGAGCCGAGCGCTCAAGCGCGCGCCAAAGCTTATTTTCGGGGCAGGCGACAGA 13947
 QY 255 -Tyr-----Lys----- 257
 Db 13948 CTGGGTGTACAGGGAAGGGCTCCAGAGGGGTTTCGTCAGATATTTCAAGTGTCTCAAGC 14007
 QY 258 ----Asp----- 258
 Db 14008 GAGCCACCGGAACTGTGGAACGACGCGTACCAGTAGACAAACTGACGTTTACCACCGA 14067
 QY 259 ----Asp----- 259
 Db 14068 GCTAAGCGCCCGCTCGGCGACTACAAAGAGGCAAAACCTCCCGCACTGACCGGTACCA 14127
 QY 260 -Lys-----Arg-----Leu-----Ile----- 263
 Db 14128 AAAGTCTCAAGCTAGACAGGAGGCTTCCACAGATACACGACAGAAATCCCTACGTGTT 14187
 QY 264 ----Glu----- 264
 Db 14188 CGTCGACCCCGAGTAGCTCGCTCCGAGCTGGCAGACACCCCGAGTAGTACGTTTAAGCA 14247
 QY 265 ----Gly-----Lys----- 266
 Db 14248 GCACGACTCGCGGTGGCGGTGACCTGTACTTCGACAAAGCTGGTACACGCGGTAGCCAA 14307
 QY 266 ---- 266
 Db 14308 CATCATCAATGCTCTTCCAGAAACACGCTGGCAACCGTAGCTATGTTGTATAACTT 14367
 QY 267 ----LysGly----- 268
 Db 14368 TTTAGACATTCGCTGACCTTTCCACGCGCTAGTACTCAGACGCGGAAACAGCGCTCA 14427
 QY 269 ----Val-----Val----- 269
 Db 14428 GAAAGTTTCTCTGCGCTATGTGGGACAACTAGAGTCCAACTGGCAAGCAGTGAGCA 14487
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 QY 274 ----Arg---ProPhe----- 276
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 Db 14668 AATACGTGACCATGCTTTGGGCTAGTGCCAAATATGAGGATCTGTTAACCCATGG 14727
 QY 277 ---- 277
 Db 14728 GTCATGCGTGGCGTAGTGGCGACGCAAAACGACAGCGGCAACGCGGACGATCGT 14787
 QY 278 ----Ser----- 278
 Db 14788 CGCGCTGGCGTGAATAACAATTTTTCAGAACCCATCGGCATTTGGGTACGCGGCCCTCC 14847
 QY 279 ----LysLeu---IlePhePheValSer----- 286
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QY 288 -----His----- 288
Db 15025 ACAGTGCAGTCCACTCGCGGAGAGATATACGGGATATCTTTCACAGCTGCTGTCCCGT 15084
QY 289 -----AspTyr-----Gly-----Asn----- 292
Db 15085 CTCTTTTGGACCTCTGACATTCGAGTTCATTTGGTGTGACACAGTGAAGGTGACCC 15144
QY 293 -----Tyr-----Thr-----Cys--Va 296
Db 15145 CGAGCAATTGACACCAAGTACTTGACGTTACGCGAGCGGAGAGAGACTTTGCAAGT 15204
QY 296 lalaSer-----Asn-----Lys----- 300
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QY 300 ----- 300
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QY 301 -----LeuGly----- 302
Db 15322 CCCTCTGGAGCCAGGTATTGCACTTATCCAGACTGTGAGAAACTATCCACCTCA 15381
QY 303 -----His-----ThrAsnAla----- 306
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QY 320 -----Ser-----Asn----- 321
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QY 322 -----Gly-----ThrSer----- 324
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QY 328 -----Gly--Cys-----Va 330
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QY 330 lTrp-----Leu-----Leu----- 333
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QY 334 -Pro-----LeuLeu----- 336
Db 15162 GCGTGGGAGGCTCAAAATAATAATACTTGTCTCACCTGTCATGCCAAGGAGTG 16221
QY 337 -----Val-----LeuHis-----LeuLeu----- 341
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QY 342 -----LeuLysPhe 344
Db 15282 GAGGTGCTGAGCAGCGGGTTTGAGCGCGAGTTTACCGTAACGTGGCATTC 16330

RESULT 7

US-08-757-669A-17
; Sequence 17, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-669A-17

Alignment Scores:
Pred. No.: 2,89e-23 Length: 35100
Score: 1727.60 Matches: 302
Percent Similarity: 10.41% Conservative: 35
Best Local Similarity: 9.33% Mismatches: 5
Query Match: 71.74% Indels: 2895
DB: 3 Gaps: 250

US-10-017-084A-523 (1-344) x US-08-757-669A-17 (1-35100)

QY 1 Met---Lys----- 2
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QY 3 -----ThrIle----- 4
6688 CTTCTTAGTACGACACCGGCAACACTGGACACTAAAGTCTGGCCCTCACTACAGG 6747
QY 5 -----Gln-----Pro----- 6
6748 AAGTTTCAGAGCTTCAGGCACACTACTCCCTCTCTCAGACGACAAACGACACGAA 6807
QY 7 -----LysMet-----His----- 9
6808 TGCTCAGGTCTGTCTAGTAATTTGAGCAGCTTTTGGAAAACGTGCTGATGTCTGGCCA 6867
QY 10 -----Asn-----SerIle----- 12
6868 CGTTGGAGTGTGCTAGCAGAAACTGTCTCCAGAAAGCAATTTTCCCTCTGCAAT 6927
QY 13 -----Ser-----TyrAla 15
6928 TGGACACAATGCAACAAGCAACCGAGCGTTAGGTTTAATTTTACGGAAATTTGGCC 6987
QY 16 -----IlePhe----- 17
6988 TTGGAGTTAAAGCTGTCTCAATAAAGACGTTGAAATTTTCTTTAAACGCTTAGTAGC 7047
QY 17 ----- 17
7048 GTTTTTATTGTATAGGATCGGCAGTCTCTGGAGGGTTTAGGGAGGATTTGCGTTTC 7107
QY 17 ----- 17
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QY 18 -----Thr-----Gly-----Leu----- 20
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QY 21 AlaAlaLeu-----Cys----- 24
7228 GCCATGCTCCAGACAGCGCTGCAGTCACATATGTACCCCGCATCGGTGAGCCGTGC 7287
QY 25 -----LeuPhe-----Gln-----Gly-----ValPro 30
7288 CGGGCGCTCTTTTGAGAACGAGCTAAACAGCTCGGGCTTCAAAACCCGTGAGTCCATACCT 7347
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7348 ACTACCCCTGTCACTCCCGGTAAAGCAAGATGATGAATTCAGACAGAGCTCTTAATG 7407
QY 32 ----- 32
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QY 38 -----Phe----- 38
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QY 40 ----- 40
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QY 47 -----ValArg-----Gln-----Gly 50
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7828 AAATGTTCCACTGAAGCTTGCATCCGAGCCCGTAGCAGCTGGTAGTGGGGGCAAA 7887
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QY 54 -----ThrLeuArg----- 56
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QY 57 -----Cys----- 57
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QY 58 Thr-----Ile----- 59
8008 ACCCTGGTCTAAGACTGTGGGGTCTGTCTATCTACACGAGGCATCTGCCCTACAAAAC 8067
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QY 67 Ala----- 67
8308 GCGGCGATGTTCCCATCAAAAGATGATGGTATCAGAGATGATCTGGCCAGCATAGAG 8367
QY 68 -----Tyr-----Leu 69
8368 CCGAAGACTGGATAGAGCCCACTCAACAGTCTTATAGCTTGTGAGAATCAAGACATA 8427
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8428 AACCATCTGCAAAAGAGAGCTTGGGAATATATCAGAGAGCTGTATATATCGGTTTCTG 8487
QY 73 -----Thr-----Ile----- 74
8488 TACACAGAACTTGGGAGAGGGAGCTAAATAATCTTCTCAGCCTCAGGGCTCACCGGG 8547
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8548 TTTGAGAAACGAAACCCGCGAGACTCACAAACGGGCTGTACCTAATTTTGAGACATCT 8607
QY 77 Ala-----Gly----- 78
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QY 81 -----Lys----- 81
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QY 81 ----- 81
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Db

QY 82 -----Trp-----Cys-----Leu----- 84
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QY 85 -----Asp-----ProArg----- 87
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QY 88 -----Val-----ValLeuLeu----- 91
DB 8968 CAAGTACCACCAAGAGAAATTTTACTGGTGTACAAAAAACAATAGTGCCTCATATCTT 9027
QY 91 ----- 91
DB 9028 TAAGTGGCGCGCTATAGGAAATTCACCTCTGTCAAGTCTACAGGGGCTTGACAGA 9087
QY 91 ----- 91
DB 9088 GTCCGCCATCACCACCAAGTATGAACTCCCGAGACCGGTGCCACTCTATGAGATAAGCCA 9147
QY 92 -----Ser----- 92
DB 9148 CATGACAGCACTATCAGTGTCTTATAGTTCCATGAAAGTAAATGTCAACGGGGTAGAAA 9207
QY 93 -----AsnThr-----Gln----- 95
DB 9208 CACATTTACTGACAGACGATGTTAAACACACAGTATTCCTCCAAACAGTAGAGGGGT 9267
QY 96 -Thr-----Gln-----Tyr-----Ser-----Ile-----Glu----- 101
DB 9268 TACGGATAACATTCAAAGGTACTTTAGCCAGCGGTCTATCAGCGGAACCGGCTGGTT 9327
QY 102 -----Ile-----Gln-----Asn-----ValAsp-----Val----- 107
DB 9328 TCCCGCATATACAGAGTTAGACCACTGTCAATTGGAGATAGTGACATGATGCCAG 9387
QY 108 -----Tyr----- 109
DB 9388 GTCTGTGAACATACAAATTACTTTGTACAGTCACTGGGTGACAGGTGGAAGTCTCCCC 9447
QY 110 -----Glu----- 110
DB 9448 TTTTGTCTATAAGAACTCTCATGAGCAGACACCCCGCAGCAAAATATGGCTTAGCGT 9507
QY 111 -----Gly----- 112
DB 9508 CCAAGTAGTCTCAACCAACACTGTGTGTCAGTACTCTGACAGAGGAACCAAGTCCACTCC 9567
QY 112 0-----TyrThr----- 114
DB 9568 CCAAAACAGGATCTTTGTGAAACGGGAGCGTACACGCTTTTCGTGGGCTCCGAGAGCAA 9627
QY 115 -----Cys-----SerValGlnThr----- 119
DB 9628 GACCACGGCGGTGTTCGGTGGCACTGTGGAAACCTTTCGGCGCTCCATCCAGACTAC 9687
QY 119 ----- 119
DB 9688 CCACGAGGACAGTTCCTCACTTTGTGGCCAAACAGATACAGGCCACTTCACGGCTCTCT 9747
QY 120 -----Asp----- 120
DB 9748 AACGCCAGTGGCAACTTTACGACACGTAFTCTTTGTCTGACCTCGGATATCAACACCAC 9807
QY 121 -----Asn-----His-----ProLys----- 124
DB 9808 GCTAAACGCCAAGGCCAAACTGGCGAGCACTCACTGCTCCCTAACGGGAGCGTCCAGTA 9867
QY 125 -----ThrSer-----Arg-----Val----- 128
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DB 9928 TCACGCTCAGGGCGACAGCGGGAACCCACGTCATCGCGCGCCCTTCGCGATCCCCCAT 9987
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DB 10048 GGGGTCCACGGACAACTGTCTTTACACGAGCTGCAGTTTGGCTACGACAAACTCGCGGA 10107
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QY 142 -----SerSer----- 143
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QY 143 ----- 143
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QY 144 -----AspIleSer----- 146
DB 10528 GCGCATATAAACACCACCTGACATATCCACCTTGACACTTTTATCGCCCTGAATCTATC 10587
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QY 149 -----Glu----- 149
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QY 154 -----Ser-----LeuThr-----Cys----- 157
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QY 158 -----IleAla----- 159
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QY 160 -----Thr----- 160

Db 11008 CGTAGATCGCAGGGCACCTCTAGCGGGAGCCCAACACGGGAGGAAATCAAAAACAT 11067
QY 161 -----Gly-----Arg----- 162
Db 11068 CCTGCTGGGATGACACAGCTACAAACAGAGGAGGAGGAGGCGGATGATCTGA AAAA 11127
QY 163 -----Pro----- 163
Db 11128 AAGTACACCCCTCGGTGTTTTCAGCGTACCGCAACGGCCCTTCGTGAGCGTCTGAGAGGATA 11187
QY 164 -GluPro--Thr-----Val-----Thr-----Tyr----- 169
Db 11188 TAAACCTCTGACTCAATCGTAGACATCAGTCCGGAACCGGGGAGTGACAGTGGATTTCG 11247
QY 170 -----Arg----- 170
Db 11248 AGGTATTGTTGATGATAATTTAGGAACACGGCCCGCTCTGAAGCACACATACAGA 11307
QY 171 -----His----- 171
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Db 11368 TTTTTCATCCATTATCGACCACTCGCGGAGGCCGAGAAACACTGTGAGGCAACC 11427
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Db 11488 CTGTTTCCAAACCCCGGGGACCCCGCGTGTGTCGCTGGACACCAACATTCACCCAC 11547
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QY 183 p-----Glu-----Tyr-----LeuGlu----- 187
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Db 11728 TGATATCATTTCCAGCGGCACCGTCTCAAGCTGCTCGGAGAACACTAGATGCGGCCAG 11787
QY 189 -----Thr-----GlnGlyTl 191
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Db 12088 CCACGGGTTCCTGACATTCCGGGTGTTACGAGTGCAGCAATCCGGCCCCCGCCAGCC 12147

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QY 210 -----Pro----- 210
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QY 211 -----Val-----Arg----- 213
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QY 214 -----Arg-----ValLys----- 216
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QY 217 -----Val-----ThrVal----- 219
Db 12688 GTACCAAGTTTCAGGGAAGAGCTGAGTGTGCAGACTACAAAGCTGGACACAGTGGCTAA 12747
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Db 12748 GCAATGCTCGGTGCAACAAAAGATGACATCTCATACAGGACATACCCCGCTTTTAA 12807
QY 224 -----Tyr----- 224
Db 12808 ATCTGGCCCTGATGTTTCGCGCAAGGTGGAAACTACTGTGTTATTGACTCGTCTGCT 12867
QY 225 -----IleSerGlu-----Al 228
Db 12868 TATGGATCTTCTGCTACGGTTTCAGACCCATGTTGAGATCTCGGAATAGCCAGCTGGC 12927
QY 228 aLys-----Gly----- 230
Db 12928 CAAGATCCCAACCCCTAGGCTACTGACGACGGCCACACAGATCAGGGTATTTCTCTGCT 12987
QY 231 -----Thr--Gly-----ValPro----- 234
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QY 237 -----Gln----- 237
Db 13108 CGTGTGATTTTGCAGCTTGTACCCAGTATCATCCAAGCGCACAACTTGTGCTACTC 13167
QY 238 -----Ly 238
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 Db 13288 TCTTGCCAAAGCTTTGACGGTATGCTCGCGAAGAGAAAGAAATAAGAAAGACCTCGC 13347
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 Db 13348 ATCATGCGAGCCCGCAGCTGAAAACATTTCTAGACAAAACAACAACCTGGCCATCAAGGT 13407
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 Db 13408 TACCTGCAACGCCGTTTACGGCTTCACGGCGTTCCTCTGCACTACTGCTTGCCTAAA 13467
 QY 243 ----- 243
 Db 13468 CATAGCGAGACCGTGACACTACAAGGGCGAAAGATGCTGGAGAGATCTCAGGCCCTTGT 13527
 QY 244 -GluAla---Ser-----Ala-----Val---Pr 249
 Db 13528 AGAGCCCATCTCGCGGAACGCTAGCGGTCTCTGCGGAGGCCAATAGAGCTCTCACC 13587
 QY 249 o----- 249
 Db 13588 CGACGCCGATTCAAGGTCAATACGCGGACACTGACTCTCTTTTCATATGCTGATGG 13647
 QY 249 ----- 249
 Db 13648 TTTCACATGGACAGCGTGCAGACTTCGCGGAGGAGTACGGTCAATCACCACCAAC 13707
 QY 250 -----Ser-----AlaGlu----- 252
 Db 13708 GCTGTTTGAGCCCCATCAAGCTGAGCGCTGAAAAGATCTTCAAGTCCCTTCTGCTCCT 13767
 QY 252 ----- 252
 Db 13768 GACTAAAAAGAGATACGTGGGGTACTCAGTGACGACAAGGTCTCTGATGAAGGGCGTAGA 13827
 QY 253 -----Phe----- 253
 Db 13828 CCTCATTAGGAAAACAGCCTGTGTTTGTCCAGGAAAGAGCAGTCAAGTCTCTGGACCT 13887
 QY 254 -----Gln----- 254
 Db 13888 CATACTGCGGAGCGAGCGTCAAGCGCGGCCAAGCTTATTTCGGGGCAGGCGACAGA 13947
 QY 255 -Trp---Tyr-----Lys----- 257
 Db 13948 CTGGGTGTACAGGAAGGGCTCCAGAGGGGTTCGTCAAGATAATTCAGTGTCTCAAGCC 14007
 QY 258 -----Asp----- 258
 Db 14008 GAGCCACGGGAAGTGTGCGAAGCAGCGGTACAGTAGAACAACCTGACGTTTACACCGA 14067
 QY 259 -----Asp----- 259
 Db 14068 GCTAAGCGCCGCTGCGGACTACAAGACGCAAAACCTCCGCACTGACCGGTGTACCA 14127
 QY 260 -Lys-----Arg-----Leu-----Ile----- 263
 Db 14128 AAAGCTAAAGCTAGACAGGAGAGCTTCCACAGATACACAGAGAATCCCTACGTGT 14187
 QY 264 -----Glu----- 264
 Db 14188 CGTCAGCGCCCGAGTACCTGCGCTCGAGCTGGCAGAGCAACCCGAGTACGTTAAGCA 14247
 QY 265 -----Gly-----Lys----- 266
 Db 14248 GCACGGACTGGCGTGGCGGTGGACTGTACTTCGACAGCTGTGTACACGGGTAGCCAA 14307
 QY 266 ----- 266

Db 14308 CATCATCCATGCTCTTCCAGAAACAACGTCGGCAACCGTAGTATGTGTATAACTT 14367
 QY 267 -----LysGly----- 268
 Db 14368 TTTAGACATTCCTCGTACTTTTCCACGCCCTAGTACTCAGACGCGGAAACAGCGCCTA 14427
 QY 269 -----Val----- 269
 Db 14428 GAAAGTTTCTCTTTCGCTATGTGGGACAACTAGAGTCCAACTGGCAAGCAGTGGAGCA 14487
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 Db 14548 TGACTGGGAGATAACGGGTGTCTAACTGCGCGTTTACTTTCAGCAGCCCTAACATGTGGCCC 14607
 QY 274 -----Arg---ProPhe----- 276
 Db 14608 CCTTTACAGATCTAGCGGCGACTACACGCGGCTAAGAAATCCCTTCTCTCTGGATCGACT 14667
 QY 277 -----Leu----- 277
 Db 14668 AATACGTGACCATGCCATCTTTGGGCTAGTGGCCAAATATTGAGGATCTGTTAACCCATGG 14727
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 Db 14788 CGCGCTGGCGGTGATAACAATTTTTCAGAACCCATCGGCATTTGGGTACGCGGCCCTCC 14847
 QY 279 -----LysLeu---IlePhePheAsnValSer----- 286
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 QY 288 -----His----- 288
 Db 15025 ACAGTCGATCCACCTCGCGGACGATATACGGGATACCTTCACAGTCTCTGTCCGCT 15084
 QY 289 -----AspTyr-----Gly-----Asn----- 292
 Db 15085 CTCTTTTGGACCTCTCGACTTCGAGTCCATTGGGTGTGACAAACGTGGAAGTGACCC 15144
 QY 293 -----Tyr-----Thr-----Cys---Va 296
 Db 15145 CGAGCAATTGACACCCCAAGTACTTGAGCTTCAGCAGACGGGAGAAAGACTTTGCAAGT 15204
 QY 296 -IleAsn-----Lys----- 300
 Db 15205 A---ACGTTTACACACCCATTTCGACAGCATGCAAGAGCCCGTGTTCGTTTCGTCTA 15261
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 QY 301 -----LeuGly----- 302
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QY 310 -----Le----- 310
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QY 310 uphe-----GlyProGly-----AlaVal-- 316
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Db 15742 GGCCGACCGCACAGGAAACCCATGCAATCGTGAATGTCGAGCACATATGGCGAGAG 15801
QY 320 -----Ser-----Asn----- 321
Db 15802 TCAGAGCAGTGTCTCCCGTGGTTTGCAAGTGCAGTAGTAGTAACGACAGCTGGCGGGC 15861
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QY 330 lTrp-----Leu----- 333
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QY 334 -Pro-----LeuLeu----- 336
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QY 337 -----Val-----LeuHis-----LeuLeu----- 341
Db 16222 TACCTCGGTGCGTAAGGACCTTTCTACACACACTGCGCACCTATTGTTTCAGCGT 16281
QY 342 -----LeuLysPhe 344
Db 16282 GAGTGTGAGCAGCGGGTTTGAGCGCGAGTTTACCGTAACCTGGCATTC 16330

RESULT 8

US-09-230-371A-17
; Sequence 17, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 35100
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-230-371A-17

Alignment Scores: 2.89e-23 Length: 35100
Pred. No.: 1727.60 Matches: 302
Score: 10.41% Conservativity: 35
Percent Similarity: 9.33% Mismatches: 5
Best Local Similarity: 71.74% Indels: 2895
Query Match: 4 Gaps: 250
DB:

US-10-017-084A-523 (1-344) x US-09-230-371A-17 (1-35100)

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QY 3 -----Thrile----- 4
Db 6688 CTTCTTAGTTACGAGACCCGCGACACACTGGACACTAAAGTCTGCCCTCTACTACAGG 6747
QY 5 -----Gln-----Pro----- 6
Db 6748 AAGTTTCAGAGCCTTCACGCGCACACTACTCCGCCCTCTCAGACGACAAACGACACGAA 6807
QY 7 -----LysMet---His----- 9
Db 5808 TGCTCAGGTCTGTCTACTAGAAATGGAGCACTTTTGGAAAACGTGGCTGATGCTCTGGCCA 6867
QY 10 -----Asn-----Serile----- 12
Db 5868 CGTTGGGAGTGTGCTAGCAGAAAACCTGTCTCCAGAGAGCATTTTCCCTCTGCTGCT 5927
QY 13 -----Ser-----TrpAla 15
Db 5928 TGGACACAACTGCAACAAACGACGAGCGGTAGGTTTAATTTTACGAAATTTGGGCC 6987
QY 16 -----IlePhe----- 17
Db 6988 TTGGAGTTAAGCTGTCTACTAATAAACGACGTTGAATTTTCTTTAAACGCTTTAGTAGC 7047
QY 17 ----- 17
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QY 17 ----- 17
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QY 18 -----Thr-----Gly-----Leu--- 20
Db 7168 CCTGCGCTAGAAATGCTTCAGGAAGTGTGTGACTCCCAACGAGGCCAGGCTGTGAG 7227
QY 21 AlaAlaLeu-----Cys----- 24
Db 7228 GCCATGCTCCAGACACGCGCTGCAGTCACATATGTACCCCGCATGGGTGAGGCTGTC 7287
QY 25 -----LeuPhe-----Gln---Gly-----ValPro 30
Db 7288 CGGGGCGCTTTTGAAGACGAGCTAAACACAGCTCGGGCTTCAACCCCTGAGTCCATACCT 7347
QY 31 -----ValArg----- 32

Db 7348 ACTACCCCTGTGTCAGTCCGGGTAAAGCAAGATGATGAATCAGACAGAGCTCTCTAATG 7407
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Db 7468 CTGATCTATTGGAGCTCTGCCACTCGGATGCCACTCGCGACGGAGACAGAGCTGCTCT 7527
QY 38 ----- 38
Db 7528 CACCTGGCTCGTGTGTTACTCAGAGGCTGACATGATAAAAGCGCGTCGACCTGGCC 7587
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Db 7588 GGATGCTGGCGAAGCGGCGACGCCAACCACTTTTGTGACTGTCTTCGCCCACTCC 7647
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QY 41 AlaMetAsp-----AsnValThr----- 46
Db 7708 CAAAGGACTGCTCTTCGCTCTTCTACCAACAGGTAAACTACACTACTGCACTGCAAAAA 7767
QY 47 -----ValArg-----Gln-----Gly 50
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QY 51 -----GluSer-----Ala----- 53
Db 7828 AAATGTTCACTGAAAGTTGCCAATCCGAGGCCCTAGGCAGCTGGTAGTGGGGCAA 7887
QY 54 -----ThrLeuArg----- 56
Db 7888 CCAGGAAGTGTCTGAGGATGCAAAACACCGGCAAGAACTATACCTTCAGAAAGTGCA 7947
QY 57 -----Cys----- 57
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QY 58 Thr-----Ile----- 59
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QY 60 -----Asp----- 60
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QY 61 -----Asn----- 61
Db 8128 CCAAGCGGTTTGAATTTCTAAATATATCAAAAATTTCTGTACTGCGCAGGCTCGGG 8187
QY 62 Arg-----ValThr----- 64
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QY 65 -----Arg-----Val----- 66
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QY 67 Ala----- 67
Db 8308 GCGGCGATCTTCCCATCAAAAGATGATGTATCAGAGATGATCTGSCCCAGCATAGAG 8367
QY 68 -----Trp-----Leu 69
Db 8368 CCGAAGGACTGGATAGAGCCCACTTCAACAGTTCTATAGCTTTGAGAATCAAGACATA 8427
QY 70 Asn-----Arg-----Ser----- 72
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QY 73 -----Thr-----Ile----- 74
Db 8488 TACAACAGAACTTTGGGAGAGGGAGCTAAATAATCTCTCACGCTCAGGGCTCACGGGG 8547
QY 75 -----LeuTyr----- 76
Db 8548 TTTGAGGAACCGAAACCCGACAGGACTCACACGGGGCTGTACCTAACTTTGAGACATCT 8607
QY 77 Ala-----Gly----- 78
Db 8608 GCGCCCTTGGTGTGGTGAATAAAATATGGCTGGATATTTAAAGACCTGTACGCCCTT 8667
QY 79 -----AsnAsp----- 80
Db 8668 CTGTACCACCACTGCAACTGAGCAACCACTAGCTCCAGGCTCTAGATTGGCCACCTC 8727
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Db 8728 GGGGACTGTCTATCTGTGTGGTCTGCTTTTGGCAGGCGCGGCACTCGAGGGGTGACAC 8787
QY 81 ----- 81
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QY 85 -----Asp-----ProArg----- 87
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QY 88 -----Val-----ValLeuLeu----- 91
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QY 92 -----Ser----- 92
Db 9148 CATGGACAGCACTATCAGTGTCTTTAGTTCCATGAAGGTAAATGTCAACGGGGTAGAAA 9207
QY 93 -----AsnThr-----Gln----- 95
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Db 9268 TAGCGATAACATTCAAAGTACTTTAGCAGCGCGGTCTATCAGCGGAACCCGGCTGTT 9327
QY 102 -----Ile-----Gln-----Asn-----ValAsp-----Val----- 107
Db 9328 TCCGGCATATACAGAGTAGGACCACTGTCAATTGGAGATAGTGGACATGATAGCCAG 9387
QY 108 -----Tyr-----Asp----- 109
Db 9388 GTCTGTGAACCATACAATTTACTTTGTCACTGCTGCTGGTGGACACGCGTGAAGTCTCCC 9447
QY 110 -----Glu----- 110
Db 9448 TTTTGTCTATAAGATCTCTCATGACAGCAACCCCGAGCAACAAATAATGGCCTTAGCGT 9507
QY 111 -----Gly-----Pr----- 112
Db 9508 CCAAGTAGTTCTCAACCACTGTGTGTCAGTACTCTGTGACAGAGGAACCACTCCACTCC 9567
|||

QY 112 o-----TyrThr----- 114
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QY 115 -----Cys-----SerValGlnThr-- 119
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QY 119 ----- 119
Db CCACGAGACAGCTTCCACTTTGTGGCCACGAGATACGGCCACTTTCACGGCTCCTCT 9747
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QY 121 -----Asn-----His--ProLys----- 124
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QY 129 ----- 129
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QY 130 -----Leu----- 130
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Db 11848 AAACCTGACCCACGTCCTCCAGCAGGCCCTCCAGSGCTGGCTTCGGTTCGGCATCCTGGG 11907
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Db 11908 CTTCTCCACGAGCGGTTCAGAAAAAATCTTGGCGGTACGACACACAACATATGC 11967
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Db 12028 AACCTGTGGTGGAGGTGTTTGTAGTCCAAATGTGGACGCCATTAGGCGCTTCGTCTGGA 12087
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Db 12928 CAAGATCCCAACCCGTAGGTACTGACGACGGGCAACAGATCAGGGTATTTTTCTGCT 12987
QY 231 -----Thr-----Gly-----ValPro-----234
Db 12988 CTTGGAGGCTGTGCCACGGAAGGTATCATTTCTCCCGTCTCCAAAAGAGAGCGGTAG 13047
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Db 13048 CGGTATCAGGGGCGCACTGTAATAAGCCCTCTCCGGGATTTCTATGACGACCCCGTACT 13107
QY 237 -----Gln-----237
Db 13108 CGTGTGGATTTTGGCAGCTTGTACCCAGTATCATCCAGCGCACACTTGTGCTACTC 13167
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Db 13168 CACACTGATACCCGCGGATTCGCTCCACCTGCACCACACACTCTCCCGGAGACTACGA 13227
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QY 242 -----Gln-----242
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QY 253 -----Phe-----253
Db 13828 CCTCATTTAGAAACACAGCCTGTCTGTTTTGTCAGGAAAAAGAGCAGTCAAGTCTCTGGACCT 13887
QY 254 -----Gln-----254
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QY 255 -Tyr-----Lys----- 257
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Db 14008 GAGCCACCGGAACTGTGCGAAGCAGCGGTACAGTAGACAACTGAGTTTACCACCGA 14067
QY 259 -----Asp----- 259
Db 14068 GCTAAGCGCGCGCTGGCGGACTCAAGACGCAAAACCTCCCGACCTGACCGGTACCA 14127
QY 260 -Lys-----Arg-----Leu----- 263
Db 14128 AAAGCTACAAGCTAGACAGGAGGACTTCCACAGATACACGACAGATCCCTACGTGTT 14187
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QY 269 -----Val----- 269
Db 14428 GAAAGTTTCTCTTCGCTATGTGGGACAACTAGATCCAACTGGCAAGCAGTGGAGCA 14487
QY 270 -----LysVal----- 271
Db 14488 AGAGCCAGACAGCGGATCTCGAAAAAATAATGCAGACAGAGCAACGTTTCCTTAGG 14547
QY 272 -Glu-----Asn----- 273
Db 14548 TGACTGGGAGATACGGTGTCTACTCCCGTTTACTTTCGAGCAGCCTAAACATGTGCC 14607
QY 274 -----Arg-----ProPhe----- 276
Db 14608 CCTTACAGATCTAGCGGCGACTACACGCGCTAAGATCCCTTCTCTCTGATCGACT 14667
QY 277 -----Leu----- 277
Db 14668 AATACGTGACCATGCCATCTTTGGGCTAGTGCCAAATATTGAGGATCTGTAAACCCATGG 14727
QY 277 ----- 277
Db 14728 GTCATGCGTCGCGTAGTGGCGACGCAAAAGCCACAGCGCGCAACGCGCGCATCGT 14787
QY 278 -----Ser----- 278
Db 14788 CGCGCTGGCGTGATAAACAATTTTCAGAACCCATCGGCATTTGGTAGCGCGCCCTCC 14847
QY 279 -----LysLeu-----IlePheAsnValSer----- 286
Db 14848 GCGCAAAACGCGAAGGAGCTATTAAAGTTCTGCATATTTTTT---GTACGTCCTCCGTC 14904
QY 286 ----- 286
Db 14905 CCGCGGAGATGACACATATGTGTTCAAGGGCGGCGATTTCCTCCCGGACGAGCA 14964
QY 287 -----Glu----- 287
Db 14965 ACCGAAACACTACACTCCGCGGAGGCAACCTTACCTCGTCGCGGAGACGCTGTGTAAGTGG 15024

QY 288 -----His----- 288
Db 15025 ACAGTCGGATCCACCTCGCCGGAACGTATACGGGATACTTTACAGTCTCTGTCCGCT 15084
QY 289 -----AspTyr-----Gly-----Asn----- 292
Db 15085 CTCTTTTGGACCTCTCTGACATTCGAGTCCATTCGGGTGTGACACAGTGTGAAGGTGACCC 15144
QY 293 -----Tyr-----Thr-----Cys-----Val 296
Db 15145 CGAGCAATTGACACCCCAAGTACTTTCAGCTTTCACGCGACGGGAGAAAGACTTTGCAAGT 15204
QY 296 lAlaSer-----Asn-----Lys----- 300
Db 15205 A---ACGTTTACACACCCATTCGACAGCATCAAGAGGCCGCTGTCTGTTTCTGTTCTA 15261
QY 300 ----- 300
Db 15262 CAGACCGACGCGCTCGCCGCTCAGCTTGTTCATGGGTTCAGGCTTCACCCCTCATACAC 15321
QY 301 -LeuGly----- 302
Db 15322 CCTCTGGAGCGCAGGTTATTCGAGTCTATCCAGACTGTGAGAAACTATCCACCTCA 15381
QY 303 -----His-----ThrAsnAla----- 306
Db 15382 GGAACCAACACCCCTGAGGATTCATTTGCTGTTCGAGCAGCATGGTGCCACCCGGAGA 15441
QY 307 -----Ser----- 307
Db 15442 CTGCGCTTTGTTCATCATGGGCTCGCCGTGAAACAAAGTTTGTCTCTCATTTCCGCGAGT 15501
QY 307 ----- 307
Db 15502 ACTCTTCGCGGCAACGACACACCTTATGTATTTCATCCACAGACACATCTCTGAC 15561
QY 308 -----Ile-----Met----- 309
Db 15562 CATTCACGGGACACATAGTGGCGTGGCAATGGCTTCTATATCCACCCCGGTAAAGC 15621
QY 310 -----Le 310
Db 15622 AGCCAGCCAGGACCATACAGCTTTCAGACTGCAAGGAAGAGAGCTGCACGTGGGGCT 15681
QY 310 uPhe-----GlyProGly-----AlaVal--- 316
Db 15682 CTTCCAGATCAACGCGGACCGGAGGGGTCTGTACACACCTTGCCAGTAGCGATTAG 15741
QY 317 -----SerGlu---Val----- 319
Db 15742 GGCGGACCGCCAGGAGAACCCATGCAATCGTGTCTGCTGCGAGCACATATGGCGCAGGAG 15801
QY 320 -Ser-----Asn----- 321
Db 15802 TCAGACAGTGTCTCCGCTGCTTTTCAGTGTGCGAGTAGTAAACGACAGCTCGCGCGCGC 15861
QY 322 -Gly-----ThrSer----- 324
Db 15862 GAGCCCGTGTGGGATTCGTCATTCACCGAGCCCATCTCTCTTAATCGAGTACCC 15921
QY 325 -----Arg----- 325
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QY 326 -----Arg-----Ala----- 327
Db 15982 CACAGAGCTACCCCAACTTTTACATTTGACACACGCGCACCGCAAGCAGCAACGAGGAGCC 16041
QY 328 -----Gly-----Cys-----Val 330
Db 15042 TACACTGCATTCACGCTTTTGGGAGCCAAATAAACAAGTTAGGATTTGCCCTACTGTT 16101
QY 330 lTrp-----Leu----- 333

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Db      16102 GTGGAAGCTCTCGAGCGTGCTGATTTTATAGACTCGTGCATCGGTCTCTCGAACATC 16161
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Qy      334 -Pro-----LeuLeu-----
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Db      16162 GCCGTGGAGGGCTCAAAATAATAATACTTGCTCTCACCTGGTGCATGCCCAAGGAGTG 16221
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Qy      337 -----Val-----LeuHis-----LeuLeu-----
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Qy      342 -----LeuLysPhe 344
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RESULT 9
US-09-661-596A-76
; Sequence 76, Application US/09661596A
; Patent No. 6528066
; GENERAL INFORMATION:
; APPLICANT: Santos, Richard
; APPLICANT: Grose, Charles
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
; FILE REFERENCE: 140.0011 0101
; CURRENT APPLICATION NUMBER: US/09/661,596A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/153,779
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella zoster
US-09-661-596A-76

Alignment Scores:
Pred. No.: 7,19e-21 Length: 124884
Score: 1725.90 Matches: 291
Percent Similarity: 11.93% Conservative: 41
Best Local Similarity: 10.46% Mismatches: 8
Query Match: 71.67% Indels: 2442
DB: 4 Gaps: 245

US-10-017-084A-523 (1-344) x US-09-661-596A-76 (1-124884)

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Qy      7 -----Lys----- 7

Db      75448 TAATTGTAATACACTGGATCGGCTTCTAATGGAGCAAGGCTGTGGCGTCGCAAGGTC 75507
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Qy      7 ----- 7

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Qy      8 -----Met-----His----- 9
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Qy      10 -----Asn----- 10
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Db      75628 AACGGCTACGCGGGAGAACCGGGGCAGATGAAGTTCATTAGCCCAATATCTGATTCTG 75687
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Qy      11 -----Ser-----IleSer----- 13
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Db      75688 AGACGGGTGCGCCCTTAGGGGATGTCTTCCTCTCCGGATAAATTTACACAGCGCCACAT 75747
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QY 62 -----Arg-----Val-----ThrArg-----Val----- 66
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QY 67 -----Ala----- 67
Db 76888 GAACTGCCAATATACACGGACATATTAATGCAACATCAGATCATCTGACATTTGTTCC 76947
QY 68 -Trp-----LeuAsn-----Arg----- 71
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QY 72 ----Ser-----Thr----- 73
Db 77008 TCTGTCAGGTATCCAACTGTTTACATAGATATCCACGGGGTCTACACCTAATCTTACT 77067
QY 74 ----Ile-----LeuTyr----- 76
Db 77068 GTTAGGATACAAGCTCCTGTGAGGCTATTAATTTCCGGAGTTAAATCGTTTAACAAA 77127
QY 77 -----Ala-----Gly----- 78
Db 77128 TAGTCTACGGCCGGCTGTTTGTGTAATAAAAAAGGGTACGCCACGCTACAT 77187
QY 79 -----AsnAspLys----- 81
Db 77188 CCGGAGGTATGGAATGATAAAACAGTAACACTGGAGCGGAAGATAGCACGTTTCCCTTT 77247
QY 82 -----Trp----- 82
Db 77248 TCGAGACAGCAAACTGTTGCTGTATAGCAACGATATGCAACTGCAAACTCTGGCTG 77307
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QY 89 1-----Leu----- 90
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QY 91 -Leu-----SerAsn-----Thr-----Glu 95
Db 77425 GCTCTAAGAAAAAAGTGCTCCAATCCAATATAATCCAATCCGATTTATATACGACCAAC 77484
QY 95 nThr-----GlnTyr----- 98
Db 77485 ATCGCTACACCAAGTACCAAGACGCTCGTGTATTGTAGTAAGTACGAGGCTCTACGTAAACG 77544
QY 99 -----Ser-----IleGlu----- 101
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QY 102 -----Ile-----GlnAsn----- 104
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QY 104 ----- 104
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QY 104 ----- 104
Db 77725 CGCATGGCTCCATCCATTGTGATGAACCGGCTTATTATATACATAACAGCAAGCT 77784
QY 105 -----Val----- 105
Db 77785 GTGACATCGTATGTGCTAAACACGCGCATGTGATCGTCATACATATGTAACACG 77844
QY 106 -----Asp-----Val----- 107
Db 77845 TTTAACAACCTGATCGACGATCCACGTAAGTTATACAAAAAAGTTGACTGTCTTTCCG 77904
QY 108 -----Tyr-----Asp----- 109

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QY 110 -----Glu----- 110
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Db 78025 TGACCTCGGATACCTTCCGTGGAAACGATAGAAAGATATATAGTTACCCACCACAAAGTTAAATG 78084
QY 115 -----Cys-----Ser-----Val----- 117
Db 78085 TATCCTTAATACCACGTACGTAAAAAATGTTTGAATAGCTACATATTTCTTTTCTTTT 78144
QY 118 -Gln-----Thr----- 119
Db 78145 CCAGTACAACCATATCCCGTGTATATGGAAGCCCATTTGGCAATGAAACCAACATGC 78204
QY 120 -----Asp-----Asn----- 121
Db 78205 ACTTTGGCATATGATACACAAAAGGATTACTACACGTGTGTGATACCTAACGGGGCT 78264
QY 121 ----- 121
Db 78265 TATTGGCGCGGATAGATCCGCAATTACTGATTTTTAAAGAAACCCGGACACGCTTCAA 78324
QY 122 -----His----- 122
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QY 123 -----ProLysThr----- 125
Db 78385 CGCCGCTACATTCGGTAAAGCGCTTAAACAATCTTTAATATACCAAAACGGAACCACT 78444
QY 125 ----- 125
Db 78445 TGTTTACACAGTTTTCGGCCACGATATTCAGGGGATTTGATTTTATCATTTCCCTGT 78504
QY 126 -----Ser-----ArgVal----- 128
Db 78505 TTATCTTAGCCCCGTTTATTTCTTTGATGATTTAAACGTTGTAGCGATACGAATAAATAC 78564
QY 129 -----His-----LeuIle----- 131
Db 78565 TGGAAACCGCAAGCACCGTGATTTGTATTGTATGTCAGAACTAATCCCAACGGAAAC 78624
QY 132 -----Val-----Gln-----Va 134
Db 78625 GCGTTATTTTGTGATGACAAACCGGTACTTTTATTATGCAACAGCTGATTGCGTATAT 78684
QY 134 1-----SerPro-----LysIle-----Val----- 139
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QY 140 -----Glu-----Ile-----SerSer----- 143
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QY 143 ----- 143
Db 78805 TCTTGATGACAGTTAACTTCTGAGGTATTGATGACTCCCTCTGCTGAACACAGCATACA 78864
QY 144 -----Asp-----Ile----- 145
Db 78865 GGAATAATTCGGGACGCTCCTTGAGCTATAAATAACGGCGGTAAACATTTGTTAACTCCAG 78924
QY 145 ----- 145
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QY 146 -----Ser-----IleAsn----- 148

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Qy 149 -Glu-----Gly-----AsnAsn-----Ile-- 153
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Qy 154 -----ThrCys-----IleAlaThrGly-----SerLeu----- 155
Db 79105 ACCTTTACAGACGTTCTATTGTTTACCCAGCTTCGACAGAACCCCAAGCTCTTATGGA 79164
Qy 156 -----ThrCys-----IleAlaThrGly-----SerLeu----- 161
Db 79165 ATGTTTCAGATCTGTTATGCCCATTAGTTAGCGGGGACACTCCAGCAGATTTCTGGAA 79224
Qy 162 ---ArgPro-----Glu--ProThr----- 166
Db 79225 ACGGCGTCCCTATCAATTGTCGCGACATTAGCGAGATCCCCAGCTCGTTGATGT 79284
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Db 79285 AGTATCTTACACGATCTCTGCTGGGAGGAGCTATTACCGAAGTCCCAATTTATA 79344
Qy 171 -His-----Ile----- 172
Db 79345 TCATCTGCACAGGCTATTATTGAGTGCTGTATATAAATCCCGGTTGACAAATCCCCA 79404
Qy 173 -Ser-----ProLys-----Ala--Va 177
Db 79405 AAGCTCATGTGACAGTCCGCAAGAGCTAGTCGCGGTTTACCGTTTGGGTAAAGT 79464
Qy 177 1-----Gly----- 178
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Qy 182 -----Glu----- 182
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Qy 184 ----- 184
Db 79705 AATGTCATCGATCGGTTTATACAGCTCCTTGATGATGCGGTTTGGGTATCTGTC 79764
Qy 185 -----TyrLeu----- 186
Db 79765 ATCTGTATATACAGCACCAAGTGCGGGGTATATACCTTACCTTCAAGCTTCCCTCCC 79824
Qy 187 -----Glu11 188
Db 79825 ATGCTGTTAGGTAATCGTTCTATATATTATTTGACTATTATAATTCAGGAGGGAAAT 79884
Qy 188 e----- 188
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Qy 199 -----Tyr----- 199
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Qy 213 ---Arg--Arg-----Thr-----Val----- 215
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Qy 219 -----Val----- 219
Db 80722 AGACCATGTTTGTGGAGCAACGTTTAAAGAACCGATCGGTCACCCCTTCCAACTCAT 80781
Qy 220 -----As----- 220
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Qy 220 nTyr-----Pro-----ProTyr-----IleSer----- 226
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Qy 227 ---Glu-----AlaLys----- 229
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Qy 230 -----GlyThr----- 231
Db 80962 AGGGCTATGTCGCGCGGATGCGATGCTCGATATCTTGCTCTGTATTAAATCGACTCCT 81021
Qy 232 -----Gly-----Val----- 233
Db 81022 CAGCCATGCGGACGGATGTGATGAATGTAATCATAGATTCACGTGGGGCACTGTATGC 81081
Qy 234 ---Pro-----Val----- 235
Db 81082 GTTACCCCATGTCAAAATCATCGGAAGGTTGTGTGTGTGGCTCCGGTGTATGGAG 81141
Qy 236 ---GlyGln-----Lys-----Gly--ThrLeuGln----- 242
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QY 253 -----Phe----- 253
Db 81379 TGGTCTGCTTCAGCGAATTGCTTCCCGGAGACACAAAGATTATCGGGTGAACCGGAACC 81438
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QY 268 -----Gly----- 268
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QY 272 -----GluAsn-----Arg-----Pro-----Phe----- 276
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QY 277 -----LeuSer-----LysLeuIle-----Phe 283
Db 82159 ATGAGGTGCTCTTCTCCGGTGAATATTCATAAACTGTACACTTGTGACGCTTTT 82218
QY 283 eAsn-----ValSerGlu-----His----- 288
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QY 295 -----Cys-----Val-----AlaSerAsn----- 299
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QY 300 -----Lys-----Leu----- 301
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QY 302 -----Gly-----His----- 303
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QY 304 -----Thr-----Asn-----Al 306
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QY 313 -----Pro-----GlyVala-----Val----- 316
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QY 317 -----Ser-----Glu-----Val----- 319
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QY 321 n-----Gly----- 322
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QY 326 ----- 326
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QY 327 -----Ala----- 327
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QY 328 -----GlyCysVal-----Trp----- 331
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QY 332 -----LeuLeu----- 333

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QY 334 -----Pro-- 334
Db 83416 AGATCCAATACATCAACGCGAAAGGTTGGACGTTTTTCCACAATTTAAACAAACCCCATG 83475
QY 335 -----LeuLeuVal----- 337
Db 83476 GGTTTTGAATTTCCAAATTAATCCCGTTTAAATGTGTACCCATCTTCAGCTCAATGAACA 83535
QY 338 -----Leu----- 338
Db 83536 GTTATGTTTTTCTAAATTAACAGATTGAGATAGACCCAGGTTTGGGACGCGGAACGTA 83595
QY 339 -----HisLeuLeu-----LeuLys----- 343
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QY 344 -Phe 344
Db 83656 TTTT 83659

RESULT 10
US-09-913-514-1
; Sequence 1, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124884)
; OTHER INFORMATION: Dumas Strain
US-09-913-514-1

Alignment Scores:
Pred. No.: 7,19e-21 Length: 124884
Score: 1725.90 Matches: 291
Percent Similarity: 11.93% Conservative: 41
Best Local Similarity: 10.46% Mismatches: 8
Query Match: 71.67% Indels: 242
DB: 4 Gaps: 245

US-10-017-084a-523 (1-344) x US-09-913-514-1 (1-124884)

QY 1 Met-----LysThr-----IleGlnPro--- 6
Db 75328 ATGGGCATCAACAAAACATCTTACGGTGCAGGCTATACACGGAACATACACCTTAC 75387
QY 6 -----Lys----- 6
Db 75388 AGGCGCTTCTCCTATCTACAGCCATGCTTTAAAGTTTTTTTACACCAGCGAGGTTAAAC 75447
QY 7 -----Lys----- 7
Db 75448 TAATTGTAATACATCGGATCGGCTTCTTAATGGAGCAAGGCTGTGGCGTCGCAAGCTC 75507
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QY 7 ----- 7
Db 75508 CACGCACATGAATATCAATTTAAACGCCCTCCGGTTCTACCGAAATGACACAGGATCC 75567
QY 8 -----Met-----His----- 9
Db 75568 GTGTGGCCTTTTCAAGAAGCATATCCACCACATATGCTCAAGCATGGGCCCATGTTACG 75627
QY 10 -----Asn----- 10
Db 75628 AACGCTCACGCGGAGAAAACCGGGGAGATGAAGTTTCACTTAGCCCAATATCTGATTCG 75687
QY 11 -----Ser-----IleSer----- 13
Db 75688 AGAGCGCTCGCCCTTAGGGGATGCTCTCTCTTCGCGGATAATTTCCACACGCCACAT 75747
QY 14 -----Trp----- 14
Db 75748 ACCCACTCCCAATAAAAGCCCTGTAGAGCGCATTTGGCATCTTACTTGAGATTGGATACG 75807
QY 14 ----- 14
Db 75808 CTGCGCGACTTGTCTGTCTTTTCAAGCTTCTTAAACAACATGGCTATGCCAATTGAGATA 75867
QY 14 ----- 14
Db 75868 GAGGTATTGTACAGGAGAACTATATCCCGCGGGAACATCTGCATTACAGAAATGTGAG 75927
QY 15 -----Ala----- 15
Db 75928 GGAATAATTTACTTCTCAACCTCGCTATCGAGCTTCACTGGTGGATATAGCGCTG 75987
QY 16 -----Ile----- 16
Db 75988 TCGTCATATTACATTAAACGGTGTCCAACAGACACGCTCTCGCTGTAGAGCATACCGA 76047
QY 17 -----Phe-----Thr-----Gly-----LeuAla-----Ala--- 22
Db 76048 ATGGATTTCGGGCGGAGTATATAACACGGGTATCCCGGGAAGTGTGTGGCGCATGCCATT 76107
QY 23 -----LeuCys 24
Db 76108 GGCCTGGGTACTCTACACCGGGTGTGTTTATTCAAATAATATATCCCGCTGTGATCTTTGT 76167
QY 24 ----- 24
Db 76168 AATGGCGATTACATCTGCTTACTTCTCTCGGTTTTTCGGGTCCGAGACTCAATTCGGTTG 76227
QY 25 -----Leu-----Phe-----Gln----- 27
Db 76228 GACTCTGTAGGACTTGGAAATTTTCCCTTTAACCATCCCCAGACCTTAATGCGAGAA 76287
QY 28 -----Gly-----Val--- 29
Db 76288 ATCATCGCCAAAGTGTGTGACGCGGCGTGTAGCGCACGCGCGGGTGTCTCAAAATTTTA 76347
QY 30 Pro-----Val----- 31
Db 76348 CCCACGAAGTTCTTACGAGCGCGGATGTCTTTTGTACAATGGAGGCGCTTATGAACCTC 76407
QY 32 -----ArgSerGly---AspAla-----Thr----- 37
Db 76408 GAAACAAATTTTCAACATCGGACGCGATCGATGCGGCTATTTCGCACATTTGGTTTTAAAT 76467
QY 38 -----Phe-----Pro----- 39
Db 76468 CTAATGTTTCCATAAAACGAGGATGTCTGCTTTTATTGGCGGTGATTCCAACTTTGTTA 76527
QY 40 -----LysAlaMetAsp-----Asn-----Val-----Thr-----ValArg 48
Db 76528 GTCCAAGGAGCACACGACGGTTATGTAATTTTATGATACAAAACGCGCAATTCGCTTAGA 76587
QY 49 -----Gln-----Gly----- 50
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Db	76588	GAACCGGCAGTAAATAATATATACCGCCAATGCCCGGGAATTCAGACGGCCATCGCCGA	76647
Qy	51	-----Glu-----SerAla-----	53
Db	76648	TTTCCCATATGAAACTATTTCACTCTGGATATCAACATCATCTAGACTGGGGATACC	76707
Qy	54	-----Thr-----LeuArg-----Cys-----ThrIle-----	59
Db	76708	TTGGGAACCTCGCGAATTTTACCGCGTCTGTGTGTTGATGAGACCTCTACTGTTTCATCCG	76767
Qy	60	----Asp-----Asn-----	61
Db	76768	GGAGACGCACGCCGTGATTCAGAGGTAAACAGGTGTTAATAAACAACACACAGTCTA	76827
Qy	62	-----Arg--Val-----ThrArg-----Val-----	66
Db	76828	GTTACATTTACCGCGTCTGTTGTTTATTAATAGGCATAAACACGGAATCCGGTATACAT	76887
Qy	67	-----Ala-----	67
Db	76888	GAATGCCATATACAGGCACATAATTAATGCAACCATCAGATCATCTGACATGTTTCCC	76947
Qy	68	---Trp-----LeuAsn-----Arg-----	71
Db	76948	GTGGTACCTTTACCCCGTGAAGTTTTGTGCTCTAGATTACCCATACCGCCTTAATTACC	77007
Qy	72	---Ser-----Thr-----	73
Db	77008	TCTGTCAAGTTATCCAACTGTTTACATAGATACTCCACGGGCTTACACCTAACTTTACT	77067
Qy	74	---Ile-----LeuTyr-----	76
Db	77068	GTTAGGATACAGCTCCTGTGAGGCTATTATTTCGGAGTTAAATCGTTTAAACAAA	77127
Qy	77	-----Ala-----Gly-----	78
Db	77128	TAGTCTACGGCGCGCTTTTGTGTTTGTATAAAAAAAGGCTACGCCACGCTACAT	77187
Qy	79	-----AsnAspLys-----	81
Db	77188	CCGGAGGTATGAAATGATATAAAACAGTAACTGGAGCGGAAGATAGCACGTTTCCCTTT	77247
Qy	82	-----Trp-----	82
Db	77248	TCGAGGACAGCAACTGTTGTCTATAGCCACGATATGGCACTGCAGAAATCTGGCTG	77307
Qy	83	---CysLeuAspPro-----ArgVal-----	89
Db	77308	CTGTTTC--CCTCTATAGAAACAGTGTACGTTTGTAAATGTATTGGGGGTAAAGCGAGT	77364
Qy	89	1-----Leu-----Ileu-----	90
Db	77365	ATGTGSCCTAAGCAITGAGTAAGCAACGCCCTATCTCACTGGAAGAGCTGCCAGTTAAA	77424
Qy	91	---Leu-----SerAsn-----Thr-----Glu-----	95
Db	77425	GCTCTAAGAAAAAAGTGCTCCAATCCAAATATAATCCCAATCCGACTTATAACGCCAACCA	77484
Qy	95	nThr-----GlnTyr-----	98
Db	77485	ATCGCTACACCAAGTACAGACGCTCGTGTTTGGTAAATGCAGGCTCTACGTAACG	77544
Qy	99	-----Ser-----IleGlu-----	101
Db	77545	TACAACACTGACGATTAATATAGCAACATTCGCAACGGTTGACGGCCGATATAAAATAAAC	77604
Qy	102	-----Ile-----	104
Db	77605	CTCTACGGGCAGTTTTTTGTAATTAATGCGCGGTCAAACCCCAACACCCCGAGATTTCTGT	77664
Qy	104	-----	104

Db	77665	TTACGCCCACTACAAATTCCTCGACGAAGGAGTGGCCATAAATAAATCTCGAGTGGCG	77724
QY	104	-----Val-----	104
Db	77725	CGCATGGCTCCATCCATTGTGATGAAAAACGGGCTTATTTAATACATAACACGAAACAAGCT	77784
QY	105	-----Val-----	105
Db	77785	GTGACATGGTATGTGTCTAAACACACGGCGATGTGATCGTCGCATACATATGTAAACAAG	77844
QY	106	-----Asp-----	107
Db	77845	TTTAAACAAGTACCGGAGATCCACGTAAAGTTATACAAAAAAGTTGTACTGCTGTTTCCG	77904
QY	108	-----Tyr-----	109
Db	77905	GTAATTTGTTGATGAAACAAAAATAATTTTACAAATTTGGTTTGAATTTAAAAATCCGACTATA	77964
QY	110	-----Glu-----	110
Db	77965	GTTTGTACAGCATCAGTTCGAATAAAATTTAGCTTCATCCACAAACGAAGATTAAATCT	78024
QY	111	-----Gly---Pro-----	114
Db	78025	TGACCTCGGATACCTCGGAACGATAGAAAGATATATAGTTACCCCAACAAAGTTTAAATG	78084
QY	115	-----Cys-----Ser---Val-----	117
Db	78085	TATCCTTAAATACACGTAGTAAAAAATGTTTGAATACGTACATATTTCTTTTTTTTT	78144
QY	118	-----Gln-----	119
Db	78145	CCAGTACACCATATCCGGTGATATATGAAGCCCATTTGGCAATGAAACCAACATGC	78204
QY	120	-----Asp-----	121
Db	78205	ACTTTGGCATAAATGATACACAAAGAGATTACTACAGTTGTGATACCTAACCGGGGCT	78264
QY	121	-----	121
Db	78265	TATTGGCGCGGATAGATCCCGCATTTACTGATTTTAAAGAAACCGGACACGCTTCAA	78324
QY	122	-----His-----	122
Db	78325	GGTTGAAGTACAAACAAGATATCATGCTACAGTCAATCGAACCGTGGTGTCAAGTTTT	78384
QY	123	-----ProLysThr-----	125
Db	78385	CGCGGGTCATTTCCCGATAACGCCTTACAATCTCTTAATACCAAAACGGAACCATT	78444
QY	125	-----	125
Db	78445	TGTTTCACAGTTTTTTTCGGCCACGCATAAATTCAGGGGATGTGATTTATCATTTGCCCTGT	78504
QY	126	-----Ser-----	128
Db	78505	TTATCTTAGCCCGTTTATCTTTTGATGCATTTAAACGTTAGGATACGAATAAATAC	78564
QY	129	-----His-----	131
Db	78565	TGGAACCGCAAGCACCGTGATATTGTTATGTATGTATGCAGAACCTAATCCCCAACGGAAC	78624
QY	132	-----Val-----	134
Db	78625	GCATTATTTTGTGATGGACAACGGGTACTTTTATTTATGCAAACAGCTGATTGGGTATAT	78684
QY	134	1-----SerPro-----	139
Db	78685	CCGATGCACCCCTCTTCTTGGATCGTCTATAAATAATATACGAGAGCATATGTTGGGACG	78744
QY	140	-----Glu-----	143
Db	78745	CATGGGTGAATCACACACGTCAAATGGGGACAATATTCGACCCGTTTTCATCCATAATCGA	78804

Qy	188	e	-----	188								
Db	79885	ACTTAAAGCTTTC	CAAGGTC	CCCGGTC	CCCGTAGCCTTAGAAAAGTTGGTATTGGTAATTC	79944						
Qy	189	-----Gln-----	Gly	-----Ile	Thr	arg-----	193					
Db	79945	CACACAACTGAGGGTAAATTTATA	-----CGCAGCGGGATATGTTGATATGTTGAATTTGGAATTTG	80001								
Qy	194	-----	Gln	-----	Glu	Gln	-----	195				
Db	80002	TTCTAAGTATTAC	CCGGTCA	ATGTTAC	GGGTACATTTGCTAGGATTTAAC	CAGCAAT	80061					
Qy	195	-----	-----	-----	-----	-----	195					
Db	80062	ACAATCCATTTAG	TTTTTAC	CGGGGGATTT	CGGCAATGTTTTTGTAATACGATACCC	80121						
Qy	196	-----	Ser	-----	Gly	-----	Asp	-----	198			
Db	80122	ACAGGCAGCACTAC	TGCACTCGT	CACTGTTAATCGGACCTATTCTAGACAGATTC	TGCTCTCTAT	80184						
Qy	198	-----	-----	-----	-----	-----	-----	198				
Db	80182	TCCCAACCCCATAA	ATAAATAGT	GTACATATAAABACATAAC	CACAGATCTCTTCAT	80241						
Qy	198	-----	-----	-----	-----	-----	-----	198				
Db	80242	ATGTAATTTTAC	GTCAATTTCTCCGTTCT	CCGCTTCCACCCCTCTTAAATATAAAATAAC	CGGGT	80301						
Qy	198	-----	-----	-----	-----	-----	-----	198				
Db	80302	GGTGGCANTAA	ACCCACAGTAC	CGGGGGGCAATCCGCTAGACTGTTTCTGCTCAT	80361							
Qy	199	-----	Tyr	-----	-----	-----	-----	199				
Db	80362	GGAAATTACAA	CGATATTTCCGCTGTAC	CCGCTACGGGTGCAGCGCGCAATTAAC	CCCC	80421						
Qy	200	Glu	-----	Cys	Ser	Ala	-----	Ser	-----	204		
Db	80422	CGAGGCAGTT	TCAGACTCTCGATGCATTAAC	CGCTGGATGGGATATGGAAGTCCAT	80481							
Qy	205	-----	Asn	Asp	-----	Val	-----	Ala	-----	Al	209	
Db	80482	CTGACCGATCC	CCGGGTGAATAATCGATCACTGCTTTTAACTTTAAGGATGC	80541								
Qy	209	aPro	-----	Val	Val	-----	-----	-----	-----	212		
Db	80542	TCGGTTATCC	CCCTTCAACCGATAC	TACTAATATTCGGTGTGTGTGAGCCACAATTA	80601							
Qy	213	-----	Arg	-----	Arg	-----	Val	-----	Val	-----	215	
Db	80602	CATCAGCCGCC	ACGTCCAGATGAACTTAC	TCTCCGAAGACTTTTCATGTAATGTGTAATTT	80661							
Qy	216	-----	Lys	Val	-----	Thr	-----	-----	-----	-----	218	
Db	80662	TAATTACGAGG	TCGTGCGAATGAC	CGGCACTTAAGAATTTATCGGTTGAAAAACAT	80721							
Qy	219	-----	Val	-----	-----	-----	-----	-----	-----	-----	219	
Db	80722	AGACCATGTTT	TGGAGCAAGTTTAA	GAAACCCGATCGGTAC	CCCCCTTCCACATCTAT	80781						
Qy	220	-----	-----	-----	As	-----	-----	-----	-----	-----	220	
Db	80782	TCCGATCCT	CGAGATCC	CACCCCGCAGATCTTAC	CAACGCGCAACTTAAGCA	80841						
Qy	220	nTyr	-----	Pro	-----	Pro	Tyr	-----	Ile	Ser	-----	226
Db	80842	CTACTTACA	CCCCCGCGCTCC	CGAAAAATCCATAC	GATGTAAGTATTTCTCGGG	80901						
Qy	227	-----	Glu	-----	Ala	Lys	-----	-----	-----	-----	-----	229
Db	80902	AGTGGTGGT	CAGAGAACGA	AGCGGTTTATATGTACTGCTATGGAACTAATTAAT	80961							
Qy	230	-----	Val	-----	Gly	Thr	-----	-----	-----	-----	-----	231

Db 80962 AGGGCTATGTCGCGCGGATGGCATGCTCGGATACCTGCTCTGTATTAAATCGACTCCT 81021
QY 232 -----Gly----- |||||
Db 81022 CAGCCATCGGACGGATGTGATGAATGTAATCATAGAGTTTCAGTGGGGGCACTGTATGC 81081
QY 234 ---Pro---Val----- |||||
Db 81082 GTTACCCCATGTCAAAATCATCGGAAGGTGTGTGTGGTCCGCTGTATGTGGAG 81141
QY 236 -----GlyGln-----Lys-----Gly-----ThrLeuGln----- 242
Db 81142 AAAGCGCGTTCAGCGGGAATTAAAGTGGAGGTAGACATTTGGCGCCACG---CAGGTTCT 81198
QY 243 -----Cys-----Glu----- 244
Db 81199 TTTTGTAGATGTCAACACCTGCATTCGAATTCAGTACTAAATAATCTCGCATACCGC 81258
QY 245 -----AlaSer-----AlaValPro-----Se 250
Db 81259 AAATCTTGGCGGTTATAGCGGGAACCAACGCGTGTCTCTCTGTACCGTAATTC 81318
QY 250 rala-----Glu----- 252
Db 81319 ATCTGGGTGGCAGCTTTATATGTTTGGAGAAACATTAAGCGGGCTATTATTAAACGGCTG 81378
QY 253 -----Phe----- 253
Db 81379 TGGTCTGCTTCAGCGAATTTGCTTCCCGAGACAAAGATTATCGGGTGAACCGGAACC 81438
QY 254 -----Gln-----Trp----- 255
Db 81439 TACAACCACTAGTATACCTTAACCTCAACCGCGTGTGGAAAGGTATATGTCAACATTT 81498
QY 256 -----Tyrlvs-----Asp----- 258
Db 81499 ACGTAAATATTAAGGTTAAATTTATAAACAACCTCACGTTTGTGTGTGACTTGACGC 81558
QY 259 -----Asp-----Lys----- 260
Db 81559 GAACACCGTGTCTGTAGACCCGTCGGTAAATGAAGTAATAGATTGCTTTTAC 81618
QY 260 ----- 260
Db 81619 ATGATCCAGTAAATTTGCCCCAAACCACTGTTCCAGCGGAGACTTGATACCTCAAACAC 81678
QY 261 -----Arg-----Leuile----- 263
Db 81679 GGGTTCGGTGTCTTGGTATATGAGCGGTATAACCCACTTTAAATTCCTCTAAACGTGC 81738
QY 263 ----- 263
Db 81739 CATTACTAAAGCTATTAAATGGTACAAAGCAACATGTTTCCCATGCTACGTGTACCAA 81798
QY 264 -----Glu-----Gly----- 265
Db 81799 AAACACAGTTGATTTTGTGTGAAGTGTCTTAAACACTGTCAAAACACTTTGGCGTGT 81858
QY 266 -----Lys----- 266
Db 81859 AAACACTGTACGAGAAAGCAGTCAACTGTGCGGATGATGCCCAATAGCAACGATGA 81918
QY 267 ---Lys----- 267
Db 81919 AATAAAATGCGTGTGTCATGAGGATCATTTTTTGAACAGTTCCAACTCCCTTTATA 81978
QY 268 -----Gly----- 268
Db 81979 TCTGCCATAGATTGGAAACGTCACCTTTGGCGGTTTGGCCATGACTTCCCACTCTTCAAT 82038
QY 269 -----VallyVal----- 271

Db 82039 ACTCTCAAAAGATGTTTCCACAAGGTACGAAAAACGTTGTGTAAAGGTAGACAACACTGACA 82098
QY 272 -----GluAsn---Arg-----Pro-----Phe--- 276
Db 82099 GAACTATCCGACAGAGAAAACGCGGAAATGTGTTCATAACACCGCTATACGCAATTTGCG 82158
QY 277 -----LeuSer-----LysLeuile-----PhePh 283
Db 82159 ATGAGGTGCTGCTTCTTCGGGTGAATATTCAAAACTGTACACTACTGACAGCCTTTT 82218
QY 283 eAsn-----ValSerGlu-----His----- 288
Db 82219 TAAATTCAGGGCTTACGTTTGCATTTACCGAATATCGCATGTTTCAAAACTACATTTGGG 82278
QY 289 -----Asp----- 289
Db 82279 GGTACAGTTGTACCTGTTCAGTATAGAAACGCGCAACATTTGCCCTCGAGCAGTAGC 82338
QY 290 -----Tyr-----Gly----- 291
Db 82339 CGAGAACAGTGGAAATATATTCACACAGTTGTGAGCGTTCCAATTCGSGAATAACCGC 82398
QY 292 -----Asn-----TyrThr----- 294
Db 82399 CTGATGACGTCGGGTACATCTATAGCAAAATTCAGAAACGGGATTTGGTTGCGTTTCC 82458
QY 295 -----Cys-----Val---AlaSerAsn----- 299
Db 82459 CAGAGACCTTTCGCCCGGTGGAAACACGCGGTGAGGACTCCACACGTCCCAAGCGTTTC 82518
QY 300 -----Lys---Leu----- 301
Db 82519 CCTACGACGCTTAGACGTTCAAAATATCTTACAGATTCTTCAACCAAGCGTACGACCAA 82578
QY 302 -----Gly-----His----- 303
Db 82579 CATTATCAATGACATTTAAACATCAATTCAGGAATCCGCTCATCTCTGTAAAGCAGTAA 82638
QY 304 -----Thr-----Asn-----Al 306
Db 82639 AACAGGAACCGCGTCATCTTACGTTACTCGTTACGTATATATATATATATATATATATAT 82698
QY 306 aSer---IleMetLeuPheGly----- 312
Db 82699 CGCAATTCATTCAC---TTTGGTCACTCAGGCCACACTCCAACCTACGCTCTCATAGC 82755
QY 313 ---Pro---GlyVala-----Val----- 316
Db 82756 GTAACCGTGTCAAACTAGTTGAGCGGCATAACCGCGGGGTATTATTAAAGAACCGAAC 82815
QY 317 ---Ser-----Glu-----Val----- 319
Db 82816 TCGATCTAATCCGTGGGGTGGAGTGTACAAGATCCAGCATTTCTGTATGCTTTACTG 82875
QY 319 ----- 319
Db 82876 CTGCAAAAGAGCCTCGCGCGATTTAAATAACACAGCTCGCTCTGAGCTGCGATAGCTT 82935
QY 319 ----- 319
Db 82936 CAGTTGAACAGAGATTCTGTGATATACAAATCAAGTTGAGGAACAACAAGTATTCAAC 82995
QY 320 -----Ser----- 321
Db 82996 AGATTTTAAATACAAACAGACGCTATATAGCACCGGATTTTATTCGCGTTTGGATAAAA 83055
QY 321 n-----Gly----- 322
Db 83056 CAGAAGACGATAATACCGATAATATAGACACTGGAAGACGCGGTAGGACCGAATCG 83115
QY 323 ---Thr---Ser-----ArgArg----- 326
Db 83116 AACACGAAATCATACTTGGTTTGGAGAAAGACGACGAAAGCGTTACTTACAAATGATGC 83175

Qy	326	-----	326
Db	83176	TGAGCAGACACCCCCCAACCTCCAATATCTCCAATCTGAGGACCTTTGCGTTCCCA	83235
Qy	327	-----Ala-----	327
Db	83236	CANTACGAGGCATGAACCAATGCAACCGCAGCCGATCAGCAAGAACGAGATCCAC	83295
Qy	328	-----GlyCysVal-----Trp-----	331
Db	83296	CAACCCACACACGATGTGTAAATCATCTGGGCCAATCGTCAACTGCAACATGCAT	83355
Qy	332	-----LeuLeu-----	333
Db	83356	GGNATCACCAGACGATCACAACAGACAGCTATTTTATTAAGACGCGTTAACGAG	83415
Qy	334	-----Pro-----	334
Db	83416	AGATCCAATACATCAACGGGAAAGGTGGACGCTTTTCCACAAATTTAAACACCCCATG	83475
Qy	335	-----LeuLeuVal-----	337
Db	83476	GGTTTTAGAAATTCAAATTTATCCGTTTAATGTATCCCATCTTCACGCTCAATGAACA	83535
Qy	338	-----Leu-----	338
Db	83536	GTTATGTTTCTTCAAAATTACAGATTCGAGATAGACCAGGTTTGGCGGACGGGGAACGTA	83595
Qy	339	-----HisLeuLeu-----LeuLeu-----	343
Db	83596	TGGCGGTGTTTCATATATACCATCGTCAAAAAATAGCTGTAAAAAACCATGGACATCGTGT	83655
Qy	344	-Phe 344	
Db	83656	TTTT 83659	

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RESULT 11
US-09-661-596A-76/c
; Sequence 76, Application US/09661596A
; Patent No. 6528066
; GENERAL INFORMATION:
; APPLICANT: Grose, Charles
; APPLICANT: Santos, Richard
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
; FILE REFERENCE: 140.0011 0101
; CURRENT APPLICATION NUMBER: US/09/661,596A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/153,779
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 76
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella zoster
US-09-661-596A-76

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Alignment Scores:
Pred. No.:          7.44e-21      Length:      124884
Score:             1725.30      Matches:     293
Percent Similarity: 11.34%      Conservative: 43
Best Local Similarity: 9.89%    Mismatches:  8
Query Match:       71.65%      Indels:     2618
DB:                4           Gaps:       253

US-10-017-084A-523 (1-344) x US-09-661-596A-76 (1-124884)

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Db AAAAGCGACAGCCACCTTGGATCACATCGAGCTAGCAGTTCACCTCTGAAGATGTACG 54703
Qy 7 ---Lys-----Met----- 8
Db TATAAACTTGAACAGTAGAACCAAAATGTTTCGATTAAATCCAAATCCATGTTATCGG 54643
Qy 8 ----- 8
54642 GCTGTTACTGTCCACTGAGCTGAAGCTGAATGGTTGGAGACACACTATATTACAGGTCA 54583
Qy 9 -----His-----AsnSer-----Ile----- 12
Db TATGGGTAAGGACTACACACAAAAAAGAAACACACACAGAATATGTAAATTATGACTTGT 54523
Qy 13 -----Ser-----Trpala----- 15
Db TTATTACGTACATCAACCCGCGTGTGGGCTTTAAATGGATAAAGAGGAGGTAAATCAT 54463
Qy 16 ----- 16
54462 TTCCATTGTAATGTTCCCATGTTTATGGGAATACCCTAAGATCAAGAGTTCGTCACTC 54403
Qy 17 Phe-----Thr----- 18
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Qy 19 -----GlyLeuAlala----- 22
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Qy 23 -----LeuCysLeu----- 25
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Qy 26 -----PheGlnGly----- 28
Db AGCGCCTTCTACGGTCCAGGGCGTTTCCAGGGTTTGGATAATCTGGTCGTGAACCTCTC 54163
Qy 29 -----Val-----ProVal----- 31
Db CAAGTCTCTGGTAAAACTCATCTGTCTGAAGACTTAACCAAGTCGTCAAAATGCCATATG 54103
Qy 32 -----Arg----- 32
54102 TTGTGCTCGAGCGCCACTGTCAGCAGCAACCGTGGCGTATATGGTAATTGAACCATGGC 54043
Qy 33 -----Ser----- 33
54042 CCGCCACTGACAAATATATACCGCAACTTGGTTCGATAGGGTGGTTTCTCGAATTTCCGA 53983
Qy 34 -----Gly---Asp-----Ala 36
53982 CGAGGACCTGTTACCGGGCAGATAAAACCTCCTCTAGGACATGCTATTATAAACCGCG 53923
Qy 37 Thr-----Phe----- 38
53922 AGTGGATCAATGTAATAGCGGGCATACATTTTACC CGGTTTAAACCGCTCCAATT 53863
Qy 39 Pro-----Lys----- 40
53862 CCCTGCTGAAAGACGCGGTTGTTTCTCGCGCTCCGTGATATTACTAATGCTTAATTC 53803
Qy 41 -----Ala-----Met----- 42
53802 TAAAAAGCATGGGACGTTGATCATGGCCGCGGCACTAAATGAGTTGAAGTAAAGC 53743
Qy 42 ----- 42

Qy 124 LysThr---Ser---Arg-----Val--- 128
Db 51522 AAAACCTCTCCGATGACCTGTGATGAGTGTGAATGGGTGCGGTACGACGCGTTAAC 51463
Qy 129 -----His-----Leu----- 130
Db 51462 ATCGGCATGAAAGTTGTACCGGNAATAACGGTATACGTATACATCCCATGGTTAAAT 51403
Qy 131 -----Ile-----Val----- 132
Db 51402 ATGAACAATATCGAGTCCCTCATATATGCAGAAACACGTTGCACATAAATACGGCTTCCTT 51343
Qy 133 -----GlnVal----- 134
Db 51342 AAACAAATCCGTGACCAACCAAGTATAATATTGTATTCTTGCTCTAATCCAAGCGGGT 51283
Qy 135 -----Ser----- 135
Db 51282 GCATATCTCAGCGCGGTCTCTCAACAGCACCGTCAACAGGAGGCCCTTGGCAGCGTGA 51223
Qy 136 ---ProLys-----IleVal-----GluIle----- 141
Db 51222 AAACCCAAACCGTCTCGAGCGCGGTACACGCGGTGTGAGATTGGGGCCGCGGAGCT 51163
Qy 142 -----SerSer-----Aap----- 144
Db 51162 GGGTAAACGTGTTTGGCTCCGTGAAAGACAAGACAGATGATAGAAATGACTGTAGT 51103
Qy 144 ----- 144
Db 51102 GAGTTTAAAGTAATACAGCTCCGCAAGACCCGTAGTGGTGTCTCCAGAAACACCGC 51043
Qy 144 ----- 144
Db 51042 CAGGTGGATGTAAAGTTTTTCCACGGTCAAAATTCAGCATCAAAAGGTAAAGCAAA 50983
Qy 145 Ile-----Ser----- 146
Db 50982 ATCAGAGTCCGTGCTACGAGCGGCCAAAAATGAAATTTCTCCAGATCCAAATCTTCAAC 50923
Qy 147 ---IleAsn----- 148
Db 50922 CCGGCACGATAAACGTAACACCGGGGCCCGTGGGCACGTGTACAGTCTTCTGAGTATT 50863
Qy 149 -----Glu-----Gly----- 150
Db 50862 TTCATTTTGGTGAAGTACTCGTAATATGCGGGGTGTTGGCAGGGTCAAAATGACCAAC 50803
Qy 151 ---Asn----- 151
Db 50802 CAAAACCCAGTCTGTCGATACATTAAAGAGAGAGGCTTTTAAACGGGTATTACATATCG 50743
Qy 152 -----Asn-----Ile----- 153
Db 50742 GAAACCAACAATAACAGTATACACTTTATGTATTAGAGGCGGTGGGTGTGTGTTA 50683
Qy 154 -----SerLeuThr----- 156
Db 50682 CTCAGTAACACATGGCTTTTACAGATTATCAATCGTTAACTAAATGGCGATCAGAAC 50623
Qy 157 -----Cys-----IleAla-----ThrG1 161
Db 50622 GGGTTTTTGTAAATCCCTTTTAAACCAAGCATCAGGGATTAAATATAACCCAGAACCGG 50563
Qy 161 YArg----- 162
Db 50562 GCGCGGTAGTAACAGAGAAATTTCTTCATAGTTTACAAACTACCATGTCTCATCGTTTCAATT 50503
Qy 163 ---Pro-----Glu-----Pro----- 165
Db 50502 TTTGGCCCTTAAATGTTTATAGATGAGATGTGCCATGGGAAGAACGAAAGGGGTTCACGT 50443
Qy 166 ---Thr-----Val-----Val----- 167

Db 50442 CGGTACACTTAGTCGACCGCTAAAGTTTACTGTAAATGGAAGAAAGTTCGGATTCTGGA 50383
Qy 168 -----Thr---Trp---Arg----- 170
Db 50382 TTTTCGTGTTCCAGCCCTGGCTAGACGCGTGAATATTGGGGGGAATTCGACTTTTCG 50323
Qy 171 -----His-----Ile----- 172
Db 50322 TGGGATAAGTTTGACCCCGCTTTAAACATTCATGTATATGATATTTCGAAACAAC 50263
Qy 173 -----Ser-----Pro----- 174
Db 50262 AGAAGCGCGTCTAATGGAGATGTATCCCGTTTGCAACTGCAACACGCGCTGGTAC 50203
Qy 175 -----Lys-----AlaVal-----G1 178
Db 50202 CGTTATTACTTTTACTTGGCATGTCCCGATGTGGAAGAAAGGTGGCAGTTTATGTATACGG 50143
Qy 178 Y-----Phe-----Val----- 180
Db 50142 CATCTGCAATATTTTATATAACAAGCGGAGTGGATACCGCTTGTGGCATACGTTTC 50083
Qy 181 ---SerGlu----- 182
Db 50082 CGGTAGCGAGTTATCTGTATTACTTGCAGTGTTTACGCACTTCTATGATAACACAAA 50023
Qy 183 -----Aap----- 183
Db 50022 TGATGCAACGTTAAATGGAGACAAGACGCTTTTCATGGTACCTGTTTAAAGCGCATC 49963
Qy 184 -----Glu----- 184
Db 49962 TCCAGAAAGCTTTCGCGTTGAGGTATTGAGCGCACAGATGTTTATTACTACGATACACA 49903
Qy 185 -----TyrLeu----- 186
Db 49902 GCCATGTCGTTTTACAGGGTGTATTCTCCCTCATCTAAATTTACAAATATCTTTGTGA 49843
Qy 187 -----Glu----- 187
Db 49842 TAACTTTACCCGGAGTTGAAAAAGTATGAAGGTGCGGTAGACCTACCATCTGTTTTCT 49783
Qy 188 -----Ile-----Gln-----GlyIle----- 191
Db 49782 AATGATAATCCCGCTTTGTAGTTTGTGTTGGTATCACTAAACCTCGAGTTGATGG 49723
Qy 192 -----ThrArg-----Glu----- 194
Db 49722 GGAACGTGTCGAGTTCGACCGCAAGTCGCCAATTAACGTTAAGCGACGTTGAAATTTGA 49663
Qy 195 -----Gln-----SerGly---AspTyr----- 199
Db 49662 CTGCATGTCGATAATCTGACGGCTATACCAACGATGACTATGGCCTGACTACAAGTT 49603
Qy 200 -----GluCys---Ser---AlaSerAsn----- 205
Db 49602 GTTATGTTTCGATATTGAATCTAATCAGGAGGATCTAATGAGCTGGCGTTTCCCGATGC 49543
Qy 205 ----- 205
Db 49542 AACACATCTGAGGATCTTGTAAATCCAAATTTCTTGCTATTATATTCAATCCCTCGACA 49483
Qy 205 ----- 205
Db 49482 GTCTTTAGAACACATTTTACTGTTTTTCCCTTGGCTCTTGTGACTTACCAAGGTAATGT 49423
Qy 206 -----Aap----- 206
Db 49422 ACAAGAAATGAAGNCGCGGGTTACCGAGCCGACTGTGCTGGAGTTTGTATGTAATTT 49363
Qy 207 -----Valala-----AlaPro----- 210

Db 49362 CGAGCTATTAAATTGCATTTATGACCCCTCGTAAACAGTAGCTCCCGAGTTTGGCCACAG 49303
QY 211 -----Val----- 211
Db 49302 TTATAACATTTGTTAAATTTTGAATGGCGTTTATTTATGGAGAACTTAAATTTCTATATACAG 49243
QY 212 -----Val----- 212
Db 49242 TCTCAAGCTTGATGGTTATGGCAGTATAAACCCTGGGGTCTGTTTAAAGTATGGATGT 49183
QY 212 1-----ArgArg-----ValLysVal----- 217
Db 49182 TGGCAAAATCCGGATTTTCAGCGACCAAGCAAGGTAAAGATCAACGGTCTCATATCTCTGGA 49123
QY 218 -----Thr-----Val-- 219
Db 49122 TATGTATGCAATTTGCACTGAAATAATTAACCTCTCGAGTTATAATTTAGATTCGGTTGC 49063
QY 220 -----Asn-----Tyr-----Pro----- 222
Db 49062 ACGTGAAGCTCTAAATCGAGTCCAAGAGAGATTTGCCCTACAAAGACATTCGGGATATTA 49003
QY 223 -----Pro-----Tyr-----Ile-----Ser----- 226
Db 49002 CGCTAGTGGACCGAATACACAGAGGAATTTATGTGTAATTTGTATATCAAGACTCGGCTCT 48943
QY 227 -----Glu----- 227
Db 48942 TGTGGGGAACTGTTTAAATATTTTACCACACTTGAGTTATCCGGTTCGAAGGCT 48883
QY 228 -Ala-----Lys-----Gly-----Thr-- 231
Db 48882 AGCTAGAATTACTTTAACCAAGGCTATTACGACGACAGCAGGTAGGATTTTACACCTG 48823
QY 232 -----Gly----- 232
Db 48822 TTTATTAGACTGGCTCGCTCGAGGATTTATTTACCAGTGGGGGATACCCAGCTAC 48763
QY 233 -----ValPro----- 234
Db 48762 TTTTGAATATAAGATGTTATTTCCGATGTCGGGATGTTGAGGAGAGATGATGAAGA 48703
QY 235 -----Val-----GlyGln-----LysGly----- 239
Db 48702 CGAGAGCGTTTCTCCCACTGGTAGCTCAAGTGGCGGAAATGATAGATATAAGAGCCAG 48643
QY 240 -----Thr----- 240
Db 48642 GGTTTTGGCCCTGATACGGGATTTTATATCGATTCGGTGGTGTGATTTGCAAG 48583
QY 241 -Leu-----Gln-----Cys----- 243
Db 48582 TTTTATCCAAGTATAATTCAGGCCCATATTTATGTTTACCAGCTAACGTTAAATTT 48523
QY 244 -Glu-----Ala----- 245
Db 48522 TGACAGCGTTTAAACGTTTGAATCCATCCGATATGCCACCTTTACAGTTGGAGAAAACG 48463
QY 246 -----Ser----- 246
Db 48462 TCTTTTTTTGTGGCTCTAACGTTTCGAGAAAGTCTGCTGGGTGTTCTTTTAAAGACTG 48403
QY 247 -----Ala-----ValPro-----SerAlaGlu----- 252
Db 48402 GTTGGCTATGGCAAGGCTATTAGAGCGCATACCCGGAAGTCTTCAGATGAAGCAGT 48343
QY 252 ----- 252
Db 48342 GTTATTAGCAACAACAAGCCGGGATAAAGTAGTTTGTAAATTCGCTACGTTTAC 48283
QY 253 -----Phe----- 253
Db 48282 TGGAGTTGGCAGGAGTTTCTGCCATGTTTATACGTAGCGGCCCACTGTCACATAAATTGG 48223

QY 254 -----Gln-----Tyr----- 255
Db 48222 CCGTCAAAATGTTTAAAGTACGAGAGATTAATTCATATAACTGGCGGCAATTGGAAG 48163
QY 256 -----Tyr----- 256
Db 48162 TTTTATTACAGGTTTCCAGACATTTAAAGTAGCGTCTCTCCCAAAAAGCGTACGAGT 48103
QY 257 -Lys-----Asp-----AspLys-----Arg----- 261
Db 48102 AAAGGTTATATGAGATACGAGATTCGTGTTTATCCGATTCAGAGGTGTTAGTGTGA 48043
QY 262 -----Leu----- 262
Db 48042 GGGGATAGCTAAATCGCGAGAAAATGGCACATATAATTTCAACGGCTCTGTTTGTCC 47983
QY 263 -----Ile-----Glu----- 264
Db 47982 TCCTATAAAGTTGGAGTGTGMAAAAACCTTTTATAAACTTTTGTCTTATAACAAGAAAAA 47923
QY 265 -----GlyLys-----LysGlyVal----- 269
Db 47922 GTACATGGGGTAAATTTACGGCGAAAGGTTTAAATGAAGGGAGTCGACTTGGTTAGAAA 47863
QY 270 -----Lys-----ValGlu----- 272
Db 47862 AAACAACCTGCTCAATTTATTAACGATTTATGCCCGCAAACTTGTAGAACTGTTGTATATGA 47803
QY 273 -----AsnAr----- 274
Db 47802 CGACACCGCTCTCGCGTGTCTCGCGAGGCGTCTGTGTTTCCATTGCTGAATGAATAG 47743
QY 274 g-----Pro-----Phe----- 276
Db 47742 ACGGCGCATGCGCTCTGGGATGCGCGGTTTGGACGCAATTTGAGATGCACATCGCCA 47683
QY 277 -Leu-----Ser-----LysLeu-----Ile-----Phe----- 282
Db 47682 GATTACATCACCCAAATTCGATATTAATAAGTTTGTATGACGGCGAGCTTAGTCGTCC 47623
QY 283 -----Phe----- 283
Db 47622 ACCATCGCTTACATAAAACCGTCTGCTGGTGCCTCACTTAACAGTATATTTATAAATAGTAAT 47563
QY 284 -----AsnVal----- 285
Db 47562 GAGACAGGCTCAATCCCAAAAGTTTCGAAACGCTTCGAAACGCTTATGTTTGTGGCCCCC 47503
QY 285 ----- 285
Db 47502 AGACGAAGTGGAGCTGATGCAAAAAGTGTAGCTTTGCTACGTGGAGATCCTTTTACAGAA 47443
QY 286 -----Ser-----Gly 287
Db 47442 TACCGCAGGTAAACCGTGTGGGGAAGCAAGCGTAAGTTAATAATCTGACTTAGCGGA 47383
QY 287 u-----His-----AspTyr----- 290
Db 47382 AGATCCCATTCAGTTAAACATCACAACGGGCTGCTTTAAACATTTGACTATTTTCTCA 47323
QY 291 -----GlyAsn-----TyrTh 294
Db 47322 TCTCATTTGGAGCGGAGTGAACCTTTTAAAGCGTTTATTTGGAACGACACTAAACTCAC 47263
QY 294 r----- 294
Db 47262 AGAAGCGCTTTTAAACGTTTATTCAGAGACACGAGTGTGTAAAGTAAATGTCAA 47203
QY 295 -----CysVal-----Ala-----SerAsnLys----- 300
Db 47202 CCGCTTGCAGGCGGAGGCTTTGTTTGTATACAGGCCCGCTGCTGGGATAATAATGA 47143

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Db 47082 TATTCCAAAGCAATCTCCATCAAGTTAAGTTCACACATTTTACAGTAACGTCGAT 47023
QY 305 ----- 308
Db 47022 GTTCCAAATGGATGGACACACAGTCTCTGTTTCTGTTCTGTTGTTGCGACATACCGACAGT 46963
QY 309 ----- 311
Db 46962 AAAAAATGTTGTCTGCCAAAGTGTGGGACTATTTATACCCCGGACACGCGCCCTGTATA 46903
QY 312 ----- 312
Db 46902 TGNATCGATTAGTCTGTAAATGGAGGTGMAACAGATTTCCCGGAAATATAACATACATCATATA 46843
QY 312 ----- 312
Db 46842 AACCTCCGGCATCTCCATCAGCATAAAAAGTACGCGTATATCTGCGATGCCGCCCTCC 46783
QY 313 ----- 313
Db 46782 CTCATAATATGATACATAAAAAATATTCGGTGTGCCAATACGCTCGACATAGGGT 46723
QY 314 ----- 314
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QY 315 ----- 318
Db 46662 ACACGATATTCTGTATATGTTTAAAGTCTGTAACATATGCTAGTATCAGAGCCGCCGA 46603
QY 319 ----- 320
Db 46602 TCGGTTGACATAGACGCGGTTCTCCAGATGAGTGCATGTCGGACATAAATCTCCGAGA 46543
QY 321 ----- 322
Db 46542 CCTAATGATAACCCATTCGGGATAACGACAGGCAAGTATTCGCCCACTGTCTGACCCAAG 46483
QY 323 ----- 326
Db 46482 TTAACGGAAGGGTGCAGGGGTCGTCTTAATAATTGGCAGATTAAGCTCTAACGGTA 46423
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Db 46422 GCTAGTCTCTCGGGGGACCTTGCAGTGAATTAATAATGCGGTACACAGACCGC 46363
QY 330 ----- 331
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QY 332 ----- 333
Db 46302 CGCATCGAAGCCCGCTCCGAGATACGGATTTATATCGCCTAGACATACATTCGATAGGGT 46243
QY 334 ----- 334
Db 46242 GTGTTGAGGAGACAGCATATTGTCATGTCGGAAGCATTAAGTCTCCATCTCGTAT 46183
QY 335 ----- 338
Db 46182 GAATGCGGCATTTGCGGTTGTTGCGTGGGAAATCTGTTAGGCTTTAAATGCATACGC 46123
QY 339 ----- 339
Db 46122 CAATGTCCAAGGCCACACATACACAGCCTTCAAAATCTGTTTGTGACGCCAGTTGGGC 46063
QY 340 -LeuLeu----- 343
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Db 46062 TTTATATAACTCCACACTTCTCTTATCCGCGTGTGTAGATGGCAATAAAATTTTAGG 46003
QY 344 -Phe 344
Db 46002 GTTT 45999
RESULT 12
US-09-913-514-1/c
; Sequence 1, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(124884)
; OTHER INFORMATION: Dumas Strain
US-09-913-514-1
Alignment Scores:
Pred. No.: 7,44e-21 Length: 124884
Score: 1725.30 Matches: 293
Percent Similarity: 11.34% Conservative: 43
Best Local Similarity: 9.89% Mismatches: 8
Query Match: 71.65% Indels: 2618
DB: 4 Gaps: 253
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QY 1 Met-----Lys----- 2
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QY 2 ----- 2
Db 54822 CCGGAGAAACAGCTTTTAATAATACGAACGTGTCAACAGTTAGCGCTAACCGATATA 54763
QY 3 -----Thr-----Ile-----GlnPro----- 6
Db 54762 AAAAGCGACACGCCACCTTGGATCAGTCGAGTAGCAGTTTCAACCTGAAAGATGTACG 54703
QY 7 ---Lys-----Met----- 8
Db 54702 TATAAACTTGACCCAGTAGAACCAACATGTTTCGATTAATATATCCATTCATGTTATCGG 54643
QY 8 ----- 8
Db 54642 GCTGTTACTGTCCACTGGACTGTAACTGAATGTTGGAGACACACTATATTACAGGTCA 54583
QY 9 -----His-----AsnSer-----Ile----- 12
Db 54582 TATGGGTAAGACTACACACAAAAAAGAAACACACAGAAATATGTAATATTGACTGT 54523
QY 13 -----Ser-----TyrPala----- 15
Db 54522 TTATTAGTACACTCACCAGCGTGTGGGCTTTAAATTTGGATAAAGAGGGAGGTTAAATCAT 54463
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QY 16 -----Ile 16
Db 54462 TTCCATTGTAATGTTCCCATGTTTTATGGGAATACCACTAAGATCAAAGAGTTCGTCATC 54403
QY 17 Phe -----Thr-----
Db 54402 TTGCGGGGGTTCGTTTAAGACACAGGACAGTTGACCTGGAATGTTTGACCTGAAATGTT 54343
QY 19 -----GlyLeuAlaAla-----
Db 54342 TAATACGTTAGATGTGTGTCATGCTGCTGTTTACAGAAATCAAATTAATAATCTAGGTT 54283
QY 23 -----LeuCysLeu-----
Db 54282 TGTGGGGGTTCCCATCTCCCGCTGCTGTTTTTTCATCTAGAACTCTTTACTGCTCTAG 54223
QY 26 -----PheGlnGly-----
Db 54222 AGCGCCTTCTACGGTCCAGGGCGTTTCAGGGTTTGGATAATCTGTCGTGTAACCTCTC 54163
QY 29 -----Val-----ProVal-----
Db 54162 CAAGTCTCTGGCTAAACAACTCATGCTCTGTAAGACTTAAACGAGTCGTCAAATGCCATATG 54103
QY 32 -----Arg-----
Db 54102 TTGTGCTCGAGCGCCCACTGCACGCACACCGTGGCGTATATGGCTAAATTAACCATGGC 54043
QY 33 -----Ser-----
Db 54042 CCGCCACTGACAAATATACCGGAACCTTGTGTCGATAGGTGGTTTTCTCGAATTTCCGA 53983
QY 34 -----Gly-----Asp-----Ala 36
Db 53982 CGAGGGACCTGTTACGGGGCGAGATAAAACCTCTCTAGGACATGCTATTATAAACGGCG 53923
QY 37 Thr-----Phe-----
Db 53922 AGTCGATCAAAATGATAAGCGGCATACATTTTTTACCCCGTTTAAACCGCTCCAATT 53863
QY 39 Pro-----Lys-----
Db 53862 CCCTGCCTGAAGACGCGGTTGTTTCTCGCGCTCCGCTGATTAATTAATGCTTATTC 53803
QY 41 -----Ala-----Met-----
Db 53802 TAAACGACCATGGACGTTGATTCATGCGCGCGGACTAAATGAGTTGAAGTAAAGC 53743
QY 42 -----
Db 53742 CGTAGTCCATAATCCCGTAAGTTTTCGTTTTTTTCAAGAACGCTTTGCTGGGTTTC 53683
QY 43 -----Asp-----Asn-----ValThr 46
Db 53682 TATGTCGCGCGGACGTCATCTTTACGAATCCAATGCAAAACGGAATGATGGTCACG 53623
QY 46 -----
Db 53622 CGGGCGCTGCGCACCGTAATATAGAGTTAAGGTATTTATAGGTACTGTGAATGATC 53563
QY 46 -----
Db 53562 GCAGTATTTAAGAAATAGATTTCGCATATAAACTGGGCTAATTTCTCTATGCGAGTTGG 53503
QY 46 -----Val-----
Db 53502 GGGTAGATTAATAAGTTTATTTGTCGCATATTCCTCGGTAAACCGTTTAAACAGCTGCAAT 53443
QY 47 -----Val-----Arg-----GlnGly 50
Db 53442 AGTGGAATCTCTTCGTGTGAAGTTTATCTGCGCGCATCTGTTGCGTTGTAACAGGGT 53383
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QY 50 -----
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QY 51 -----Glu-----Ser-----
Db 53322 GCGGTGAACACTGTTTAAGCAAAACCCCTAGGGCCCGCGTGAACATATCCACTCTTTTTC 53263
QY 53 -----Ala-----Thr-----LeuArg-----
Db 53262 TTGGCCTTGGTAGCAGCTTTCGAAAGCCCTACAAGCCCTGCGCGGCTGCTCAGAGAGAT 53203
QY CysThrIle-----Asp-----Asn-----
Db 53202 TGTACAGTTACCTGAAACCAACGACCTATTTTAACTCGTATATCCGGAATAACTTCCAC 53143
QY 62 -----Arg-----Val-----Thr-----ArgVal-----
Db 53142 GCTTACGCGCGCTAAATCCCATCAAGAGTACGCCCGCGCGCGCTCTTGTCCCAATGT 53083
QY 67 -----AlaTyr-----
Db 53082 CGGATTTGGCGGATACAGGACCTTCAGATAATGTTACGGTTATAGAGCGTGTGATAT 53023
QY 70 -----AsnArg-----
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QY 72 -----Ser-----Thr-----
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QY 74 IleLeuTyr-----
Db 52902 GTCTTGTACACGCGTAGTGTGTTTAACTAAATAATGGTAATGGGACAAATGCG 52843
QY 76 -----
Db 52842 TCCTGATATGGATCAACAGTTAAACGCCATTAAGTGGTGGCTTCGGATAATCCTTCACG 52783
QY 77 -----AlaGly-----
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QY 79 -----AsnAspLys-----
Db 52722 ACGCGACGCGAGTGTCTAATATGCGACGAAACGTTGGATGATCCACAATGACAGACGA 52663
QY 82 -----Trp-----
Db 52662 TAGTCCCTCGGAAGAACATGGGGCACCGCGATCCAGTAGTCGCTCTTGTCTAGATCGAT 52603
QY 83 -----CysLeu-----
Db 52602 AAACAGCGTTCTAGTGTAGCCCTATAAGTGTCTCTGATGTTGCCCTTTCCTGCTTCOGT 52543
QY 85 -----Asp-----
Db 52542 TTGATCCCGGGTTTTCGAAGGATTAATATGAGCATAGTTTCCTAGAGATCGCAGTC 52483
QY 86 -----Pro-----
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QY 87 -----Arg-----Val-----
Db 52422 TCGGGCATCGTTGTTCTAAGTGTGCTGCTGTTGTTGTTGAGCGCATACCGCGCGGTGTG 52363
QY LeuLeuSer-----
Db 52362 TTTTTCACATAAACTACATGGAATTTTCAGAGTCAAAGGTCCCGGTAAACATATTTAACGC 52303
QY 94 -----Thr-----
Db 52303
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Qy	95	---Gln---Thr---Gln---	97	Qy	142	---SerSer---Asp---	144
Db	52242	CGCCACAGGGGTCTCCAAATCCAAATGAGTGCCCAATAATCCACGCTAAACTCTGT	52183	Db	51162	GGTAATAACGTGTTGCTCCCTGTAAGAACAAAGACAGATGAGTAAGATGACTGTAGT	51103
Qy	97	---	97	Qy	144	---	144
Db	52182	GTTTGATGAACCCGTAGACTGACTGGATAGAACTGGCCATCTCGATCTGTTGGGATT	52123	Db	51102	GAGTTTAAAGTAATACCAGCTCCGCAAGACCCGTAGTGTCTCCAGAAACCCAGC	51043
Qy	98	---Tyr---SerIleGlu---	101	Qy	144	---	144
Db	52122	CGCAGCTAAATGAGGTCCGCAAACTGGTAATAATCGATTAAATGATGAGACCCGCTCCCC	52063	Db	51042	CAGCTGGATGTAAGATGTTTTCACCGTCAAAATTACGCATCAAGTAAATAAGCCAA	50983
Qy	102	---IleGln---	103	Qy	145	Ile---Ser---	146
Db	52062	ATCCTTGGCTTCGGTCATCCCGCTATCTCCACCTCAGTTAGATACACGCAAGATTGG	52003	Db	50982	ATCAGAGTCGTGTACAGCGGCCAAAATGAAATTTCTCCAGATCCAAATCTTCAAC	50923
Qy	104	---Asn---Val---Asp---	107	Qy	147	---IleAsn---	148
Db	52002	GCTGAAACCCATCGCACCAATGACCCCGGCCACACGAGCGGTATATGACCCGAGCGGT	51943	Db	50922	CCGCGCAGCATAAACGTAACCCAGGGCCCGTGGGCACTGTCAAGTCTTCTGAGTATT	50863
Qy	108	---Tyr---Tyr---Asp---	109	Qy	149	---Glu---	150
Db	51942	TAGCCTTGGCAAGTGCCCTCATGCTATATAACATTGGCCATCTTTGATATCTGTTGG	51883	Db	50862	TTCCATTTTGGTGAAGTACTCGTAAATAATGGGGGGTGTGGCAGGGTCAAAATGACCACC	50803
Qy	110	---Glu---	111	Qy	151	---Asn---	151
Db	51882	AGTTTCTTCGTAATTCAGTGTGAATATAACTTCTGGTCAAGGCTGTGTACGCGC	51823	Db	50802	CAAAACCCAGTCTGTGATTAAGAGAGAGGCTTTTAAACGGGTATTACATATGCG	50743
Qy	112	---Pro---Tyr---	113	Qy	152	---Asn---Ile---	153
Db	51822	CATAATAGACCAACCGTCTTTCAACCCCGCATGGGTAGGCTTAGCGTGAGTT	51763	Db	50742	GAAACCAACAATACAGTGTATACACTTTATGTATTAGAAGGCGTGGGGTGTGTTA	50683
Qy	114	---Thr---	114	Qy	154	---SerLeuThr---	156
Db	51762	GACATCGTTTCAGCGGCTCCAGGGCGGTAGTGTTCACCTGAAGAGACTGAAATA	51703	Db	50682	CTCAGTAACACTGGCTTTTACAAGATTATCAATCGTTTAACTATAAATGGCGATCAGAAC	50623
Qy	115	---Cys---	117	Qy	157	---Cys---	161
Db	51702	CGTGACGTAATGTCAGGGGAGTACTGCCCTCGTGATTTTCATCAAAAGCAAGGTG	51643	Db	50622	GGGGTTTGTATCCCTTTTAAACCAAGCATCAGGATTAATAATAACCAAGAACCGG	50563
Qy	118	---Gln---ThrAsp---	122	Qy	161	Yarg---	162
Db	51642	GGCGCTCTCGGGCGACGCGATTTACTGACGCGCAAGGCAACGGCATGGGAGC	51583	Db	50562	GGCGGTAGTACAGAGATTCTTTCATAGTTACAAACTACCATGTCTATCGTTCAATT	50503
Qy	123	---Pro---	123	Qy	163	---Pro---	165
Db	51582	AATAACACAGTCATGTATTAATGGCAACCCGGTGTATATAAAGGTGTGGGTATAC	51523	Db	50502	TTTGGCCCTTAAATGTTTAGATGAAGATGTGCCCATGGAGAACGAAGGGGGTTCAGT	50443
Qy	124	LeuThr---Ser---Arg---	128	Qy	166	---Thr---	167
Db	51522	AAAACCTCTCCGATAGACCTGTGATGAGTGTGAATGGGTCCGGTACCGACGCTTAAC	51463	Db	50442	CGGTACACTTAGTCGACCGCTTAAAGTTTACTGTATGTAAGAAAGAAAGTTCCGATTCTGGA	50383
Qy	129	---His---Leu---	130	Qy	168	---Thr---Tyr---Arg---	170
Db	51462	ATCGGCATGAAAAGTTGTACCGGAATAACCGGTATACGTATTAACATCCCCATGGTTAAT	51403	Db	50382	TTTTCGTTGTCAGCCCTCGCTAGACGCTGAATATTTGGGGGAAATCGACTTTCG	50323
Qy	131	---Ile---Val---	132	Qy	171	---His---	172
Db	51402	ATGAACAATATCGNGTCTCTAATAATGCAGAAACACGTTGCACATAAATACGGTTCCTT	51343	Db	50322	TGGGGATAAGTTGACCCCGCTTTTAAACATTCATGTATGTATGTTCGAACAAC	50263
Qy	133	---GlnVal---	134	Qy	173	---Ser---	174
Db	51342	AAACAATGCGGTGACCAACCAAGTATAATATTTCTGGCTTAATCCAAAGCGGGT	51283	Db	50262	AGNAGCCGCTTAATGGAGATGTATCCCGGTTTGCAACTGCAACACGACCGCTTGGTAC	50203
Qy	135	---Ser---	135	Qy	175	---Lys---	178
Db	51282	GCATATCTCAGCGCGGTGCTCAACAGCACCGTCAACAGGAGGCGCTTGGCAGCGTGA	51223	Db	50202	CGTTATTACTTTTACTTGGCATGTCCCGATGTGGAAGAAAGGGTGCAGTTTCATGTATACGG	50143
Qy	136	---ProLys---	141	Qy	178	Y---	180
				Db	50142	CATCTGTCAATATTTTATATAAACAAGCCGAGGTGGATACCGCTTGTGGCATACGTTTC	50083

[illegible]

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QY	270	-----Lys--ValIu-----	272
Db	47862	AAACAACGTGCAATTTATTAACGATTATGCGCGAAACTGTGTAGAACTGTTGTATATGA	47803
QY	273	-----AsnAr	274
Db	47802	CGACACCGTCTCCGCTGCTGGCGGAGGCGCTGCTGTGTTTCCATTGCTGAATGGATAG	47743
QY	274	g-----Phe-----	276
Db	47742	ACGGCCATCGCGTCTGGATGCGCGGTTTGGAGCGATAATTGCAGATGCACATGCCA	47683
QY	277	-Leu--Ser--LysLeu--Ile--Phe-----	282
Db	47682	GATTACATCACCAAAATTGGATTAATAAAGTTTGTATGACGCGAGCTTAGTCGTCC	47623
QY	283	-----Phe-----	283
Db	47622	ACCATCGGCTACATAAACCGTCGCTCGCTCACTTAACAGTATATATAAATTAGTAAT	47563
QY	284	-----AsnVal-----	285
Db	47562	GAGACAGGTCAAATCCCAACGTTTCGAGACGCATCCCTTATGTTATTGGGCCCCAC	47503
QY	285	-----	285
Db	47502	AGACGAAGTGGAGCTGATGCAAAAAGTGTAGCTTGTCTACGTGGAGATCCTTTACAGAA	47443
QY	286	-----Ser-----	287
Db	47442	TACGCAGGTAAACGGTGTGGGAGCAAAGCGTAAGTAAATAATCTGACTTAGCGGA	47383
QY	287	u-----His-----	290
Db	47382	AGATCCCATTCAGTAACATCACACGGCTGCTTTAAACATTTGACTATTATTTCTCA	47323
QY	291	-----GlyAsn-----	294
Db	47322	TCTCATTTGGACGGCGAGTGTAACTTTAAGCGTTATTGGAACGACACTAAACTCAC	47263
QY	294	r-----	294
Db	47262	AGAACGCTTTTAAACGTTTATTCCAGAGACACAGTGTGTTAACTGTTAAATGCTAAA	47203
QY	295	-----CysVal--Ala-----	300
Db	47202	CCGCTTCAGCGCGCAGGCTTTGTTGTATACACGCCCGTCTGGGATATAAATGAA	47143
QY	300	-----	300
Db	47142	CACCTGAAGCTGAATATCACGAGGAGGAACAAAGTCATCAATAATGCGTAGAGTCTTTTG	47083
QY	301	-----Leu-----	304
Db	47082	TATTCCAAAGCAATCTCCCATCAAAGTTAAGTTCACACATTTTACAGTAAACGTCGAT	47023
QY	305	-----AsnAla-----	308
Db	47022	GTTCCATGGATGGCACACAGTCTCTGTTTGTGTTGTTCTGGGTGGGACATACCGACAGT	46963
QY	309	---Met-----	311
Db	46962	AAAAATGTTGTGCCAAACGTGTGCGACTATTATTATACCCCGACACACGCGGCTGTATA	46903
QY	312	-----Gly-----	312
Db	46902	TGATCGATTAGTCTGTAATGGAGGTGACAGATTTCCCGGAAATATAATACATCATATA	46843
QY	312	-----	312

46842	ARCCCTCGGCATCTCCATCAGATAAAAAAGTAGCGGTATATCTCGCATGCCCTCC	46788
313	-----Pro-----	313
46782	CTCATATATGATACATATAAAATAATTCGGTTGTGCCAATACGTCGACATAGGGT	46723
314	-----Gly-----	314
46722	TCAGCGAGCGCTGCTTGCATGTTGGCTCGGTCTGTATAGCGCAAAATGGATGCAAGAAC	46663
315	-----Ala-----ValSerGlu-----	318
46662	ACAGGATATCGTATATGTTGTTAAGCTGCTGAACATATGCTAGTATCAGAGCCGCCGA	46603
319	-----Val-----Ser-----	320
46602	TCGGTTCGACATAGACGCGGTTCTCCAGATCGAGTCATGTCGGACAATAACCTCCGAGA	46543
321	-----Asn-----Gly-----	322
46542	CCTAAATGATAACCCATTCGGATACGACAGCGAGTTATCCGCCACTGCTGACCCCAAG	46483
323	-----Thr-----Ser-----Arg-----	326
46482	TTAAACGGAAGGTGACAGGGTCTCTTAATAATTGGCACGATTAAAGCCTCTAACGGTA	46423
327	-----AlaGly-----Cys-----	329
46422	GCTAGTTCTTCGGGGGACCTTGGCATTAATTAAATAATANGGGGTACACAGCCGC	46363
330	-----Val-----Trp-----	331
46362	TCCTTTGACATAAGTTTCTCGAATGGTTTGACGGCGCATGGCGTCTCGAGCGGTACA	46303
332	-----LeuLeu-----LeuLeu-----	333
46302	CGCATCGAAGCCCGCTCCGAGATACGGATTATATCGCCTAGACATACTCTCGATAGGT	46243
334	-----Pro-----Pro-----	334
46242	GTGTTGAGGAGACACAGGATATTGCATGTCGTGAGCATAAAGTCTCCATCTCGTAT	46183
335	-----Leu-----Leu-----Val-----Leu-----	338
46182	GAATCGGCATTTGGCGTTGGTTTGGTGGAATAATCTGGTAGGCTTTAAATGCATACGC	46122
339	-----His-----	339
46122	CAATGTCACAGGCCACACATACAGACCTTCAAATCTGTTTTGTGACGCCAGTTGGGC	46063
340	-----LeuLeu-----Leu-----Lys-----	343
46062	TTTATATAACTCCAACTCCCTTATCCGCGGTTGTAGGATGGGCAATAAAATTTTAGG	46003
344	-----Phe 344	
45002	GTTT 45999	

RESULT 13

US-09-913-514-2

US-09-913-314-2
: Sequence 2, Application US/09913514

Sequence 2, Application
Patent No. 6653069

Patent No. 6653069
GENERAL INFORMATION:

APPLICANT: GOMI, Yasuyuki

APPLICANT: GOMI, YASUYUKI
APPLICANT: SITNAMACHI, Hiroki

APPLICANT: SUNAMACHI, HIFOKI
APPLICANT: TAKAHASHI, Michiaki

APPLICANT: TAKAHASHI, Michio
APPLICANT: YAMANTSU, Koichi

APPLICANT: YAMANISHI, Koichi
TITLE OF INVENTION: Method for

; TITLE OF INVENTION: Method for Quality Control of
 ; TITLE OF INVENTION: Method for Quality Control of
 ; TITLE OF INVENTION: Method for Quality Control of

; FILE REFERENCE: 0216-0454P
; ADDITIONAL ADDITIONAL NUMBER. IIS/09/913 514

; CURRENT APPLICATION NUMBER: US/09/913,514
CURRENT FILING DATE: 2001-12-07

; CURRENT FILING DATE: 2001-12-07
 PCT/JP01/00678

; PRIOR APPLICATION NUMBER: PCT/JP01/00678

; PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: JP 2000-62734
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 125157

TYPE: DNA
ORGANISM: Varicella virus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(125157)
OTHER INFORMATION: Attenuated Oka strain
US-09-913-514-2

Alignment Scores:
Pred. No.: 8.62e-21 Length: 125157
Score: 1722.90 Matches: 284
Percent Similarity: 11.90% Conservative: 53
Best Local Similarity: 10.02% Mismatches: 5
Query Match: 71.55% Indels: 2491
DB: 4 Gaps: 245

US-10-017-084A-523 (1-344) x US-09-913-514-2 (1-125157)

QY	1	Met-----Lys-----	2
Db	32423	ATGATAACAGAACCTAAAGATTGGATATCCTACCGAATATATCGCTAGCGTGT	32482
QY	2	-----	2
Db	32483	GTGGAACGCTGTTGTGCTTATATTATTCACAAACAGACGCTTGATGCCCTTCGGCA	32542
QY	3	-----Thr-----IleGln-----	5
Db	32543	ACAATAGCTTTGTCTTTTGATACACGGGAATACAGAACGCTTGTCTATCTTCATGG	32602
QY	6	-----Pro-----LysMet-----	8
Db	32603	GCTCGGNTTATGATCGGAACGCTGCCAATGCAGATGGATATCGCAAAACTATCT	32662
QY	9	-----His-----	9
Db	32663	GCTCTTATACAAATATTAGAACCTTTTACCGGTACACACCCCGAGTACTTTTACCATCT	32722
QY	9	-----	9
Db	32723	CACGTTTCTACTATAGATTCCTTATATGCGAACTTCATCGGACTGTTGGCATTCGCGTT	32782
QY	10	-----AsnSer 11	
Db	32783	GACCTGCTTCCCCAGCAGCTCGTCTTGTGTTCTCTGACCGTCCTTCTATTACAAATAGC	32842
QY	12	Ile-----Ser-----Tyr-----	14
Db	32843	GTTTTTTTAGCAACTCTCTATTATGATGAACCTTTACGGTCGTTGGACCGCATGATAAA	32902
QY	14	-----	14
Db	32903	ACATCGCAGCGGTTGGTTGAAATTTTACATCCAAACGGCTTAGTGGTTTCTCGGTACATG	32962
QY	15	-----Ala-----	15
Db	32963	TTAATGTTACAAAATTTTTCGGTGTCTGTTTATCCAAACCCAGATCTTCAGGCTGT	33022
QY	16	Ile-----Phe-----	17
Db	33023	GGTATCTGTAAACCAAGGTTGAACCGATGAACAATTTGGGGTATGGGTTTAAACGAT	33082
QY	18	-----Thr-----	18
Db	33083	CTTGCTGATGCGGTGCTCATATTGTTGGGCAATACAGGAATCGGAACGCAATGAGA	33142
QY	19	Gly-----Leu-----Ala-----AlaLeu-----Cys 24	

Db	33143	GTGGGAATATCCAGCTTGGCACAATATTATGCGCGATGCTTCTCAGCCCTTAGGGAATGT	33202
QY	25	-----LeuPhe-----	26
Db	33203	GAAAATTTAATGACTAAACCTCCACTTCTGCTATTGGGCTCTTTTTTCAACGATGGCT	33262
QY	27	-----Gln-----	27
Db	33263	TCCGGTATGACAGGTTTACACAGGATCAATGAGCAATTTAATGCGTGTTCACAACTA	33322
QY	28	Gly-----ValPro-----Val-----	31
Db	33323	ACAAACAGGAGAAAATATATACCCGCTCTTGCAATGTAGAGATTTTTTAAATAGTGGAA	33382
QY	32	-----Arg-----Ser-----	33
Db	33383	CGAATAGCAACAGCTTGTAGGATGCCACGGCAGTCCCGTCGGCCGAATCTATTGCAACC	33442
QY	34	-----Gly-----Asp-----Ala-----	36
Db	33443	GTGTGTAATGAATTGAGCGCGGTTTAAAAAATATACAGAGGATCGTGTAAATGCCCA	33502
QY	37	Thr-----	37
Db	33503	ACCTCATATATGATCAGCCCGAAATCTGGAAGATCACAAGCAGCAGTTTCATTCGT	33562
QY	38	-----Phe-----Pro-----	39
Db	33563	ATGGACTCCAGGCAACAGTTTATGTGGATTCTGGACCTCAGATGGCGGGTTTTAACT	33622
QY	40	-----Lys-----Ala-----MetAspAsnVal 45	
Db	33623	TCACAATGTAATATAGAACATGGAGAAATGTAATGCAACGTTTTCACACGACACGTT	33682
QY	46	-----ThrValArg-----Gln 49	
Db	33683	AAAAAATCAACACGCTCAGAGACGTAATTTACAGAGCTCCGACGTGTAATAGGACAA	33742
QY	50	-----Gly-----	50
Db	33743	AGATGGCTTCGTCAGATGAGATTTTATCTAATGTAGATTGGCTTTCGCGTACCCGG	33802
QY	50	-----	50
Db	33803	AATACAGTGGAGTGACCCTTAATATAAAACAGCGGTGTTATGTACATTAAGTATTT	33862
QY	50	-----	50
Db	33863	GTGTTTTTATGATGGCGGCTTTCGTTGTATAAAGCTGTTGTGTGTATTTTCATA	33922
QY	50	-----	50
Db	33923	ACCTCTAGGTTTTTGGAGTACACGTCCTTATTCACGCTCTTTGGGATTGTAATCATC	33982
QY	51	-----Glu-----Ser-----	52
Db	33983	GTAACGTTAGCTCCCTACCAAGTGGCGGTAAATTTTCGTAAAGCAATAAATGATATA	34042
QY	53	-----Ala-----Thr-----	54
Db	34043	ATTCGCTATAGCTGTCACTGTTTGGGAGTGGGAAGCGTAATCAATTTGACGGTGCC	34102
QY	55	-----LeuArg-----	56
Db	34103	CTGGACCGCGCTCAGGTCGTCTCATGTTTAAAGACATCTTTATCGTTTTTGCATATGACA	34162
QY	57	-----Cys-----	57
Db	34163	TATGGCATGGAATTAATGCAACCTGTCTATCAGACATGATTTGATGATGTTTACAAGAG	34222
QY	58	-----Thr-----	58

Db	34223	GGTGACGATGGACTACGAGTCTGTCTTAATATGCGGAGGGGTGCCAGATATGTGTCT	34282
Qy	59	---IleAspVal---Thr---64	
Db	34283	CTTGTGTATCTCCCAATCGAATTCATATATTAACTGGGGGACACTACCAAGTACGTGC	34342
Qy	65	---Arg---Val---66	
Db	34343	TGCGTTTGTCTAGAATATACGGCGATAGCCATTTTTTTCGTTCCAGACAGGGTTTT	34402
Qy	67	---Ala---TrpLeuAsnArg---71	
Db	34403	ATGTCCACACAAATCCCGCTAGACGGTTTTTCGATGATGTGTGGATGGAGCGTGAAGAG	34462
Qy	72	Ser---ThrIle---LeuTyr---AlaGlyAsn---79	
Db	34463	TGCTATACAAATATAACTGTAGACTCAACGGGAATGGCCATCTCTCGTCAGGGAAACATA	34522
Qy	79	-----82	
Db	34523	TCTTTTATTTTGTATCCACATGGCCATGGGACTATAGACAGGCTGTAGTTGTCGGGTG	34582
Qy	80	---Asp---80	
Db	34583	AATACACGGATGTGTACTCTTATATCGCATCGGAGTATACCCACCGCCCGATACGTA	34642
Qy	81	Lys---Trp---82	
Db	34643	GAATCCCAATGGCGCGCTGCTAGTTTGTGTACCGCAACGACGGTCCCGTAAGC	34702
Qy	83	---Cys---83	
Db	34703	GAAGAAGCGTATCTTCGGCAGTAACGCTTATATACGGAAGCTGTGATACATATTTTACA	34762
Qy	83	-----83	
Db	34763	GATGAACAATATTGCGAATACTGGTTACAGCTCAACATCCGTTGCTTCTTTCACCTCCT	34822
Qy	83	-----83	
Db	34823	AATTCACGACAAATGTGCTTAATAAATCGTCTATAGTACTCTTACCAGAAAGTTGGT	34882
Qy	84	---LeuAsp---85	
Db	34883	GAAGTGTATCTTGAAGCAACCTCATATTCAACGTTAACCAACGCTTGCACTGGAC	34942
Qy	86	ProArg---Val---88	
Db	34943	CCTAGATGTAGTTACAGCGAGGTTGATTCCTTGGCATGCGGTTCTAGAAAACAACCTCGACT	35002
Qy	89	---ValLeu---90	
Db	35003	GGGTCTGGCGTTTGGATTCGTGTGTAGAGCGCGTCTTCATGGACTCTCTCTCAGC	35062
Qy	91	---Leu---Ser---Asn---93	
Db	35063	GAGGAAATTTAGCTTGTATCGACGATGGCTTGGTAAATAATACACATTCACCGATAAT	35122
Qy	93	-----93	
Db	35123	TTACATAAACCCGCTAAAAGGTTCTCAAAATTTAAACCAACTGTAGACGTGCCGGATAAA	35182
Qy	94	ThrGln---95	
Db	35183	ACACAGTGGCACATGTATTATACCGCGCTACGAGAAGTGTGTAACACCCAGACGTTGTG	35242
Qy	96	---Thr---96	
Db	35243	TTAAATGTATCCAAATGTAGATACGCTTGAAATCCAGTCCCACTTTTTCACGGAACATGAAT	35302
Qy	97	---GlnTyrSer---99	
Db	35303	GTAGGAAGCAGTTTGAAGATCGGAAGCCATTTCTATTTTGAACAG---AGTGGTATGTC	35359

Qy	100	---Ile---GluIle---Gln---103	
Db	35360	AACATGTTTGTGCGAAAACTACTACAACTGGGCATGAAATTAGCAATGGATACGTACAA	35419
Qy	104	Asn---Val---Asp---ValTyr---108	
Db	35420	AATCGGTGGGTAGCTTGGATCTATTATACCGGTCTATACAAATGTTCCCATTTGGGTA	35479
Qy	109	---AspGlu---110	
Db	35480	ACAAGGCCCTTGGTCATGCCAGACGAAAGGATCCATTGGAGCTTTTATTAACTCACC	35539
Qy	110	-----110	
Db	35540	ATTTTTCGTTTAAACGGGATTTTGTGTGAAAAATGGAAACACGTACATCATGTGTCTACA	35599
Qy	111	---GlyPro---112	
Db	35600	AGCGTTGTATCAGACTTTTATAGGTCCCTTGGGAAATTTTAAACAGGATTTCCCTCCGCC	35659
Qy	113	---Tyr---113	
Db	35660	GGGAACTTATACGGTTTACAAAGTTTATATTAACAACATGCCGGGGCGGAATATGCT	35719
Qy	114	---Thr---CysSer---116	
Db	35720	ATTAACACTGTTCTCCGGAAAAATGTACAATTTGGCATGCTCAATTATCGCTAAGTTTGGT	35779
Qy	117	---ValGln---Thr---119	
Db	35780	CTAGTTGCCATCGCGGTTTCAAGGATACAAACCGCGCTTTTACATGCCGAACATAGATGTTA	35839
Qy	120	---Asp---120	
Db	35840	GAAGCGATCTAGGAGTTTGTGCGCCATAGACCTTATTCTAGACTGCGACAGTCTT	35899
Qy	121	---Asn---HisPro---123	
Db	35900	ATAAGTATATAAATTTGGCTATTATTCTCATCCGGACTTTTTCGCGAGCTTATCCA	35959
Qy	124	LysThr---Ser---Arg---Val---128	
Db	35960	ACCGGTACAGGTCCTGTCTGACGAATACGTCCTTTTGTGAATAGTCTCGGCCCGG	36019
Qy	129	---His---129	
Db	36020	GAGACAGCTATATGGTGAAACACACCGCGCTTGTCTTAGTGTAAAGCTTTAGAGAAAT	36079
Qy	130	---Leu---Ile---ValGln---Val---134	
Db	36080	GCATTACGGTCTACCGCAATAAATTTGATGCCAATTCAAATACCAAGTTCCTCCAGGAA	36139
Qy	135	Ser---ProLys---Ile---Val---GluIle---141	
Db	36140	CCCCCGAAGAAACCGACATTCACCCGGAAGAGTTAATTCGGCGTGTATATGAGATACGA	36199
Qy	141	-----141	
Db	36200	TCCGAAGTTACATGTATTGACCTCGGCTGTTTACAGATATCTTCCCGCGAGTGTTA	36259
Qy	141	-----141	
Db	36260	TATAGCACACGGGCTTTGATCGCTGAACAATCCCTAGGCGTTTTCGGGTTCGCGACCGCA	36319
Qy	142	Ser---Ser---Asp---144	
Db	36320	AGTAGCGCACCAATCAACGGCTTTTAGATTCTCTCCGGAATTCGACGCTTAATTAACG	36379
Qy	145	IleSer---Ile---Asn---148	
Db	36380	GCAATCATATCGTCCCTGTCTATACACCTCTCTCTGAGACTATACAAATCTCCCGTCTC	36439

QY 149 -----GluGly-----Asn----- 151
Db 36440 GTATCTGTATAAGAGCTTATTAAAGAGGGGAAGATTAAACACAGACAGCGGCTCTC 36499
QY 151 ----- 151
Db 36500 GTATCGTGTATTCTGTAGTCGGGAAGCTCAACCGCAGGTTACTTATCCAGACGAGAG 36559
QY 152 -----Asn-----IleSer 154
Db 36560 TTCGATGAATTATCAGCTACAAATTAACCAATTAATACACGCGCAACGCAACGGGCTTCC 36619
QY 155 -----LeuThrCys----- 157
Db 36620 GCGAAGCAGAGTTGTCTGCTTTAATACGCTAAGCGCGCCGTAGACACGCGGTAAAG 36679
QY 157 ----- 157
Db 36680 GACTATGAACATATAACAATGGTGAGGTCAAGTATCTCTGAATAACACGGGATGATTTA 36739
QY 157 ----- 157
Db 36740 TTAGCAACAATTGTACGTCTACAGACGATTGGTGCACAGATAAATAATTTTAAGTGAT 36799
QY 157 ----- 157
Db 36800 CCAATGATCCAATCCGGTTTACAACTTCGATTAAAGACGATTGGNAACAGGCTTAA 36859
QY 158 -----Ile----- 158
Db 36860 GAGGTTCAAGCTATGCAACAGAGGCCGGAACACACAGACACATAAAGAGTCAAAA 36919
QY 159 -----Ala-----ThrGly----- 161
Db 36920 CAGCGGCATATATAAATACTCGGGGGTTACTTCGCGCGTAACCGGTTTTTGTGGGACTT 36979
QY 162 Arg -----ProGlu----- 164
Db 36980 AGGCTCAGTAGATTATTATACCGGAACCTTGCTCTGAGTTAGATGTCGAAGGACCCCTG 37039
QY 165 -----ProThr-----Val-----Thr----- 168
Db 37040 GTAAATCTCAGACCAAAAGTCTTAGAGCGCGGTAGAGATCCGTTCTCAACTTACCGGT 37099
QY 169 -----Trp-----Arg-----His----- 171
Db 37100 GATTTCTGGGCGTTATTTAACCAATATCGAGACATTTTAGAACATCCCGGAACGCACGC 37159
QY 171 ----- 171
Db 37160 ACATCTGTCTTAGGAGGACTGGAGCTTGTTTTTACAGCTATTATCGAAATTTGTCCGATA 37219
QY 171 ----- 171
Db 37220 CCTAGGAGTATAGACCATCATCTGCTCGTTTTTTTGGTGCAGTGGCAGATGCTGTGCA 37279
QY 172 -----Ile-----Ser-----Pro----- 174
Db 37280 TCCGNATCGCGACCGGTATCTACTAACCCGGAAGAGTGAGTCGGCATAAACGCTGTGTT 37339
QY 175 -----LysAla-----Val----- 177
Db 37340 GCAACTCTTAGTAAGCGAGCTTAGTTTCATCTACAGTGCCAGCCTTATCTTGTGTTG 37399
QY 177 ----- 177
Db 37400 TCGTTATATAAATAATCAGGCTTTACAAACAAGAAATTACGAATPACCCATAAGTTGACT 37459
QY 178 -----Gly-----Phe-----ValSer----- 181
Db 37460 GAATTACAAAACAACTTGGAGATGACTTCTCCACCCTAGCTGTCTCATCTGGACACTTG 37519
QY 182 Glu-----AspGluTyr----- 185

Db 37520 AAGTTTATATCATCTTCAATGTAGATGATTATGAATAAATACGATCGATATTATCAATA 37579
QY 186 -----Leu-----Gln----- 189
Db 37580 CAAACAAATGTGCACGCCCTGATGATACGGTTAAACTTGTGAAGTTGAACTGCAAAAG 37639
QY 190 -----Gly----- 190
Db 37640 CTACCCCCCATTTGTTGCTGGGCACTACCTTATCTCGAGTAGTAAAGATCTTCAT 37699
QY 191 -----IleThr----- 192
Db 37700 AACTCGTCACAAATGCGACATCAGAGAAGAGAAACAGGCAAAAGTGTAAATACCGATTGT 37759
QY 193 ---Arg-----GluGlnSer----- 196
Db 37760 GAACGTGCATATAACACAAACGCACTCGGGTTTTGTATGAGCGTTGGACAGTGATATT 37819
QY 196 ----- 196
Db 37820 ATAGCATGTCTGGAGGCATGGAACGCCCATGTTTAAACGGGACAGAACTGGCACGG 37879
QY 197 -----Gly---Asp-----Tyr----- 199
Db 37880 TTGCGAGATATGCGCGCTCGCGAGGGTTTGATATACAGCGATTTTACCCCAACAGCACGT 37939
QY 200 Glu-----Cys-----SerAla----- 203
Db 37940 CAGGTTGTAGCGCATGTGAACACTACGCCGTTTACGGCAATTAGATACYGTGTTCCGCCAC 37999
QY 204 -----SerAsn----- 205
Db 38000 AATCCACATACCCCGAABATACAAATATTTCCCCACCTTTGSCCTTTGTTAAGAGGGTTA 38059
QY 206 ---Asp-----ValAlaIleProVal-----Val 212
Db 38060 ACATGTTTGATGATGATTTTCGATTACCGCTCCGTTATTCACCGTTATGTTTCCAGGTGT 38119
QY 213 -----Arg-----Arg-----ValLysVal----- 217
Db 38120 AGTATTGAAGGACTCCTCTGCTTGTGCTTATGCTGTTATTCGCGGTT---GTGTTATTATCCGCC 38176
QY 218 ---Thr---ValAsn---TyrPro----- 222
Db 38177 GATACGTCATTTAATGGAATACCTAACTACCGAGATATGATATTACGAACCTCGGGGAT 38236
QY 223 ---Pro-----Tyr----- 224
Db 38237 CTATTACAAATACCCGATTTGGCTGGGTATGTTGATTTTACACAGGCTCTTATGATCAG 38296
QY 225 ---Ile-----SerGlu-----AlaLysGly 230
Db 38297 TTTATTAACGAAAGTGAAGTTAAGTGAATCTAGAGCAGACATCAGACAGGCTGCGGG 38356
QY 230 ----- 230
Db 38357 GCTAAACTTACAGAGCAAAATAAGGCTTTGGAGGAAGTAACTCATGTTCCGGGCACACGAA 38416
QY 231 Thr-----GlyVal-----ProVal-----Gly----- 236
Db 38417 ACGGCTAAACTTGCACCTTAAGAAGGTGCTTTCATTACATTACCAAGCGAAGGTTTATTG 38476
QY 237 ---Gln-----Lys-----GlyThr----- 240
Db 38477 ATTCCGGCTATAGATGATTTTCAACTTTCGATCATTAACGATTTATAGGACGGCATAT 38536
QY 241 -----LeuGln----- 242
Db 38537 GAAAGATTTTACAAACAATGGTAGACCGGATCTAAAGAGGAGGCCAACCGACAGAGCTTGCA 38596
QY 243 ---CysGluAlaSer----- 246

QY 82 ----- 82
Db 6312 TTAATAATATCAAAATATCAATTGTGAAAAGTTGTATTTGGTTCAGGTTCAAGCTTTCCGA 6371
QY 83 ----- 85
Db 6372 ATTTGTTGAATTTTATCCCTGTTTCAATTGTTGACTTGTGTTGGAGACACCTTTTIT 6431
QY 86 ----- 87
Db 6432 GTGTTTCGTGAACATGTCACCCCTTCGGTATACATTAGCCTACAAGTAATAACGTTGA 6491
QY 88 ----- 90
Db 6492 TAAATGTCATCATGTTGTGTAATAAATAGACTTATATGTAATACAGACCCCTGTTGTTA 6551
QY 91 ----- 92
Db 6552 ATCTAATTACAAAGAAATTCATCATCTCTCCAGCAATCTGAGTAGCTCGGTGATGGAT 6611
QY 92 ----- 92
Db 6612 CTTCCATATCAGCGCCACAGTTTCACCCCGTTTGCCGTACCCATCCACGTAGTGGAGTC 6671
QY 93 ----- 97
Db 6672 AACCTGAACCGTGCAATTTCTCAGGCCCTTTGTCTGTATGATCAGTTCTCGGAACGGCTC 6731
QY 98 ----- 100
Db 6732 TTGGATATCAGCAAGCTCGACGAGTGGGTGTTGCACCCAGGATTTGCAGAAGCCATT 6791
QY 101 Glu ----- 101
Db 6792 GAAGACGTGGCGTGTGTTCCAGTTGCACTTGCCTTCATGCCCCCGAATAGGCGCG 6851
QY 102 ----- 104
Db 6852 CTGCAAGTGTGATACCTCGTCGCCACCCAGCTCTTCATTATATGTGCAACACCAATTG 6911
QY 105 ----- 107
Db 6912 CAGCGCTTGTGTCACACAGTGCATTGCTCAACTTGGCGACGCGTGTCTGTTGTCATG 6971
QY 107 ----- 107
Db 6972 ATCCGCCCTACGCGAGTGACCTCTCGCTGCAGGAATGGCTCGGGCGCAACAGATTT 7031
QY 108 ----- 109
Db 7032 TGCCACGAGTGTACAGAGGTCCGACAGCTACAGTCTTTATCGCCATCCAACCTCAGC 7091
QY 110 ----- 111
Db 7092 AGCCGATTCGTTGAGGAGGACATGTAAAGTGCACGGCGAAATGGCTTAAAGAAACC 7151
QY 112 ----- 113
Db 7152 TGCCGCTTCTTTCGTCGCCCTGCTGAGTTCCTCAGCCGTTATGATCATGTTGCCATTGGG 7211
QY 114 ----- 116
Db 7212 CCGGTGCTCTTCCATGATGAACGTGATTTGCCAGCAAACTGCAATGAGCCTCTTCTCTGC 7271
QY 117 ----- 118
Db 7272 TTGACCTGCGGTACGACTATCAGGTTTTCCTCCAGGAGTGCATGCCCATGATGGTGTG 7331
QY 118 ----- 118
Db 7332 GGGCATTTATCCGGAAGGCGCACCACTACCTAGTGTGTCATCGTAGGAGGCGGCTGTCT 7391

QY 118 ----- 118
Db 7392 GGCCTGTTGTCGCCACAGAACTACTTGGCGCTGGGTCAAGAAATCACTCTTTTCGAT 7451
QY 119 Thr-----Asp----- 122
Db 7452 ACCGTTGATGAGATCCGTAGTTTGGGGCATCCCGATGCCAAACGGCGACGCTCACCCAG 7511
QY 123 ----- 123
Db 7512 GCCTTGACCTGTTGGTGTGTCATGCTTCTCGGCCAACCACTTTGCTGTCTATCAT 7571
QY 124 ----- 129
Db 7572 CTGGATAAGCTTTAGAAATCCGTCAGCTTGGTTCCTTGTGTCGGCAACGACACACA 7631
QY 130 ----- 131
Db 7632 GCACATATTTCCGCCAGAAACGCTAOCATGGCAGCGGGGCAAGCTCCGCCGGGATA 7691
QY 132 ValGln-----Val----- 134
Db 7692 TTTACGGGTGATCATGTCCGATGGAGACACTACTCTACCAAGGTGTGAACGGATGSC 7751
QY 135 ----- 138
Db 7752 AGGAGACTGATGGCTCCGATGGATATCTCTTTCATGTTGAAAGAGCGTCTGTGTGATAA 7811
QY 138 ----- 138
Db 7812 GCCTCAGAACGACGCGAGCTTTGGCTCCGAGAGTTCCGAAATTCATCTTCCATGCCGTT 7871
QY 139 ----- 143
Db 7872 TTGCTCGATCTTTCAGCTGTGTAATTCGAGTCTCTGTTGGCAAGCATGTCGCAACACCC 7931
QY 144 ----- 145
Db 7932 CATGATTTCCAGGCTTTCCGGGATACTGAGTTGGGATACGCGCGAGTTTCTCTTATTAC 7991
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US-08-459-569-19
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; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
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FEATURE:
NAME/KEY: misc feature
LOCATION: complement (19031..19390)
OTHER INFORMATION: /label= ORF18SUBSEQUENCE
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US-08-459-569-19

Alignment Scores:

Pred. No.: 4.8e-24 Length: 21126
Score: 1721.10 Matches: 293
Percent Similarity: 11.04% Conservative: 44
Best Local Similarity: 9.60% Mismatches: 6
Query Match: 71.47% Indels: 2709
DB: 241 Gaps: 241

US-10-017-084A-523 (1-344) x US-08-459-569-19 (1-21126)

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QY 9 -----His----- 9
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QY 10 -----Asn-----SerIle----- 12
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QY 13 -----Ser-----Tyr----- 14
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QY 15 -----AlaIle----- 16
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QY 31 -----Val-----ArgSer----- 33
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QY 38 Phe-----ProLysAla----- 41
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DB 4812 TCGTCAAGGCATATGTTCTCGACTTTTTCGACGGCGGACGATGTTACGCCCGCGGACA 4871
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QY 59 Ile-----Val-----Asp----- 60
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QY 61 -----AsnArg-----Val----- 63
DB 5292 GGCACCGGTAAATCCAAAACCTGTCTGCGGCTGGCAGGAGCGCTTCACTGACTGAGG 5351
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QY 69 -----Leu-----Asn----- 70
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Qy 230 --- 230
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Qy 231 ---Thr---Gly---Val---Pro 234
Db 10572 CCCGAGAGTCCGAGGGTTAGTCTCGGCTCCGGTGAGGAGCGCGCGAGCTGATATCCC 10631
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RESULT 16
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; Sequence 19, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740

; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVULVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
; FEATURE:
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; OTHER INFORMATION: /label= ORF1SUBSEQUENCE
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; LOCATION: complement (2649..3458)
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15659..16210
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NAME/KEY: misc feature
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FEATURE:
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LOCATION: complement (18177..18743)
OTHER INFORMATION: /label= ORF17SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (19031..19390)
OTHER INFORMATION: /label= ORF18SUBSEQUENCE
US-08-458-831-19

Alignment Scores:
Pred. No.: 4.8e-24 Length: 21126
Score: 1721.10 Matches: 293
Percent Similarity: 11.04% Conservative: 44
Best Local Similarity: 9.60% Mismatches: 6
Query Match: 71.47% Indels: 2709
DB: 1 Gaps: 241

US-10-017-084A-523 (1-344) x US-08-458-831-19 (1-21126)

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QY	3	-----Ile-----	8	
DB	4095	GACCGGACATTGGAGAGGCCACCGCTGCTGATTTCTTCAGCCGAGATGAGCTCC	4154	
QY	9	-----His-----	9	
DB	4155	AAGGCTCTCCAGTTTCTGTCCATTTACCTCCAGTTTGGAGATCTGGAACTTTGTC	4214	
QY	10	-----Asn---SerIle-----	12	
DB	4215	GATGCCAGATGATGGAGATTACAAATTCATGAAGGCAATGGCACAGTACCACCG	4274	
QY	13	-----Ser---Trp-----	14	
DB	4275	GATTTGAAAAGTCAATGGAAGAACGCGTATTGACAGGCCAGGCCACGTCGCCACG	4334	
QY	15	-----AlaIle-----	16	
DB	4335	TCCAAAGTTTGAACCTCTTTCGCGCTGTGTCGCCGACAAACAGTAACTTGGCCGCCAG	4394	
QY	17	PheThr	19	
DB	4395	TTTACCCATCTCGGCCCTGTGAGCGTGTAGGAAGTACTCGGCAGCAGGTATTCGG	4454	
QY	20	LeuAlaIle	25	
DB	4455	ATTGCGGCTAAGAAACCTGGTACGATCGTTTATTCGCTGCGAAAGGTTCTCTGTTGGAG	4514	
QY	25	-----Val-----	25	
DB	4515	GTGAGGTACACGGCGATCGCGCCCTAGAAATCTTACCGCTTGGGGAAACAGGCTTAT	4574	
QY	26	-----PheGlnGlyVal-----	30	
DB	4575	AGCAATGGCGGTGGCAGTACTTC-----GGCTTCACACCGTCCGTCCTTTGCTTAAT	4631	
QY	31	-----Val---ArgSer-----	33	
DB	4632	CTTTCGCGCGCGCTCGCTACATTTTTCAAACGCTCGGATCTGTGTTCCCTTCCATTG	4691	

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DB	4752	TTCCGATCACTGCTTCTCCGCCACGAGCACCAATCAGTTTCTGAACTCGTAGAGCTCAGG	4811	
QY	42	-----Met-----Asp-----	43	
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QY	48	-----Gly-----GluSer-----	48	
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QY	49	Gln	-----LeuArg-----	49
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DB	5052	TTGGTGTGTTTAACTAGTGGATTGATTGAACAAGAGTCCGAGTTGGGATTCCT	5111	
QY	53	-----AlaThr-----LeuArg-----	56	
DB	5112	TTGCTGCTTCTGCTGCAACGATATCGTATGCTGATGATGATGATGATGATGATGATG	5171	
QY	57	-----CysThr-----	58	
DB	5172	GGCGGACGAGCCGCTTGGAGCGATTTGTCAGCTTCAACTTCTGCTCAGAAAGCAGT	5231	
QY	59	Ile	-----Asp-----	60
DB	5232	GTGGGAGCGAGATCATCTTTGATGAGCAGTGTGGTTCGGGACGCTCGGATCATGGA	5291	
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DB	5292	GGCAACCGGTAATCCAAACCTGTGCTGCGCTGGCAGGAGCGCTTCATGACTGAGG	5351	
QY	63	-----	63	
DB	5352	CGTCGATGGCTTTTTCACGACAGACAGACAGCCGCCGCAATGCGCGCTTGTATGGGA	5411	
QY	64	ThrArg	65	
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DB	5472	GACTGTTGTCGATGGCCAAAGCGGTGGGATGACGCTTCTCGGTTGTGAAGATCTG	5531	
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DB	5532	GCACGACATGCTTGTGCGCGCATGCTGCGCTCTTTTCAACTGTGCAACGACAGGC	5591	
QY	67	-----Ala-----Trp-----	68	
DB	5592	CTTTGCCGAGAAGCTTTCACGACGCTGTTGGCTCTACGCTCGCCACCGGCCCATGCCAT	5651	
QY	68	-----	68	
DB	5652	TGTCTGTCCTGATGAGAAAGCCAGATCCAGGCACTCGATCGGACCAACCGGACT	5711	
QY	69	-----Leu-----Asn-----	70	
DB	5712	CCCCTTGAAGAAAGGGCGCGCGCAATGACCCAGATACCCAGATTAAGGCCACGACCCAC	5771	
QY	71	-----Arg-----	71	

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QY 72 -----Ser-----Thrile----- 74
Db 5832 TCACCGGCATCAGAGTTTCATCGGTTTCTCAACGCCATCGAGGCGGAATCGCAAAGGA 5891
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Db 5892 CAAGGCGTCCAGCTCATTCTCGCAATTAACGGGACCCATAAGCAGCGGAAGTCCGCGC 5951
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Db 5952 CTGGCTGGCAAGGCATCGGCGCTGGAGCTTCCACTTCGTCCCAACATCATGTTTCATGGCT 6011
QY 80 -----Asp----- 80
Db 6012 GNAAGCGTGCAGGGATTCTTCGGCTAAATGACACGTCGAGCTGGAAGCAGCGGTGCTT 6071
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Db 6132 ACCAAGCCGTTTCATCTGGAGAGCAGATCCAGACGAGATCATTCGACCGGTCAACCGTG 6191
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QY 152 ---Aenile-----Ser---Leu-----155
Db 8292 TACAATATCGAACCGCGCTCGGAACTCGTCTGCCGTGTCAATTCAGCACTCTTCATG 8351
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QY 190 -----Gly-----IleThr-----192
Db 9312 CCACTTTTAAATTCCTTTGGCCCACTGGCCATTAATTTGGCACCTTACATATATTAGTGAG 9371
QY 193 -----Arg-----Glu-----194
Db 9372 AAGATAAAGTGTCACTATCGTTTCTCTGTTCAATTTTGAATTTTGAAGGATTTTCATGTTG 9431
QY 195 -----Gln-----Ser-----Gly-----197
Db 9432 TCAACTACACAGCTTGAAGGAAATCCCAATCAACGAGAGAAAGCTCAACATCTCGCAA 9491
QY 198 -----Asp-----198
Db 9492 AAAAAGAATGTTTCATCATTCGCTAGACTGCAATATGACCGCTCTTTCGGCGCTGGGCC 9551
QY 199 -----Tyr-----Glu-----200
Db 9552 TGCTTTACTTGTCTGCTAGCTTCGGACAGCCACGAGATGGCTATATAGATCCTTT 9611
QY 200 -----200
Db 9612 CATCAAAACCAAAACATTACTAAGATCATGCTGTAAAGCTTCAATACGGTGAGTGTGTTG 9671
QY 200 -----200
Db 9672 TAGGTTCAATTATTACTATTTTGAAGCTGTGTATTTCCCTTTTCTTAATATGCACCTAT 9731
QY 200 -----200
Db 9732 TTCATGTTTCAGATGGAATTAGCCGGACTAAACGTGCGCGCATGGCCAGACCTTCGG 9791
QY 201 -----Cys-----201
Db 9792 AGTATTATCGCTCGTCTGTCTTAAGCTTGTAGGCGTGCAAAAGGCCAAAGAGAGGCCAA 9851
QY 202 -----Ser-----AlaSer-----204
Db 9852 ACGGTATCCCGGGCGGAACCGGACCATCTTGTGAGCCAGCCATCTGAGCACCCTCC 9911
QY 205 -----AsnAsp-----ValAlaAla-----209
Db 9912 TTTGGCCATGACTTCCCAAGCCCGACCGGAGCTTCAACGACCCCGCGAGTTGCTCGAAG 9971
QY 210 ---Pro---Val-----211
Db 9972 GGACCTTTGTGCGCGGAGCTGAAAAATTCAGACCTTACGGGATTAATACGCCATTTTCGAAC 10031
QY 212 -----Val-----ArgArg 214
Db 10032 AAACCTACGGGATTAATACGACGTGGCTGGCGTTCGATTTCATTTCCAGCCGCGAGA 10091
QY 215 -----Vallys-----Val-----217
Db 10092 TGAATATGATATGTTCTGTTAAAGTTAAATAAGCTGGAGCCATGGCGGATTTGCTCTG 10151
QY 218 -----Thr-----218

QY 309 -----MetLeu-----PheGly----- 312
Db 12372 ATTGTCTCAATACGCTAAGAGCTCTGGATTATTAATAGTTTGGATCGCTCGAGTTATGG 12431
QY 313 -----Pro----- 313
Db 12432 GTACAAGCAACCTGTTTCTTACTTTGTTTAAATGCTGAAGAGCAGCTGTTCTCTCTT 12491
QY 313 -----Pro----- 313
Db 12492 TTTCAAGCTCAAGTGGAGGATGTGACAAAGCAGCGATGAGCTAGACATGAAAGAA 12551
QY 313 -----Pro----- 313
Db 12552 CGCTCAATGAGCGTAACCCCTGATCGAGCGGGTGAGAAATCAATCGATGATATGA 12611
QY 314 -----AlaVal----- 316
Db 12612 CGAAGAGGAGGTCGGTGGGCGCACGGGCTGCTGTACCTCTACGCTGAGCTGCCCGCAGAT 12671
QY 316 -----Pro----- 316
Db 12672 GATGCTCTGCTTCTATGAGGGTCTCTGCTTACATTTGATGCAAGCGCAGCTCTCAC 12731
QY 316 -----Pro----- 316
Db 12732 CAACCTTCCCGTACGACATGATGTGACTCTCGATGAGGTCAATAGAGGGCTCAGGCA 12791
QY 317 -----Ser-----Glu-----Val----- 319
Db 12792 AGCATCAGGTTTTTTCGGTTACGGGATCCTATGCGGAGCGCTACTTTCGCTGCAATTTTC 12851
QY 320 -----SerAsn-----Gly----- 322
Db 12852 TTTCCCTGGCGTGTCATCAAGCTGAATGAGCAGATGAGCTTAATTCGACAAAGGGGAAA 12911
QY 323 ThrSer-----Arg-----AlaGly 328
Db 12912 GTGCTGACATCGACCTCTATGCCAGCACCAGCTTAGTTCGAACCTGCTGAGTTGCT 12971
QY 329 -----Cys-----Val-----Tyr----- 331
Db 12972 GAGCATGGCGAGTGAAGTTTGAATCGGTAATGTTAGTTCGATGGGCTGACGAGTTT 13031
QY 332 -----LeuLeuPro-----Leu----- 335
Db 13032 GATGTCAGGAGAGCTGAGTGTGCTCCTGTTTCCCTTAAGAGTATTAATGTAATAAA 13091
QY 336 -----LeuVal-----Leu-----His----- 339
Db 13092 AATCAAGATCTGTTTAAATAACGATATCTTGATTTTCATCGCGCTTTTGTGAATAAATG 13151
QY 340 -----Leu-----Leu-----LeuLysPhe 344
Db 13152 TTTGTGCTTGATCTTAAAGATATCCTTTGAAATTT 13187

RESULT 17

US-09-913-514-2/c
; Sequence 2, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734

; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 125157
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(125157)
; OTHER INFORMATION: Attenuated Oka strain
US-09-913-514-2

Alignment Scores:
Pred. No.: 1,03e-20 Length: 125157
Score: 1719.80 Matches: 293
Percent Similarity: 11.10% Conservative: 43
Best Local Similarity: 9.68% Mismatches: 8
Query Match: 71.42% Indels: 2683
DB: 4 Gaps: 252

US-10-017-084a-523 (1-344) x US-09-913-514-2 (1-125157)
QY 1 Met----- 1
Db 55052 ATGTCTGTAAATAAAGTAAATTTCACTCGATACGTAACCTCGTATGTTGTTAAGCAGC 54993
QY 2 -----Lys-----Thr-----IleGln 5
Db 54992 TCATGGTGATATGGCAGGTTTTTAAAGTAAACGCTGAGCAAGTAATCTTTGATACAG 54933
QY 6 -----Pro-----Lys----- 7
Db 54932 TTTGAGTCTTTAGTCTCACCATAACAAACGCGTTTTTAAATGTTGTAGCAACTCAAC 54873
QY 8 Met-----HisAsn----- 10
Db 54872 AAACGCTCAGCTTCTCCCTTTACATAACATAAATGCCAATGCCAGTGCACAAACCGTGGGA 54813
QY 10 ----- 10
Db 54812 GTGTTTCAAAATTTAGCTGGGTATTAATCCCGGAGAACACGCTTTAATAAATAACGA 54753
QY 10 ----- 10
Db 54752 ACTGTCAAACAGTTAGCGCTTAACCGATATAAAAGCGACACGCCCTTGGATCAT 54693
QY 11 -----Ser----- 11
Db 54692 CGAGTAGCAGTTCAACCTGAAGATGTACGTATAAACTTGACCCAGTAGAACCAACAT 54633
QY 12 -----IleSer----- 13
Db 54632 GTTCGATTAATATCCAAATTCATCTATCGGGCTGTACTGTCCAGCTGAGTGAAGCTG 54573
QY 13 ----- 13
Db 54572 AATGTTGGAGACACACTATATTACAGGTCAATATGGGTAGGAGTACACGCAAAAAAGAA 54513
QY 14 -----TyrAla 15
Db 54512 AACCAACAGAAATATGTAATATGACTGTTTATTAATGATCACTACCCCGCTGTGGCT 54453
QY 15 ----- 15
Db 54452 TTAATGGATAAGAGGGAGGTAAATCAATTTCCATTGTAATGTTCCATGTTTATGGG 54393
QY 16 -----IlePhe-----Thr----- 18
Db 54392 AATACCCTAAGATAAAGAGTTCGTATCTTCTGGGGGGTGGTTTAAAGACACGAGGACAGT 54333
QY 19 -----GlyLeuAla 22
|||:|||||

Db 54332 TGACCTGAATGTTTAATACGTTAGATGTGCTCATGCTTGGTTTACAGAAATCAA 54273
Qy 22 -----
Db 54272 APTAAATGCTAGGTTTGTGGGGTTTCCCATCTCCCGTGTGCTTTTTCATCTAGAAT 54213
Qy 23 ---LeuCys---
Db 54212 CTTTACTGCTTCTAGAGCGCTTCTACGGTCCAGGGGTTTTCAGGGTTTGGATTAATCTG 54153
Qy 29 -----
Db 54152 GTCGTGAATCTCTCCAACTCTCTGGCTAAATACTCATGCTCTGTGAAGACTTAAACAGTC 54093
Qy 32 -----
Db 54092 GTCAAATGCCATATGTTGTCTGAGCGCCACTGCAACGACAAACCGTGGCGTATATGGC 54033
Qy 32 -----
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Qy 33 -----
Db 53972 TTCTCGATTCTCCGACGAGGACCTGTTACGGGCGAGATAAAACCTCTCTAGGACATGT 53913
Qy 36 -----
Db 53912 TATTATAAACCGCGAGTCGGATCGATCAAAATGTAATAGCGGGGATACATTTTTTACCCCGTT 53853
Qy 39 -----
Db 53852 TAAACCGCTCAATTCCTCGCTGAAAGACGGGTTGTTCTCGCGCTCCGATATTT 53793
Qy 41 -----
Db 53792 ACTAATGCTTATTCTTAAACGACCATGGACGTTGATTTCATGGCGCGCGACTAAATG 53733
Qy 42 -----
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Qy 43 -----
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Qy 46 -----
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Qy 46 -----
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Qy 47 -----
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Qy 49 -----
Db 53372 GCGTTGTAAAGGGTCCAAACCACTGCGGGTTGGGGATTTACTGTTTGGTGGCATACC 53313
Qy 51 -----
Db 53312 CCGAGGAATAACAGGCGGTGAACCTGTTTAAAGCAAAACCTTAGGCGCCCGTGAACAT 53253
Qy 52 -----
Db 53252 ATCCACTCTTTTCTTGGGCTTGGTACGCACTTGGCAAGGCTTACAAAGCCCTTCCCGGGC 53193

Qy 55 ---LeuArg---CysThrIle-----Asp----- 60
Db 53192 TGCCTCAGAGAGATTGTACAGTTTACCTGAAAAACGACCCATTTTAACTCGTATATC 53133
Qy 61 ---Asn-----Arg---Val-----Thr-----Arg 65
Db 53132 CCGAATAACTTCCACGCTTACGCGCTTAATCCCATCAAAGGTACGCCCGCGGGGCGC 53073
Qy 66 Val-----AlaTrp----- 68
Db 53072 GTCTTGTCCCAATGTCGGAATTGGGGCGGATACAGGACCTTCAGATAATGTTACGGTTAT 53013
Qy 69 ---Leu-----Leu-----AsnArg 71
Db 53012 AGAGCGTGTGATATAAACCCCATTAACAGGTCAACAAAAACGCCCGCCCAAAACAGG 52953
Qy 72 ---Ser-----Thr 73
Db 52952 TTGGAATTGGTTACGAAAGTTCCGCCCTCAACTTGTCTCCGTAATAATACACAATGACA 52893
Qy 74 ---IleLeuTyr----- 76
Db 52892 CTGGCTTAATGCTAAGTCTTGTACACCGCTAGGTGTTTCGTTTAACTAAAAATTTGGT 52833
Qy 76 ----- 76
Db 52832 AATGGGCAAAATGCTCCTGAGTATGGATCAACGTTAAACGCCATTGAATGGGTGGCTTC 52773
Qy 77 ---AlaGly----- 78
Db 52772 GGATAATCCTTCACGGATCTTATAATCGCGGTCTCAACCAACACTTTTCAAAAATTTGT 52713
Qy 78 ----- 78
Db 52712 TGTGCTGTTCTATACCGGACGCGAGTGTGCTTAATATGGAACGAAAGTTGGATGATC 52653
Qy 79 ---AsnAspLys---Trp----- 82
Db 52652 CACATGACAGCAGATAGTCCCTCGNAGAACATCGGCGACCGGATCCAGTAGTCGCTC 52593
Qy 83 -----Cys 83
Db 52592 TTGTTCTAGATCGATAAACAGCGTTCTAGTGTAGTGTCCCTATAAGTGTCTCGATGTTGC 52533
Qy 84 Leu-----Asp----- 85
Db 52532 CTTTGTGTTCCGTTTGTATCCCGGGTTTTCGAAGGATTAATATGGAGCATAGTTTCC 52473
Qy 86 ---Pro-----Val----- 86
Db 52472 TAGAGATCGCAGTCGTATATTGGCTGTGTCATTTGTTCCAAACACCCCAATAGGTTGACG 52413
Qy 87 ---Arg-----Val----- 88
Db 52412 GGTGGCTTTCAAATCGCGCATCGTTGTTCTAAGTCGGTGTACTGTTGTGTGAGCGCA 52353
Qy 89 ---ValLeuLeuSer----- 92
Db 52352 TACCGCGCGGTGTGTTTTTTCATATAACTACATGGAATTTTCAGAGTCAAAAGTCCCGT 52293
Qy 93 Asn-----Thr----- 94
Db 52292 AACATATTTTAAACGATCCCGTGCACCCCTGTAAACGACCGGTGACAGCGTTCTAG 52233
Qy 95 ---Gln-----Thr-----Gln----- 97
Db 52232 ATAAAAAAGCAGTCGCGCAACAGGGGTGCTCCAAATCCACAATGAGTGCACAAATATC 52173
Qy 97 ----- 97
Db 52172 CAGGCTAAACTCTGTGTTTGTATGAACCCGTAGACTGACTGGATAGAACGTCGCCATCTCG 52113

QY 98 -----Tyr-----SerIleGlu--- 101
Db 52112 ATCTGTTGGGATTCGCAGCTAAATGAGTCCGCCAAACAGTGGTAAATCGATTAAATGA 52053
QY 102 -----Ile 102
Db 52052 TGGACCCGGTCCCCATCTCTGGCTTCGGTTCATCCGCTATCCTCCACCTCAGTTAGATA 51993
QY 103 Gln-----Asn-----Val---Asp----- 106
Db 51992 CAACGCAGAAATTGGGTGAAACCATCGCACCAATGACCCCGGCCACACGAGCGGTATA 51933
QY 107 -----Val-----Tyr----- 108
Db 51932 TGACCCAGAGGTTAGCTTGGCAAGTGCCTCCATGCCATATAAACATTGGCCATTC 51873
QY 109 ---Asp-----Glu----- 110
Db 51872 TTTGATATCTGTGGAGTTTCTTCGTAAATTCAGTGTGAATATAAATCTTCTGCGTCAA 51813
QY 111 -----Gly-----Pro---Tyr----- 113
Db 51812 GGCTGTGCAGGGCCATAATAGACGCCAACCGTCTTCAAAACCCCGCGATGGGCTAGG 51753
QY 114 -----Thr----- 114
Db 51752 CTTAGACGTGGAGTTGACATCGTTTCGACGCGCTCCACGGGCGGTAGTGGTTCCACTTGA 51693
QY 115 -----Cys----- 115
Db 51692 AGAGGACTGAAATACGTGTACGTAATGTACGGGGGAGTACTGCCCCCTCGTGTATTC 51633
QY 116 ---Ser---Val---Gln-----ThrAsp----- 120
Db 51632 ATCAAAGCAAGGTGGCGCGCTCTCCGCGGACGCGAGTACATTTCTGACGCGCAAGGC 51573
QY 121 Asn---His-----Pro----- 123
Db 51572 AACGCCATGGAGCAATAACACAGTCATGTATTAATGCGCAACCCCGGTGTATATAA 51513
QY 124 ---LysThr---Ser---Arg----- 127
Db 51512 GGGTGTGGGTATACAAACCCCTCTCCGATAGACCTGTGATGAGTGTGAATGGGTCGGG 51453
QY 128 ---Val-----His-----Leu----- 130
Db 51452 TACCAGACGGTTAACATCGGGCATGAAAAGTTGTACCGGAATAACGGTATACGTATAAC 51393
QY 131 -----Ile-----Val----- 132
Db 51392 ATCCCATGGTTAATATGAACAATATCGAGTCTCCATAATGCAAGAACACGTTGCACAT 51333
QY 133 -----GlnVal----- 134
Db 51332 AAATACGGTCTCTTAAACAATGCGGTGACCAACCAAGTATATAATGTATTCTTCTGGCTC 51273
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Db 51272 TAATCAAGGGGTGCATATCTCAGCGCGGTCTCTCAACAGCAACCGTCAACAGGAGG 51213
QY 136 -----ProLys-----IleVal-----Gluile 141
Db 51212 CCCTTGGCAGCGTGAACCCAAACCGTTCTCGAGCGGTTTACAGCGCGGTGTGAGATT 51153
QY 142 -----SerSer-----Asp----- 144
Db 51152 TGGGCGCGCAGAGCTGGGTAAAACGTGTTGCTCCGTGAAAGACAAAAGACATGGATA 51093
QY 144 ----- 144
Db 51092 GAAATGACTGGTAGTGAGTTTAAAGTAATACCAGCTCCGGCAAGACCCGTAGTCGGTGC 51033
QY 144 ----- 144

Db 51032 TCCAGAAACACCCGCCAGGCTGGATGTAAAGTGTTCACAGGTCACAAATTACGCATCAA 50973
QY 145 -----Ile-----Ser----- 146
Db 50972 AGGTAATAAGCCAAATCAGAGTCCGTGCTACGAGCGGCCAAATAATGAAATTCCTCCAG 50913
QY 147 -----Ileasn----- 148
Db 50912 ATCAAATCTTCAACCCCGGCACGCATAACCAACCCAGGGGCCCCGTGGGCACTGTCCAC 50853
QY 149 -----Glu----- 149
Db 50852 AGTCTTCTGAGTATTTTCCATTTTGGTGAAGTACTCGTAATAATGGGGGGTGTGTGGCAG 50793
QY 150 Gly-----Asn----- 151
Db 50792 GGTCAATAGCACCCCAAAACCCAGTCTGTGATACATAATGAAGAGAGAGGCTTTTAAACG 50733
QY 152 -----Asn-----Ile----- 153
Db 50732 GGTATTACATATGCGGAACCAACAAATCAGTGTATACACTTATGTATTAGAGGG 50673
QY 154 -----SerIleuThr----- 156
Db 50672 CGTGGGGTGTGTACTCAGTAACACTGGCTTTTACAAGATTATCAATCGTTAAACATAA 50613
QY 157 -----Cys-----IleAla-- 159
Db 50612 AATGGCGATCAGACGGGGTTCGTAAATCCCTTTTAAACCAAGCATCAGGGATTAAATA 50553
QY 160 -----ThrGlyArg----- 162
Db 50552 TAAACCAAGAACCGGGCGCGGTAGTAACAGAGAAATTTCTTCATAGTTACAAAACATACCT 50493
QY 163 ---Pro---Pro-----Glu---Pro----- 165
Db 50492 GTCATCGTTTCAATTTTGGCCCTCTAAATGTTTAGATGAAGATGTGCCCATGGAAGAAG 50433
QY 166 -----Thr----- 166
Db 50432 AAAGGGGGTTCACGTCGATACACTTAGTCGACCGCTAAAGTTTACTGTATATGGAAGAAGA 50373
QY 167 -Val-----Thr---Tip----- 169
Db 50372 AGTTCCGATCTCGATTTTGGTTCGATGTTTCCAGCCCTGGCTAGACGCGTGAATATTTGGG 50313
QY 170 -----Arg-----His----- 171
Db 50312 GGAATCGACTTCGTGGGGATAAGTTTGACCCCGCTTTAAACACATTCATGTATATGA 50253
QY 172 -Ile-----Ser----- 173
Db 50252 TATTGTGAAACAAACAGAGCGCGTCTAATGGAGATGTATCCCGGTTTGCATGTCAAC 50193
QY 174 ---Pro-----Lys-----Al 176
Db 50192 ACGACCGCTGGTACCGTTTACTTTACTTTGGCATGTCCCGATGTGGAAGAGGGTGGC 50133
QY 176 aVal-----Gly-----Phe-----Val----- 180
Db 50132 AGTTTCATGTATACGCGCATCTGTCAATATTTTATATAAAACAAAGCCGAGGTGATACCG 50073
QY 181 -----SerGlu----- 182
Db 50072 TTGTGGCATACGTTCTGTAGCGAGTTATCTGTATTACTTCCCGAGTGTTCACGAGTTC 50013
QY 183 -----Asp----- 183
Db 50012 TATGATAACAAAATGATGCAACGTTAAATGGAGACAAAGACGCTTTTCATGTGTACCTC 49953
QY 184 -----Glu----- 184

Db 49952 GTTTAAAGCGCATCTCCAGAAAGCTTTTCGGTTGAGGTTATTGAGCGCACAGATGTTTA 49893
Qy 184 ----- 184
Db 49892 TTAACGATACACAGCATGTGCGTTTACAGGGTGATTTCTCCCTCATCTAAATTTAC 49833
Qy 185 -----TyrLeu-----Glu----- 187
Db 49832 AAAATTATCTTTGTGATACTTTACCCCGAGTTGAAAAAGTATGAAGTTCGGTAGACGC 49773
Qy 188 -----Ile-----Gln----- 189
Db 49772 TACCACTGTTTCTAATGGAATAATCCCGGTTTGTGTTAGTTTGTGGTATCACTAAA 49713
Qy 190 -----GlyIle-----ThrArg----- 193
Db 49712 ACCTGGATGTGATGGGAACGTGTGAGTTTCGACCGCGCAAGTCCCAATTAACGTTAAG 49653
Qy 194 -----Glu-----Gln-----SerG1 197
Db 49652 CGAGTTGAAATTTGACTGCATGTCCGATAATCTGCAGGCTATACCAACGATGACTCATG 49593
Qy 197 y---AspTyr-----GluCys---Ser---AlaSerAsn----- 205
Db 49592 GCCTGACTACAAAGTTGTGTTTCGATATTGAATGTAATCAGGAGATCTAATGAGCT 49533
Qy 205 ----- 205
Db 49532 GCGGTTTCCCGATGCACACATTTGGAGGATCTTGTAAATCCAAATTTCTTGTCTATTATA 49473
Qy 205 ----- 205
Db 49472 TTCAATCCCTCGACAGCTTTTAGAACACATTTTACTGTTTCCCTTGGCTCTTGTGACTT 49413
Qy 205 ----- 205
Db 49412 ACCAAAGGTATGTACAAAGATCAAGGACGCGGGTTACCGGACGCGCTGCTGGA 49353
Qy 206 ---Asp-----ValAla-----AlaPr 210
Db 49352 GTTTGATAGTGAATTCGAGCTATTAAATGCAATTTATGACCCCTCGTAAACAGTACGCTCC 49293
Qy 210 o-----ValVal----- 212
Db 49292 CGAGTTGCCACAGGTATTAACATTTGTTAATTTGATTGGCGTTTATTATGAGAAACT 49233
Qy 212 ----- 212
Db 49232 TAATCTATATACAGTCTCAAGCTTGATGTTATGGCAGTATAACCGTGGGGTCTGTT 49173
Qy 213 -----ArgArg-----ValLysVal----- 217
Db 49172 TAAGATATGGGATGTTGGCAAATCCGGATTTTCAGCGACGAAAGGTAAGATCAACGG 49113
Qy 218 -----Thr----- 218
Db 49112 TCTCATATCTCTGGATATGATGCAATTCGAATCTGAAATTAATAACTCTCGATTTATA 49053
Qy 219 -----Val-----Asn-----Tyr----- 221
Db 49052 ATTAGATTGGGTTGCACGTGAAGCTCTAAATGAGTCCAAAGAGAGATTTCGCCCTACAAGA 48993
Qy 222 ---Pro-----Pro-----Tyr---Il 225
Db 48992 CATTCGGGATATTACGCTAGTGACCGAATACACGAGGAATTATTGGTGAATTTGTAT 48933
Qy 225 e---Ser-----Glu----- 227
Db 48932 ACAAGACTCGGCTCTTGTGGGAAACTGTTTTTAATAATTATACACACCTTGAGTTATC 48873
Qy 228 -----Ala-----Lys-----Gly----- 230
Db 48872 CGCGGTTGAAGGCTAGCTAGAAATTACTTTAAACCAAGGCTATTATACGACGACAGCAGGT 48813

Qy 231 ---Thr----- 231
Db 48812 TAGATTTACACTTGTGTTTATTAGGACTGGCTTCGCTCGAGGATTTATTTTACCCGATGG 48753
Qy 232 -Gly-----ValPro----- 234
Db 48752 GGGATACCCAGCTACTTTTGAATATAAGGATGTTTATTCGCCGATGTCGGGGATGTTAGGA 48693
Qy 235 -----Val-----GlyGln----- 237
Db 48692 AGAGATCGATGAAGACGAGAGCGTTTCTCCCACTGGTACGTCAGTCAAGTGGCGGAATGTAGG 48633
Qy 238 ---LysGly-----Thr----- 240
Db 48632 ATATAAGGAGCCAGGGTTTTTGACCCCTGATACGGGATTTTATATCATCGGTTGGTCTG 48573
Qy 241 -----Leu-----Gln-----Cys----- 243
Db 48572 ATTGGATTTGCAAGTTTATATCCAGTATAATTCAGGCCCAATAACTATGTTTACCAC 48513
Qy 244 -----Glu-----Ala----- 245
Db 48512 GCTAACGTTAAATTTTGAGACGGTTAAACGTTTGATCCATCCGATTTGCCACTTTAC 48453
Qy 246 -----Ser----- 246
Db 48452 AGITGGAGGAAAGCTCTTTTTTTGTGCGCTCTAACGTTTCGAGAAAGTCTGCTGGGTGT 48393
Qy 247 -----Ala---ValPro----- 249
Db 48392 TCTTTTAAAGACTGTTGGCTATGCGCAAGGCTATTAGAGCGGCATACCCGGAAGTTC 48333
Qy 250 -SerAlaGlu----- 252
Db 48332 TTCAATGAAGCAGTGTATTATAGACAAACAAAGCGCGCATAAAGTAGTTGTTGTAATTC 48273
Qy 253 -----Phe----- 253
Db 48272 CGGTACGGTTTACTGGAGTTGCGCAGGATTTCTGCCATGTTTATACGTAGCGGCCAC 48213
Qy 254 -----Gln-----Tr 255
Db 48212 TGTCACTACAATTTGGCGCTCAAAATGTTATTAAAGTACCGAGATTTATATTCAATAACTG 48153
Qy 255 p----- 255
Db 48152 GCGCGCATTTGAACGTTTATTACAGGTTTCCAGACATTTGAAAGTAGCGTTCTCTCCCA 48093
Qy 256 ---Tyr-----Lys-----Asp---AspLys---Arg----- 261
Db 48092 AAAAGCGTACGAGGTAAGGTTATATATGGAGATACGGATTCGTGTTTATCCGATCAA 48033
Qy 261 ----- 261
Db 48032 GGGTGTGGTTGAGGGGATAGCTAAATCCGCGGAGAAATGGCACATATAATTTCAAC 47973
Qy 262 ---Leu-----Ile-----Glu----- 264
Db 47972 GGCTCTGTTTGTCTCTTAAAGTTGGAGTGTGAAAAAACTTTTATAAACTTTTACT 47913
Qy 265 -----GlyLys-----LysGlyVa 269
Db 47912 TATAACAAAGAAAAAGTACATTTGGGTAATTTACGGCGGAAAGGTTTTTAATGAAGGAGT 47853
Qy 269 l-----ValG1----- 272
Db 47852 CGACTGGTTAGAAAAAACAATGTCATTTATTAAAGATTATGCGCGCAAACTTGTTAGA 47793
Qy 272 u----- 272
Db 47792 ACTGTTGTTATAGCACACCGCTCTCGGTGCTGCGCGGAGCGCTCGTGTGTTTCCAT 47733

QY 273 -----AsnArg-----Pro-----Phe----- 276
D 47732 TGCTGAATGAATAGACGGCCATGCCCTCTGGATGGCCGGTTTGGACGCATAATTGC 47673
QY 277 -----Leu-----Ser-----LysLeu-----Ile-----Phe----- 282
D 47672 AGATGCACATGCCCGAATTACATACCCCAATTTGGATTAATAAGTTTGTATGACGGC 47613
QY 282 ----- 282
D 47612 CGAGCTTAGTCCTCACCATCGCCTACATAAACCGTCGCTGGCTCACTTAACAGTATA 47553
QY 283 -Phe-----AsnVal----- 285
D 47552 TTATAAATTAGTAATGACACAGGGTCAAAATCCCAACGCTTCGAGAACGCATCCCTTATGT 47493
QY 285 ----- 285
D 47492 TATTGTGGCCCCACAGACGAAGTGGAGGCTGATGCAAAAAGTAGCTTTGTACGTGG 47433
QY 285 ----- 285
D 47432 AGATCCTTTACAGATACCGCAGGTAAACGGTGTGGGAAGCAAGCGTAAGTTAATAAT 47373
QY 286 -Ser-----Glu-----His----- 289
D 47372 ATCTGACTAGCGGAAGATCCCAATTCAGTAACATCACACGGGTGTCTTTAAACATTGA 47313
QY 289 PTVT----- 292
D 47312 CTATATTTTCTCATCTCATTTGGAGCGCGTGAATCTTTAAGGGTTATTGGAAA 47253
QY 292 n-----TyrThr----- 294
D 47252 CGACACTAAACTCACAGAACGGCTTTTAAACGTTTATTCCAGAGACACAGAGTTGTAA 47193
QY 295 -----CysVal-----Ala----- 297
D 47192 CGTTAAATGCTAAACCGCTTGCAGCGCGGAGGCTTTGTGTATACACGCCCGCGGTG 47133
QY 298 -SerAsnLys----- 300
D 47132 GGATAATAAATGAACACTGAAGCTGAATCACCAGGAGGAGCAAAAGTCATCAATAAT 47073
QY 301 -----Leu-----GlyHisThr----- 304
D 47072 GCGTAGAGTCTTTGTATTTCAAAAGCAATCTCCATCAAAAGTTAAGGTCAACATTTTA 47013
QY 305 -----AsnAla-----Ser----- 307
D 47012 CAGTAACGTCGGATGTTCCAAATGATGGACACCAAGTCCTCTGTTGTGTTCTGGGGTTG 46953
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D 46952 CGACATACCGACAGTAAATAATGTTGTCGCCAACGTTGTGCGATTTTATACCCCGCA 46893
QY 312 -----Gly----- 312
D 46892 CACGCGGCTGTATATGATGATGATGCTGCTGTAATGGAGGTGAACAGAGATTTCCCGGAAAT 46833
QY 312 ----- 312
D 46832 ATAACATACATATAAACCCCTCGGCATCTCCATCAGTAAATAAAGTACGCGTATATCT 46773
QY 313 -----Pro----- 313
D 46772 CGCATGCCCTCCTCATATAATATGATACATAAAAAAATAATTCGGTGTGCGCAATACG 46713
QY 314 -----Gly----- 314
D 46712 CTCGACAATAGGGGTTACGCGGACGCTGCTTGCATGTTGGCTGTGATAGCGCAAA 46653
QY 315 -----Ala-----Va 316

D 46652 ATGATCAAGAAACACACACGATATTCTGATATGTTTAAAGCTCTGAACATATGCTAGT 46593
QY 316 LserGlu-----Val-----Ser-- 320
D 46592 ATCAGACCGCCGATCGGTTTCGACATAGACGGGTTCTCCAGATGCAAGTGCATGTCGGA 46533
QY 321 -----Asn-----Gly----- 322
D 46532 CAATAACCTCGAGACCTAAATGATAACCCATTCCGGATAACGACGAGCAGTTATCCGCC 46473
QY 323 -----Thr-----Ser-----Arg-- 325
D 46472 ACTGTCTGACCAAGTTAAACGGGAAGGTGACAGGGTTCGTCTTAATAATTGGCAGATT 46413
QY 326 -----Arg-----AlaGly-----Cys----- 329
D 46412 AAGCTCTAAGGTAGTAGTCTTCTTCTGGGGGGACCTTGGGATGTAATTAAATAATAGG 46353
QY 330 -----Val----- 330
D 46352 CGGTACACAGACCGCTCTTTGACATAAGTTTCTCGAATGGTTTGCACGGCGCATGGC 46293
QY 331 -Tip----- 331
D 46292 GTTCTGGAGCGTACACGATCGAAGCCGCTCCGAGATACGGATTTATATCGCCTAGAC 46233
QY 332 -LeuLeu----- 333
D 46232 ATACTTCGATAGGTGTGTTGAGGGAGACGAGGATTTGCATGCTCGTAAGCATAAG 46173
QY 334 -Pro-----Leu-----Val----- 337
D 46172 TCCTCCATCTCGTATGAATGCGCATTTGGCGTTGGTTGCGTGGAAAAATCTCGTAGGC 46113
QY 338 -Leu-----His----- 339
D 46112 TTTAATGTCATACGCCAATGTCCACAGCCAGCACATACAGACCTTCAAATCTGTTTTG 46053
QY 340 -----LeuLeu-----Leu----- 342
D 46052 TGCAGCAGTTGGCTTTATATAACTCAACACTTCTTATCCCGGTTGTAGATGGGC 45993
QY 343 -Lys-----Phe 344
D 45992 AAATAAAATTTTAGGGTTT 45974

RESULT 18

US-08-459-146-1/c
; Sequence: Application US/08459146
; Patent No. 5866405
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,146
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Endothia parasitica (Cryptonectria
; ORGANISM: parasitica)
; STRAIN: BP713
; US-08-459-146-1

Alignment Scores:
Pred. No.: 6.31e-25 Length: 12752
Score: 1718.90 Matches: 296
Percent Similarity: 11.19% Conservative: 39
Best Local Similarity: 9.89% Mismatches: 7
Query Match: 71.38% Indels: 2652
DB: 2 Gaps: 264

US-10-017-084A-523 (1-344) x US-08-459-146-1 (1-12752)

QY	1	MetLys	-----Thr-----Ile-----	-----4
Db	12533	CTAAACTCTGAGATGTTGAACACTTAACATTTCAGTTGTGAGTGGCGGAGGGTTT	12474	
QY	5	-----Gln-----	-----Pro	6
Db	12473	GTATGGTAGCTTTACACGAGCGGTAGCCCATCTTCGGGCAACCCCTTTTCGCCCA	12414	
QY	7	LysMet-----His-----AsnSer-----	-----11	
Db	12413	TTTCTTGAACATGTAGACGATCTCTACGTGACGATCCGGCTTACTTTTCCAGTCTGT	12354	
QY	12	-----Ile-----Ser-----TyrPala-----	-----15	
Db	12353	GCTTGCTTGGTCTTATTGCGGTTCCTACACGATCAGCCCTGGTCTTCTGGCGCGG	12294	
QY	16	-----IlePheThr-----	-----18	
Db	12293	GTGCTTGGTACAGCCTACACCAAGTTAAAGTATTAGTATTCTAGCCCTATTGCT	12234	
QY	19	Gly-----Leu-----Ala-----	-----21	
Db	12233	GGCGACAGTGTGACTGTGTTCTGCTCTCTTTCGAGTGGTCTCATGGTCACGTGGG	12174	
QY	22	-----Ala-----	-----22	
Db	12173	TGTGTGATGAGGACAAATTGCATCTCCGAGGCTTAACCATTCGCGGGAATGGTGTG	12114	
QY	23	-----Leu-----Cys-----	-----24	
Db	12113	TGTTGGTCTGAGACTCTTCAGCGGGTTCCTCCCTGCAATCTCTCAGAGGAGCAAAACC	12054	
QY	25	-----Leu-----Phe-----	-----26	
Db	12053	GTAGATTAAATCTACGTACCGTTCGGGTGCGGTGTTAAACAGATCAGCTCCCGGGTTA	11994	
QY	27	-----Gln-----	-----27	

Db	11993	ACGCTCTTACTGACGGGAGTGACCATGTGATAGGCTTGAAGTTATCCACTTACGGTGTG	11934
QY	28	-----GlyVal-----ProVal-----	31
Db	11933	GTTTTGGCGTGTACCGGGGTCACTCCCGTGGAAAGCAAGAAATGACAAATGGA	11874
QY	32	-----ArgSerGly-----AspAla	36
Db	11873	AGCGGTTTGTGTAAACCCCAACAGGTATATCCCGAGGACGGGTGTGCGTAAGATGG	11814
QY	37	Thr-----	37
Db	11813	ACCTGCTGTGCTTCTTCGGGTGCATGCTGATCTGAGTGTGAGGCAAGGTCTGTG	11754
QY	38	-----PhePro-----	39
Db	11753	GGCTCTGAGCTCGTTGACCTGGCTTGGCCACATGCGGATCTCTGCATGTTCCGCTGGT	11694
QY	40	-----Lys-----	40
Db	11693	TAGAAGTACCTTGTGGCATATGACTTACGGGAGGAGGATCTCCACCCACATCCCATC	11634
QY	41	-----AlaMetAsp-----AsnVal-----	45
Db	11633	ACAAGGATATCTTGTGCGCTTATTGTGGGAGCGCCACCGATGTAACTGCGGCC	11574
QY	46	-----Thr	46
Db	11573	GTTCGCCCACTGATGCGCCATGTCACACTGGTATGTGGTTAGCATACCTCAGTTTACC	11514
QY	47	-----Val-----Arg-----	48
Db	11513	CGACGTTAAGATGCGCTCCCAATGATCTTCACTCTCCCGAAAGGAGGTGAAGTTCAA	11454
QY	49	-----GlnGly-----	50
Db	11453	GTATCGATTGTAAACGCAAGGCCCATTCGGACTGCTGACGCGCCCAATGCCATGATG	11394
QY	51	-----Glu-----Ser-----	52
Db	11393	GATAACAGGAGGATTTGCTGACGCTTGTTCCTCTCTCTTGTAGCGGGTCTGA	11334
QY	53	-----AlaThr-----	54
Db	11333	AAGCTCGGATGTGACTTGAATGACATGACGAGTTCGGGTGACACACCACTTAC	11274
QY	54	-----	54
Db	11273	TTTAGTTAATCGGGGACCTTGTACTGCCCCCGGACTAACTCTGAAGAAAAGAAATCCC	11214
QY	55	-----Leu-----Arg-----Cys-----	57
Db	11213	ACTAGGATCTTACAGAGGAGGTGGCTGTGCCAGCAGCTGGCGGTGTATGACACACC	11154
QY	58	-----ThrIleAsp-----	60
Db	11153	ATCCATGCTCTACCGACAGGATGACCTCTGTTGTTGGTCTTCTGCTCGGTATAGG	11094
QY	61	-----Asn-----	61
Db	11093	GTGGGTGTGACTAGCTACCTTATGCAATGACATCTCCGCGCTGTGATCAGAT	11034
QY	61	-----	61
Db	11033	CGACGGCGGGTGTGATATCGATGCCAGTTTGTATATATGCGTGTGACACAGGCGCAC	10974
QY	62	-----Arg-----ValThr-----	64
Db	10973	AGTCTTAGGACAGAGGGGCTATTACTGCTCACTCATGCCAGTGTATAGACCTGTCCA	10914
QY	65	-----Arg-----Val-----	66
Db	10913	GTCTCCATCCAGCAATGCTCTTCTGAGTTCGTTATATGTGGGACTATGATCATTTGG	10854

Qy	67	Ala	-----	67	Qy	108	Tyr	-----	Asp	-----	109	
Db	10853	CGGGCCAA	CAATTCGGGCTGATCAGCAAACTGATTCGAGCCCGGTTCACATTTCCAA	10794	Db	9773	TATCGTATT	CATGCGATGCGTAAGGGGACTCCTTAGCGACGGCATCAATTTGGCGAA	9714			
Qy	68	-----	-----	-----	Qy	110	-----	-----	Glu	-----	110	
Db	10793	CACGTATCGGAATCAACCTTGTAAACGGTAAGATTGAAACGCTTTGGCAGTGTGGCTC	10734	Db	9713	CGTGAGCTCGTCAACGGTCGTGGTTCCAGCAACTTGAGGTATATGAATTTCTCCACATA	9654					
Qy	70	-----	-----	-----	Qy	111	-----	-----	Gly	-----	111	
Db	10733	AAGAAAGGAGATCGGGCCATTCATGAAGTGAACAGAGTTGCACACTCATGAAGATGGT	10674	Db	9653	CTGGTTGTGAGTGTGCCACGGATTCGGCATACAGCATGTCCTGTAGACGGCATGAACCT	9594					
Qy	73	-----	-----	-----	Qy	112	-----	-----	Pro	-----	114	
Db	10673	TGGTCTTCCAGTCTTCCAGTCTCCAGTCTCCAGTGAACCGTCCATTTTCGTGAACATCATC	10614	Db	9593	TTTAAACTCCTCAGGTATCATGTCGGTGTAGCATACACCCGTCACATATATCACGGAT	9534					
Qy	76	-----	-----	-----	Qy	114	-----	-----	-----	-----	114	
Db	10613	GAAGAACACAGGTTGTCCCTCGGACAGTCCACCTATCCTCGTTCGGAAATGTCGTA	10554	Db	9533	CCCTCATCTGGATTGGCCAGCGGATCCAGTTTGGCGATAAAGCATCATGCGCGGA	9474					
Qy	77	-----	-----	-----	Qy	114	-----	-----	-----	-----	114	
Db	10553	CGTGGTCAGGTAGATATCGGCGGATGGGTCTAGTGTCTTGTGCGCGTTTCAGATTGAGA	10494	Db	9473	TGGTCAAGGATCCCTTATCTCTGAGGTGTATGTCTAGAACTTGTGATAGATGAACCTT	9414					
Qy	79	-----	-----	-----	Qy	115	-----	-----	Cys	-----	116	
Db	10493	TCGGATGTCAAAATGGAATCTCCAGTTATCGGAGGATCTTCTCTGGCATACAGATCCA	10434	Db	9413	GGCTGCTGCTGATCCACGGAAGGAATGCTTCTGTCTTGTGTGACAACTTGAAGTTCCGTTT	9354					
Qy	82	-----	-----	-----	Qy	117	-----	-----	Val	-----	120	
Db	10433	CAGTTTCTGATCCGATGTTCTCTCTCGGCCACACCGCTCGGGGGAAGAAATGGA	10374	Db	9353	CCAGTTCCGGTTCCGTTTATAACCTGCACTTTCATCTTATCTTGTGACTGACGAGCTC	9294					
Qy	83	-----	-----	-----	Qy	121	-----	-----	Asn	-----	121	
Db	10373	CTTACCGAAGCGGTTTTTGGGGTACAGTAAACGTGACCGTGTCTCGATGGTTTGTGTC	10314	Db	9293	GTAGCGTGATTGATGTGGTGTCTTTCAGAGACGATTCAGGTCTCGCGGTACTCAAT	9234					
Qy	86	-----	-----	-----	Qy	122	-----	-----	His	-----	123	
Db	10313	GTACGTGTGGCGGTPACGGCGGCAAGGANTTGGACGGCACATTTAACGATTTGCGAGATCG	10254	Db	9233	TGCGAACCTCTTGTACAGTGGGGTGGAAATGCGGTACAGAGTGGTGACCGGACCCCG	9174					
Qy	89	-----	-----	-----	Qy	124	-----	-----	Lys	-----	125	
Db	10253	TGGTCTAGTGAAGTCGGTGCCTACCGATTCAGATTTCGAAACAGTCTCCACATGCGCCC	10194	Db	9173	TTCCACAGAGGTGACAGGAATTCGAGGAGTCTCTGATAATAACGGAAGACAGTCT	9114					
Qy	93	-----	-----	-----	Qy	126	-----	-----	Ser	-----	128	
Db	10193	AAATAGAACTTCGATGATCTCGGCGAGACCATCCAAGACCAAGTCAACGGGAACGATACC	10134	Db	9113	TCGCAATTAGAAATAGCGTGGGTTCTGGACCATCAGGAATTGAGTAGTGTCTCGCGTTC	9054					
Qy	96	-----	-----	-----	Qy	129	-----	-----	His	-----	129	
Db	10133	GAGACAAATCGTTCAGGATGAATCAGCCATCGTCTGACGAAACGTTTAGACCACAT	10074	Db	9053	AATGAGAGAAGTGTCTTCTACTGAACCGGCTGAGGATCGCATGTTCTCGATCCTTCC	8994					
Qy	97	-----	-----	-----	Qy	130	Leu	-----	-----	Gln	-----	133
Db	10073	GTATGGTCTCTTGGCAGGATCGAGTGTCTCTCTCTCGAGCGGCTTTACATGCCA	10014	Db	8993	CTGCTCTCATGCCCGATAGTCCGCTGAATCTTCTGCGGTTGGGCGAGGTGGCAACTCGA	8934					
Qy	100	Ile	-----	-----	Qy	134	Val	-----	-----	-----	-----	134
Db	10013	ATAAAAGTGTTCGCAGTCGTAGACTTTTGTACAATCCCGAGAACGACCATGAATAG	9954	Db	8933	TAAGTATCCACTTCCTGTTATCTTCTTGTGACCGCATCTCAAGCAGGATGCCAAATC	8874					
Qy	102	-----	-----	-----	Qy	135	-----	-----	Ser	-----	Pro	136
Db	9953	ATTATATAATGGCCCTATCAAGAACAGTGAATGAATAAACAGCTCGACCAATGCATTGC	9894	Db	8873	GGCGGAGCTTGTGTAAGCATCAACCTCGGAGAGGATAACAGGTCTCTTAGACCACA	8814					
Qy	105	-----	-----	-----	Qy	137	-----	-----	Lys	-----	-----	141
Db	9893	GAAATACATGCCGAGATGATGACAGTCATGCTTGTGTAGATGGCGACCTTATCTATCAT	9834	Db	8813	CATGTGTATCGCTCGTATGTGAGAGCTGTTTGAACAAAGAAATCTTTGGGCGGTTT	8754					
Qy	107	-----	-----	-----	Qy	142	-----	-----	Ser	-----	-----	145
Db	9833	GGCCTCGAGGCCAAGAGATCCTTCAGATAGTCAGGCTCTCTTAGGTCTTCCCGAATCTT	9774	Db	8753	ACCAGTAGCGGTGCCCGGCTGATGACGCCAAGTTTGAATGTAGTGTATTTGCCCA	8694					
					Qy	146	-----	-----	Ser	-----	-----	146

Db	7615	ATCCTCCACCAAGGCCTTGTCTCTAGCGGAAACAGCCAGAGTATTTCGGTTTCATATCGGCT	7555
Qy	192	-----ThrArg :::	194
Db	7555	TATGGATCGCGCATCCTGTCTGGGATTCCTGTCTCTCCAAAGAGGACGCCATCGACTGCCGTG	7497
Qy	194	-----	194
Db	7495	CGGGATCCCTTCGCGAAGGTAATCGTTTATCTCTTCTGTGATACCTATCATCCACTTCATA	7437
Qy	195	-----GlnSer 	196
Db	7435	CTCCCAGGCTTCAATCCACAGATTTTCGGCAGCCTGGTGAGACATGACAGGGTCTTGTA	7377
Qy	195	-----	196
Db	7375	TCGAATCGGACGTGTGTGTGGCCCTCCGATGGTGTATATACCAGTAGTCTCTTTCOCGGG	7317
Qy	197	-----GlyAsp 	198
Db	7315	TTCTTGATGTTGGAGACAAAGTTGTCAATCATCAGGGAATTCCTCTGCCCTGGTA	7257
Qy	199	-----Tyr 	200
Db	7256	TTCCATCAATGCTATGTTCTTGAGCGAGTAGGCTTCTGTACTGTCATGCCAGAAGCCAC	7197
Qy	201	-----Cys--Ser 	202
Db	7195	CAGCCCTGAGTCCCCACACAGGTCTTTCACCTGGTAGGGCGGAGCGCCATACATCAC	7137
Qy	203	-----Ala 	203
Db	7135	GTCTAGCCAATGCCAGAGGCAGTGATATACGGAACGTGTGGCAGCATCACTCAGGATTT	7077
Qy	204	-----Ser-----Asn 	205
Db	7076	GGCAGCTCTCATCGACGTACTAATAGCATAAAGATGGGTTACGCACCCATAGAGTT	7017
Qy	206	-----Asp 	206
Db	7016	CTCCCCTAGTCCTTTCAACACACAGCAGAGTTCGTTGAGAACTCGCGGTGTATATGAGT	6957
Qy	207	-----Val-----AlaAla 	210
Db	6956	AAACTGGGAGACACCCGATCGCTCTGTCTATTAACCTGGCCAGTTCGACAGTTCCA	6897
Qy	211	-----Val-----Val 	211
Db	6896	ATTGGCATGTCAGAACTTAGTTCCTTCGGTTCGGTATCGGTTCCTTTTCGTCCTG	6837
Qy	212	-----Val-----ArgArg 	214
Db	6836	GACAAAGTGGTGTGAAGCCAGTTTCGACTACATCGAGTTTGACCTCTTCAGGGATCGCGT	6777
Qy	215	Val-----Lys-----ValThr 	220
Db	6776	ATCTTTCAGGAAGGACAGCAAGTAACACAGGTCGTTAACCCACTGTGTCAATACTGTCTTG	6717
Qy	220	-----	220
Db	6716	ACTCCCCACCATTTCTTGGTCATAGTCAGAAATTTGTCATTGCTGATTTTCGGGGCTGG	6657
Qy	221	-----Tyr-----	221
Db	6656	CTCTGACTGACAGCAACCGAAGGCTTTTCTCAAGTGCTCTCTGCTATCATCTCCAT	6597
Qy	221	-----	221
Db	6596	TGGCACGTGCCACCTGCTCGGAAACCCAGCAGCATGATACAGCCTTGATGTGTCCCA	6537
Qy	222	-----Pro-----Pro 	222
Db	6536	CGATCGCTCGGGATACACCCAGTGATAAACGGTAGCGCGGCTTGGAGAGCGCGGAGAC	6477

QY 223 -----Pro-----Tyr----- 224
Db 6476 CAGGTACACCGCCACGAAACCATATACGCGAATACAAACCTAGTGCACCTACGCTACAT 6417
QY 225 -----Ile-----Ser----- 226
Db 6416 GATCCCTTGAGGATCACGGTCGTGCAATTGTGATTCGCGCTGTAAAGTGTAGTGTGCTC 6357
QY 227 -----Glu-----Ala----- 228
Db 6356 ATCCATTGAATCCAGNAGCTCTGGACGTGGAAAGCCACCGAGGTGGAAACACTGCCCCAGG 6297
QY 229 -----LysGly-----Thr----- 231
Db 6296 TCGGACCGGTCTAACGGACTTCGACAACTTGAAGGAGACCCGATGAGGTCTCACTTGG 6237
QY 232 -----Gly-----ValPro 234
Db 6236 GTTGACAAATTTTCCTTCGTAACAAATCATCGAGTTGGTTCACGCAACACACAGTGCCC 6177
QY 235 -----ValGly-----Gln-----Lys----- 238
Db 6176 GAATGGGTAGGAAACGTGTGCTTACCCGAGTTACCGGTTCCGAAGATCAATTCAACCG 6117
QY 238 ----- 238
Db 6116 TTTGCTCGCGTAGTTGAGCCCGTCTTGGGATTAACGCCACCAACCAATTGTATACCGAAAC 6057
QY 239 -----Gly-----Thr----- 240
Db 6056 CGTTACATGAACGGCAGCATCCACTTGGGGTGACCATGAAATTTGGAACCGCACAG 5997
QY 241 -----LeuGln----- 242
Db 5996 CGCCTTCAGCATTAGGAGACGGGTTCACTTAACCAAGCCATGCCAACCAAGTACTTCTT 5937
QY 243 -----Cys-----Glu-----Ala----- 245
Db 5936 AACGAACCTTGGTGCATGATCGCGCTGCCATGAATGGTAGTGTGCAAGCACCCATA 5877
QY 246 -----Ser-----Ala 247
Db 5876 CCACAGAACACCCAGCCCTGATCAGCAAGTACGCGGGAATTCAGATGTTTAGCG 5817
QY 248 -----Val-----ProSerAla-----Glu-----Phe----- 253
Db 5816 GATGAGTAATGAACACTTCAGCCA--GCCTATGACGAGCAACACGCGTGGCAGTTTAAC 5760
QY 254 -----Gln-----Tyr----- 256
Db 5759 ATCAAAACCTTCCTCCACAGCCATGCGGAAGTATGGCAGTATGGAGGGTGTGTAAGTC 5700
QY 257 -----Lys-----AspAspLys----- 260
Db 5699 TTTCTCGTAGGCAATTGTGTGATAATCTCTGTCAAGTTGACGTCTGTGACGACGACTTC 5640
QY 261 -----Arg-----LeuIle 263
Db 5639 GCATCCACAAGCGATTGGGTTTGGACGCGCACCGGCTCCACGAGCATGTAAATCTTATC 5580
QY 264 -----Glu----- 264
Db 5579 ATAATGCCCTGAAGATCTCGTTGTGTGTCACCGTTCGGAACCGAGGGGTACTGTCCCTGAT 5520
QY 265 -----Gly----- 265
Db 5519 GTCTTAGGCAACACAGCTGGATCAGCGGAGCCATGTAGCCATCCGATTTCCCTGTGTTT 5460
QY 266 Lys-----LysGly-----Val----- 269
Db 5459 AAGGTTGGGTTGTTGGTGATCAGGGAAACACCACTCCGCGGAACCGGGTAAATTCGAACC 5400

QY 270 ---Lys-----Val-----Glu----- 272
Db 5399 TCTAAGCAACCAATTTGCCAGTCCGGCCAGAACGTTCTGCCAGTTCTTCGGCGAACCA 5340
QY 273 ---Asn-----ArgPro-----Phe----- 276
Db 5339 GGTCAACGCGCATCAATCATACTGGCGCCGACCGATTTCATCGGTCAAGTACCGTAT 5280
QY 277 Leu-----Ser-----Lys 279
Db 5279 CTGTTGATGTAGTGCAGGCGGTGTAAAGTTGTACGAAGTTGGTTCGGCATGTCAAG 5220
QY 280 Leu----- 280
Db 5219 CTCGACATCGGAGTGAACCGCGGTTTGTAAACCCCTCAGCACCGAGTAATGGTTCGTAAG 5160
QY 281 Ile-----Phe----- 282
Db 5159 ATAGCTGGCAACAAAGCTTCCGAGTTCCTTCTTGAGGTTCTCCAAATCGCCGTACGT 5100
QY 283 ---Phe-----Asn-----ValSerGlu 287
Db 5099 CGCAGTCTGCAGTTCAAGAGATGGGTCTTGACACCTCGGAGGACCGCATGTTGGCGAA 5040
QY 288 ---His----- 288
Db 5039 GAACCGTGGTGGCAGTGATCTCCTCTTGTTCCTATGTCGGGATCAAGAGCGTGGATGA 4980
QY 289 ---Asp-----Tyr 290
Db 4979 CGGTCACGTGAAACCTCCTCACTTGAATGCAAGTTCTTTCTTCCGCGCTCTCTAC 4920
QY 291 ---Gly----- 291
Db 4919 GAAGAAATAAACCGCACCGGCTCACACGCTAGCCGTAGCAAAAGATTGGTCCAGAC 4860
QY 292 ---Asn----- 292
Db 4859 CAACGAGACACCGGTGAAGCAATATGTAATCGCTGGGTCAACATCAAGTAGAATTG 4800
QY 292 --- 292
Db 4799 CAGGTACGGCACATAGAGTGTGAAGTATAATGGCACTAGAAACCGCAGATGAAGCGAT 4740
QY 293 ---TyrThr-----Cys----- 295
Db 4739 CATGATGTTATATTGCCATACACTACACACCTTGGCGCGGTGCTCTCCAGTTTGTCTG 4680
QY 296 ---ValAlaSer----- 298
Db 4679 CAAGTTTCTTCCGGGGGGTTGCGGC--GACAGGTTTTTGTATTTCGATTAACTGTCAA 4621
QY 299 Asn----- 299
Db 4620 AATCGTGTGGTTTCGTGGACCTCAGTTCCAGTCCGCGTCAACCAAAACCTTCTG 4561
QY 300 ---Lys-----Leu----- 301
Db 4560 CTTGCAACTTGTAGTTCTTGCAACGAGCGAAGGAATCTCCCTCCCTCGACGGGAG 4501
QY 302 Gly----- 302
Db 4500 GGGATACACTCTCAGATGATGCGTGAACGGAAGAGGTTCTCTCAGCGCATACA 4441
QY 303 ---HisThr-----AsnAla----- 306
Db 4440 CCGTCGAGTGTGACTAGATACCTCTAGTGTCTATACCTACCTAGGAGGAACCGAGTG 4381
QY 307 ---Ser-----Ile-----Met 309
Db 4380 GGTACATTGATCTCCAGCGCGACGCGCTCCACGTAGAGAGTCCATCTGAGGCAATG 4321
QY 309 --- 309

Db 4320 GGATGACCGGATTGAACACTGGCCCAACCAATAATTGTTCATAATCAGACTGCCTACCGTTTA 4261
Qy 310 -----Leu----- 310
Db 4260 ACAAGACCGGCTGAAACGGTTTGACCTCTGATGATAGAGGCGAAGCCTGATGC 4201
Qy 311 PheGly----- 312
Db 4200 TTCGGTTGCGATGCCCTCGCAAGGAGGATGTCAAAACCCCATCTTCGCGAGGAC 4141
Qy 313 -----Pro----- 314
Db 4140 GTGACTGAGCCTTGCCGGTTGGTCAGAGATPAAATTTATCGTCTCTCTGACCGAACCC 4081
Qy 315 -----Ala-----Val----- 316
Db 4080 AGTCTGATAGCAGTCAAGTTGAGCACCGGTGAACATTTGTCGCCGAATTCAGCTTCA 4021
Qy 317 Ser-----Glu----- 318
Db 4020 TCAGTATGCCGATGACATCATCCCAAAATCCCGAGGCGATGAATACAGGCGTAGGCA 3961
Qy 319 Val-----Ser-----Asn----- 321
Db 3960 GTCTAGGTAATTCGACAAAGAAATCCCGAGTACGCCATGGATGCCGTGTCTCTCAAC 3901
Qy 322 -----Gly-----Thr----- 325
Db 3900 TCCTAATGTGGCATTTGTCATGTTGACGTAACTCGTCACTTCAAGCGGTGACCC 3841
Qy 326 -----Argala-----Gly----- 329
Db 3840 ATTGGTCGACCTCCCGGAGGGGCTGTCGGTTGTCAAAAGGATGAATGTAGTCAGCGT 3781
Qy 330 -----Val-----Leu-----Pro----- 334
Db 3780 CTTCAATCGGCTAGGTGTCGAAGGGTTGTTATTTCTTGGCCCTTTGGCCAGTTTCAG 3721
Qy 335 Leu----- 336
Db 3720 CTAGACCTTCGCTAGCTTGAGCCCATTTCTGACCCACTGCTGTTTTCAAACAGAGAT 3661
Qy 337 Val-----Leu-----His----- 342
Db 3660 GTTGGCCGCTTTCACATAATCAGCGACTGAACCTCTCTCAGCTCCAAACAGGAGTGTAG 3601
Qy 343 -----Lys-----Phe 344
Db 3600 GCTCGTTCTCAAGATGACCTCGAGACGGCTTTGATTT 3562

RESULT 19

US-08-459-065-1/c
; Sequence 1, Application US/08459065
; Patent No. 5882642
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,065
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Endothia parasitica (Cryptonectria
; ORGANISM: parasitica)
; STRAIN: EP713
; US-08-459-065-1

Alignment Scores: 6.31e-25 Length: 12752
Pred. No.: 1718.90 Matches: 296
Score: 11.19% Conservative: 39
Best Similarity: 9.89% Mismatches: 7
Best Local Similarity: 71.38% Indels: 2652
Query Match: 2 Gaps: 264
DB:

US-10-017-084A-523 (1-344) x US-08-459-065-1 (1-12752)

Qy 1 MetLys-----Thr-----Ile----- 4
Db 12533 CTAAACTCTGAGATGTTGAACACTTAACATTTTCAGTTGTCGCGAAGGTTT 12474
Qy 5 -----Gln-----Pro 6
Db 12473 GTATGGTAGCTTTTACAACGAGCGGTAGCCCATCTTTCCGGCAACCCCTTTTCGCCCA 12414
Qy 7 LysMet-----His-----AsnSer----- 11
Db 12413 TTTCTTGAACATGTAGACGATCCTACGTCGACGGAATCCGGCTTACTTTCCAGTCTCTGT 12354
Qy 12 -----Ile-----Ser-----TrpAla----- 15
Db 12353 GCTTGTTCGGTCTTATTCGGCTGCTAACAGCATCAGCCCTGTCTTCTGGGCGGG 12294
Qy 16 -----IlePheThr----- 18
Db 12293 GTCGTTGCGTACAGCCTACCAAGTTAAAGTATTTAGTATTTCTAGCCCTATTGCT 12234
Qy 19 Gly-----Leu-----Ala----- 21
Db 12233 GGCCGACAGTTCAGCTGTGTTTCTCTCTTTCGGAGTTGGTCTCATTTGGTCACTGGG 12174
Qy 22 -----Ala----- 22
Db 12173 TGTGTTGATGAGGCAAAATTCATCTCCCGAGGCTTAACCATTCGCCGAATGTTGGTGC 12114
Qy 23 -----Leu-----Cys----- 24
Db 12113 TGTTCGCTCTGGAATCTTCAGCGGTTTTCCTCTGCCAATCTCTCAGGAGGAGAAACC 12054
Qy 25 -----Leu-----Phe----- 26

Db 12053 GTAGATTTAATCTACGTACCGTTCGGCGTGGCTGTGTTAAACAGAAATCAGCTCCCGGGTTA 11994
Qy 27 -----Gln----- 27
Db 11993 AGCTCTTTACTGACGGGCGAGTACCATGTCATAGGCTTGAGTTATCCACTTCAGGTGCTG 11934
Qy 28 -----GlyVal-----ProVal----- 31
Db 11933 GTTTTGGCGTGTACAGGGGTCACTACTCCCGTGGAAAGACAAAGGAATGACAAATGGA 11874
Qy 32 -----ArgSerGly-----AspAla 36
Db 11873 AGCGGTTTGTGTTAAACCGCAACAGGTATATCCGAGACGGGTGTCTCGTAAGATGCG 11814
Qy 37 Thr----- 37
Db 11813 ACCTGCTGTCTCTTCGGGTGCATGCTGATCTCAGCTGTGACTGAGGGCAAGTTCTG 11754
Qy 38 -----PhePro----- 39
Db 11753 GGCTGTGAGCTCGTTGACCTGGCTTGCCACATGCCGATCTCTGCATGTTCCCGCTGGTG 11694
Qy 40 ---Lys----- 40
Db 11693 TAGAAGTAACCTTGTGCGCATATGACTTAGGGAGGAGGATCCTCCACCCACATCCCATC 11634
Qy 41 -----AlaMetAsp-----AsnVal--- 45
Db 11633 ACAAGGATATCTTGTGCGTATTGTGGGACGCCACCGATGCCCATGTAACTGTGCC 11574
Qy 46 -----Thr 46
Db 11573 GTTGCCAGCAACTGCATGGCCATGTCAACTGGTATGTGTTAGCATACCTCAGTTTACC 11514
Qy 47 -----Val-----Arg----- 48
Db 11513 CGAGTTAAGATCGCTCCAATGATCTTCATCTTCCCGAAAGGAGGTGAAGTTCAA 11454
Qy 49 -----GlnGly----- 50
Db 11453 GTATCGATTGTAAACGCAAGGCCATTCGGACTGCTGACGCCGCCAATGCCATGAGATG 11394
Qy 51 -----Glu-----Ser----- 52
Db 11393 GATAAACAGGAGCGATTCGTACAGCTTTGTTCTCTCCCTTGTAGCGGGGTCTGA 11334
Qy 53 -----AlaThr----- 54
Db 11333 AAGCTCGGATGTGATTGATTGACATGTACGGCAGTTCCGGGTGGACACCACTTGAC 11274
Qy 54 ----- 54
Db 11273 TTTAGTTAATCGGGGACCTTGTACTGCCCGCGACTAACTCTGAAGAAAGAAAATCCC 11214
Qy 55 -----Leu-----Arg-----Cys----- 57
Db 11213 ACTAGGATACCTTGACAGAGGGTTCCTGTGCCAGCGAGTTGCGGCTGTATGACACACC 11154
Qy 58 -----ThreAsp----- 60
Db 11153 ATCCATCGTCTACCGACACGATTGACCTCTGTTGCTGTTGCTCTCTGTCGTCGTTAGGG 11094
Qy 61 -----Asn----- 61
Db 11093 GTGGGTGTGACTAGCTTACCCTTATGCACAATGACATCTGCGCGCTGTGCGATCAAGAT 11034
Qy 61 ----- 61
Db 11033 CGACGGCGGGTTGATATCGATGCCAGTTGTACATATGGGTGTCACAGGCCACC 10974
Qy 62 -----Arg-----ValThr----- 64
Db 10973 AGTCTTAGGCACGAGGGGCTATTACTGCTCACTCATGCCACGTGTAGTACCTGTCCAA 10914

Qy 65 -----Arg-----Val----- 66
Db 10913 GTTCTCCAATCCAGCAATCGTCTCTTGGTTCGTATATGTTGGGACTATGATCATTTGG 10854
Qy 67 Ala----- 67
Db 10853 GCGGGCAACAATTCGGGCTGATCAGCAAACTGATCCGAGCCCGTTCCACATTTCCAA 10794
Qy 68 -----TyrLeu 69
Db 10793 CACGTATCGAATCAACCTTTTAAACGGTAAGATTGAACCGTTTGGCAGTGTGGCTC 10734
Qy 70 -----AsnArgSer----- 72
Db 10733 AAGAAAGGATGCCGCCATTCATGAAGTGAACAGAGGTTGCACCTCATGAAGATGGT 10674
Qy 73 -----ThrIle-----Leu--- 75
Db 10673 TGGTCTTTCCAGTCTTCCAGTCTCTGTAGCATGAACCCGTCATTTCTGTAACATCATC 10614
Qy 76 -----Tyr----- 76
Db 10613 GAAGAACACCAAGTTGCTTCGGGACCACTCCACCTATCTCTGTCGGAATGTCGTA 10554
Qy 77 -----AlaGly----- 78
Db 10553 CGTGGTCACGTAGATATCGGCCGATGGTCTAGTGTGTTGCCCCGTTTTCAGATTGAGA 10494
Qy 79 -----Asn-----Asp---LysTrp--- 82
Db 10493 TCGGATGTCAATGAATCTCCAGTTATCCGAGGATCTCTCTGTCGATAACGATCCA 10434
Qy 82 ----- 82
Db 10433 CAGTTTCTGATTCGAGTGTCTCTCTCGGCCACACCGCTCGCGGGAGAAAGTGA 10374
Qy 83 -----Cys-----LeuAsp----- 85
Db 10373 CTTACCGAAGCGTGTGCGGTACAGTAACGTGACCGTCTCGATGGCTTTGTTGC 10314
Qy 86 -----ProArgVal----- 88
Db 10313 GTAGTGTGGCGGTACGCGGCCAAGGATTGGACGGCACAATTAAACGATTTCGCAGATCG 10254
Qy 89 -----Val-----Leu-----Ser----- 92
Db 10253 TGGTCACTGAAGTCGGTGTCTACCGATTTCAGATTTCGCAACAGTCTCCACATGCGCCC 10194
Qy 93 -----Asn-----Thr-----Gln----- 95
Db 10193 AAATAGAATCTCGATGATCTCGCGAGACCATCCAAGACCAAGGTACGGAACGATAACC 10134
Qy 96 -----Thr----- 96
Db 10133 GAGAGCAATCGTTTCAGGATGAATCAGCCATCGTCTGACGAACGTTTAGACCAT 10074
Qy 97 -----Gln-----TyrSer----- 99
Db 10073 GTATGGTCTCTTGGCAGGATCGAGCTGATTCTCTGCTCGAGCGGGCTTTACCATGCCA 10014
Qy 100 Ile----- 101
Db 10013 ATAAACGTGTTCGCCAGTCCGTAGACTTTTGACAAATCCCGAGAACGACCACATGAATAG 9954
Qy 102 -----Ile-----Asn----- 104
Db 9953 ATTATATGTCCTTATGAAGAACAGTGAATGAACAGCTCGACCCCAATGCAATGC 9894
Qy 105 -----ValAsp----- 106
Db 9893 GAAATACATGCCGAGATGATGACAGTCAATGCTCTGTTAGTATGCGCACCTTATCTATCAT 9834

QY 107 -----Val----- 107
Db 9833 GGCCTCGAGCCCAAGAGATCCTTCAGATAGTCAGGGTCTCTTAGGTCTTCCCAAGACTT 9774
QY 108 Tyr-----Asp----- 109
Db 9773 TATCGTATTCATGCAGATGCCGTAAGGGGACTCCTTAGCGACGGCATCAAAATTTGGCGGAA 9714
QY 110 -----Glu----- 110
Db 9713 CGTGAGTCGTCACGGTCGTGGTTTCCAGCAACTTGAGGTATATGAATTTCTCCACATA 9654
QY 111 -----Gly----- 111
Db 9653 CTGTTGTGAGTGTGCCAGGAAATCTCGGCATACAGCATGTCCGTAGACGGCATGAACCT 9594
QY 112 -----Pro-----Tyr-----Thr----- 114
Db 9593 TTTAAACTCTCAGGTATCATGTCCGTGTAGCGATACACCCGTCCTATATACCGAT 9534
QY 114 ----- 114
Db 9533 CCCCTCATCTGAAATGCGCAAGCGCATCCAGTTTGGCGATAAAGCATCATGCGCGGA 9474
QY 114 ----- 114
Db 9473 TGGTCAAGATCCCTTATCTGAGGTGTATGTCTAGAACTTGTGATAAGATGGAACCT 9414
QY 115 -----Cys-----Ser----- 116
Db 9413 GGCCTGCTGATCCACGAAGAAATGCTTCTGTCTGGTGACAACTTGAAGTTCGGTT 9354
QY 117 -----ValGln-----ThrAsp----- 120
Db 9353 CCAGTTCGGGTTACAGTTTATTAACCTGCACTTCTCATCTTCTGTTGACTGACGAGCTC 9294
QY 121 -----Asn 121
Db 9293 GTAGCGTGATGATGGTGTCTCTTGCAGACAGATTCAGGTCTCTCGCGTACTCAAT 9234
QY 122 -----His-----Pro 123
Db 9233 TGGCAACTCTGTACAGTGGGGCTGGAATGCCGTACAGGTGCGTGACGGGACCCCG 9174
QY 124 -----Lys-----Thr----- 125
Db 9173 TTCACAGAGGTGTACAGGAACCTTCGAGGACTGCTCTGTATAATAAGGAAGCAGTCT 9114
QY 126 -----SerArg-----Val----- 128
Db 9113 TCGCATTTAGATAGCCGTGGGTTCTGGACCATCAGGAATGAGGTAGTGTCTCGCGTTC 9054
QY 129 -----His----- 129
Db 9053 AATGGAGAGAAGTGTCTTCACTGAACCGCGCTGAGGATGCGATGTTCTCGATCCTTCC 8994
QY 130 Leu-----IleVal-----Gln----- 133
Db 8993 CTGCTCCATGCCCGATAGTCCGCTGAATCTTCTCGGTTGGCGACGTGGCAACTTCGA 8934
QY 134 -----Val----- 134
Db 8933 TAAGTATTCACCTCTGTATCTTCTTGTGCGACCCGATCTCAAGCAGGATGCCAAATC 8874
QY 135 -----Ser-----Pro 136
Db 8873 GCGCGCAGCTTGTGAAGCATCAACTCGGAGAGGATAACAGGTCTCTTAGACCACCA 8814
QY 137 -----LysIleVal-----GluIle----- 141
Db 8813 CACTGTGTCATCGCTCGTATTTGTAGAGCTGTTTGAACAAAGAAATCTTTGGCGGTTT 8754
QY 142 -----SerSer-----Asp-----Ile----- 145

Db 8753 ACCAGTAGCGGTGCCCGCGCTGATGACGCCAAGTTTGAATGTAGTCTATTGTGCCA 8694
QY 146 -----Ser----- 146
Db 8693 CGAAGTGGCACTCTGTGACAGTGCCTCCACACGGTTCCTTGTGTGCGACGTGGATATGAC 8634
QY 147 -----Asn----- 148
Db 8633 TTGCGCAATTTGGCAAGACATACGCTTTATATCTTCTCTCAATGCCGCTTCGAATCATA 8574
QY 149 -----Glu----- 149
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QY 150 -----Gly-----Asn----- 152
Db 8513 CCATGACGAGCCTTGCATTCGCAATGCAATGCTGGATCATTTGGTAAGGAAACCTTGCAGGAAC 8454
QY 153 -----Ile-----SerLeuThrCys----- 157
Db 8453 GGCCTGCATGTACAGAGC-----ACATGCTTTCGGTTCCTCCCAAGATAACCTCTTCCACTC 8397
QY 158 -----Ile-----Ala----- 159
Db 8396 AGTGACGTTTCAATTTATGTGAGCCAGAAAGCTCGCTGAACGTCGCAAAAGTGTGACGGTA 8337
QY 160 -----Thr----- 160
Db 8336 CTTGGATTCAGTTTCAATGCTCACGCCACGTCAGGACGTGGAAAGTCAAGCGGTATA 8277
QY 161 GlyArg-----Pro-----GluPro----- 165
Db 8276 GGAAGGTTTCGGTTATCCCCATGACCATTCATTTTGCATGGCTCGAATTTGCACTGGAC 8217
QY 166 -----Thr-----Val-----Thr----- 168
Db 8216 AACTGTGCGAATTTGTCGTCCTTTGCCACTCGGATGATTTTGGAAACCTCAACTCAACCAG 8157
QY 169 -----Tyr----- 169
Db 8156 TTTGCCACGCCCATGGAACAATGCTGGTTTACAGTTTGAAGTGTAGGAGTCGCATCAGC 8097
QY 169 ----- 169
Db 8096 AATGATGAATGCTCTTCGGTTTCTCAAATCATGCAGCTCGTCCCAATGCGAGC 8037
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Db 8036 CATCGATTGTGACAAAGGCATGCCAGACCGGACCGTACGTTTCCAGGTTATTCGCTT 7977
QY 175 -----Lys----- 175
Db 7976 GTTGGCTCGATCTGAAGATCTGTGTCGACCATGTAAAGCGGATAGATCTCGGAGACCAC 7917
QY 176 -----Ala----- 176
Db 7916 CGTTCCGAAGTCTTCATCGGGGAGCCAAAGGTTGGCCAGGAACCGCTTGTGACTT 7857
QY 177 -----Val-----Gly----- 178
Db 7856 CGGGAACGGTGGTAAATTTGCTAGGTTATTTACCGGTACTGATGCACTCCAGTCCGTT 7797
QY 179 Phe-----Val-----Ser----- 181
Db 7796 TTTACGGATCACATCCATGACACCAGCTTGTCTTAAGAGCCTTCTTACTCTTATAGAACA 7737
QY 181 ----- 181
Db 7736 GCTTATGAACGGGGTCCCGCGAGTACTTCTTTGATGTAAAGTTCTACACCTTTAGG 7677
QY 182 Glu-----Asp-----Glu-----Tyr-----Leu-----Glu----- 187

Db 7676 GAGCATGATGCTCGATCGCGCAACACTTCTGCGCAATTGTTGCAACATGCGCCCTGCGCGT 7617
Qy 188 Ile-----GlnGly-----Ile----- 191
Db 7616 ATCTCCACCAAGCGCTTGCTCCTCAGGCGACAGCCAGAGTATTGCGGTTCAATATCGGCT 7557
Qy 192 -----ThrArg-----Glu----- 194
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Qy 194 ----- 194
Db 7496 CGGATCCCTTCCCAAGGTAACTGTTATCTCTTTCGTGATACCTATATCCACTTCATA 7437
Qy 195 -----GlnSer----- 196
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Qy 197 -----GlyAsp----- 198
Db 7316 TTCTTGATGTGGAGACAAAGTTGTCTATATCATCAAGGAATTCCTCTGCGCTCGTA 7257
Qy 199 -----Tyr-----Glu----- 200
Db 7256 TTCCATCATGCTATGTTCTGAGCGAGTATGGCTTCTGACTGTGTCATGCGAAGCCAC 7197
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Qy 203 -----Ala----- 203
Db 7136 GTCTAGCAATGGCAGGCGAGTATATACGAACGTGTGCGCAGTCACTCAGGATTT 7077
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Qy 206 -----Asp----- 206
Db 7016 CTCCCCTAGTCTTCAACACACAGCAGGTTCGTGAGAACTCGCGGTGTATATGAT 6957
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Qy 211 -----Val----- 211
Db 6896 ATTGCGCATGTCCAGAACTTAGTTCCTTCTGCTGCTGTTCTGTTGATGCTTCTTTGCTCTG 6837
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Db 6836 GACAAGCTGGGTGAAGCCAGTTGCACTACATCGAGTTTGACCTTCTCAGGGATCGCCGT 6777
Qy 215 Val-----Lys-----ValThr-----ValAsn----- 220
Db 6776 ATCTTTCAGGAAGGACAGCAAGTAACACAGGTCTGTTAAACCACCTGTGTCAATACTGTCTTG 6717
Qy 220 ----- 220
Db 6716 ACTCCCCCACCATTCTTGGTTCATAGTCAGAAATTTTGTCTATGTCGATTTTCGGGGCTGG 6657
Qy 221 -----Tyr----- 221
Db 6656 CTCTGACTGACCAACCGAAGGCTTTTCTCAACGTGCTCTTCTGCTATATCACTTCAT 6597
Qy 221 ----- 221
Db 6596 TGGCACCGTGCACCTGCTGCGAAACCCAGCAGCAGATGATACAGCCCTTGATGTGTCCTCA 6537

Qy 222 -----Pro----- 222
Db 6536 CGATCGTCCGGATACACCCAGTGTATAACGGTAGCGCGCTTGAGGAGCCGGAGGAC 6477
Qy 223 -----Pro-----Tyr----- 224
Db 6476 CAGGTACACCGCCGCAACCATATACGGAATACAAAACCTAGTGCACATCGGTACAT 6417
Qy 225 -----Ile-----Ser----- 226
Db 6416 GATCCCTTTCAGGATCACGGTCTGCAATTGTGCGCTGTAAAGTATAGTGTGCTC 6357
Qy 227 -----Glu-----Ala----- 228
Db 6356 ATCCATTGATCCAGAAGCTTCTGGAGCTGAAAGGACCAGGTGGAACTGCGCCAGG 6297
Qy 229 -----LysGly-----Thr----- 231
Db 6296 TCGGACCGGTCTAACGAGCTTCGACAACTTGAAGGGAGACCCGATTCAGGTCTCCTGG 6237
Qy 232 -----Gly-----Valpro 234
Db 6236 GTTGACAAATTTCTCTCGTAAACAATCATTCGAGTTGGTGTACGCAACACCGAGTCCC 6177
Qy 235 -----ValGly-----Gln-----Lys----- 238
Db 6176 GAATGGGTAGGAAACCGTGTGCTTACCCGAGTTACCGGTTTCGAAGATCAATTCAACCG 6117
Qy 238 ----- 238
Db 6116 TTGCTCGCTAGTTGAGCCCTGTTGGGATAACGGCCACACCAATTTGATATACCGAAAC 6057
Qy 239 -----Gly-----Thr----- 240
Db 6056 CGTTACAAATGAAACCGCAGCATCCACTTGGGGTGCACATGAAATTTGGAACACCCACAG 5997
Qy 241 -----LeuGln----- 242
Db 5996 CGCTTCAGCATTTAGGAGACCGGTTTCAGTTAACCCAGCCATGCCAACCAAGTACTTCTT 5937
Qy 243 -----Cys-----Glu-----Ala----- 245
Db 5936 AACGAACTTTGGTCCCATGATCGCGCTGCCAATGAGTGTAGTGTGCAAGCACCATA 5877
Qy 246 -----Ser-----Ala 247
Db 5876 CCACAGAACACCCAGCCCTGATGACGAAGTCAAGCGGCGAAATTCAGATGCTGTAGCG 5817
Qy 248 -----Val-----ProSerAla-----Glu-----Phe----- 253
Db 5816 GATGAGTATGAAACTTCAGCCA---GCCTATGACGAGCAACACGCGTGGCAGTTTAAAC 5760
Qy 254 -----Gln-----Tyr----- 256
Db 5759 ATCAAACTTTCCTCCACAGCCATGCAAGTATGCGAGTATGAGGGTTGGTGAAGTC 5700
Qy 257 -----Lys-----AspAspLys----- 260
Db 5699 TTTCTGGTAGGCATTTGTGTGATAATCTCTGTCAAGTTGACGCTGTGTGACGAGACTTC 5640
Qy 261 -----Arg-----Leuile 263
Db 5639 GCATCCCAAGCGATTGCGGTTTGGAGCGCACCGGCTCCACACGAGCATGTAAATCTTATC 5580
Qy 264 -----Glu----- 264
Db 5579 ATAATGCTGAAGATCTGTTGTGTCACGTTTCGGAACCGAGGGGTACTTGTCCCTGAT 5520
Qy 265 -----Gly----- 265
Db 5519 GTCCTTAGGCACACAGCTGGATCAGCGGAGCCATGTAGCCATTCGATTTTCCCTGTTTT 5460

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QY 273 ---Asn-----ArgPro---Phe----- 276
D5339 GGTACAGCGCGATCAATCATACTGCGCCCGACCGATTTTCATCGGTACAGTACCGTAT 5280
QY 277 Leu-----Ser-----Lys 279
D5279 CTTGTTGATGTAGTCTGCGAGCGGTGTAACTGTACGAAGTTGCGTTGCGCATGTCAAG 5220
QY 280 Leu----- 280
D5219 CTCGACATGGGAGTGAACCGCGCTTTGTAAACCCCTCAGCACCGAGTAATGTTCTGAAG 5160
QY 281 Ile-----Phe----- 282
D5159 ATAGCCTGGCAACAAGCTTCGAGCTTCCCTTCTTGAGTCTTCCAAATCGCGTACGT 5100
QY 283 ---Phe-----Asn-----ValSerGlu 287
D5099 CGCAGTCTGCAGTTTCAAGAGANGGTTTGACACCTGCGAGGACCGCCATGTTGGCGAA 5040
QY 288 ---His----- 288
D5039 GAACCGTGGTGGCAGTGAATCTCTCTTCTGTTCCATTTGTCGGGATCAAGAGCGTGGATGA 4980
QY 289 ---Asp-----Tyr 290
D4979 CGGCTCACTGAAACTCTCTCACTTGAATGACAAGTTCTTCTTCCCGCTCTCTAC 4920
QY 291 ---Gly----- 291
D4919 GAAGAAAATAAAGCGCACCGCGCTCACCGGTAGCCGTAGCAAGATTGTTCCAGAC 4860
QY 292 ---Asn----- 292
D4859 CAACGAGCAGCAGCGTGAAGCAATATGTAATCGCTGGGTCAACATGCAAGTAGAATTG 4800
QY 292 --- 292
D4799 CAGGTACGGCACATAGAGTGTGAAGTATATGGCACTAGAAACCGGACAGATGAAGCAT 4740
QY 293 ---TyrThr-----Cys----- 295
D4739 CATGATGTTATNTGCCATACACTACACCTTGGCGCGGTGTCTCCAGTTTGTCTTG 4680
QY 296 ---ValAlaSer----- 298
D4679 CAAGTTTCTTCGGGGGGTTTGGCGC-GACAGGTTTTTGTATTTCGATTAACTGTCAA 4621
QY 299 Asn----- 299
D4620 AATCGTGGTGGTTTGTGAGCCCTCAGTTTCCAGTCCGCGGTATACCAAAACCTTTCTG 4561
QY 300 ---Lys-----Leu----- 301
D4560 CTTGCACTTGTAGTTCTTGCAACGAGCGGAAGGAATCTCCCTCCCTGGAGGGGAG 4501
QY 302 Gly----- 302
D4500 GGGGATACACTCTCATGATGGGTGAACGGAAGAGGCTTCTCAGCGCCATACA 4441
QY 303 ---HisThr-----AsnAla--- 306
D4440 CCGTGGCAGTGTGCTAGATACCTTAGTCCGTATACCTACCTACCTAGGAGGAACCGAGTG 4381
QY 307 ---Ser---Ile-----Met 309

D54380 GGTACATTGATCTGCCAGCGGCGACGGCTCCACGTAGAGGAGTCCATCTGAGGCAATG 4321
QY 309 ----- 309
D54320 GGATGACCGGATTTGAACACTGGCCAAACCATATAATGTCTATAATCAGACTGCTACCGTTTA 4261
QY 310 -----Leu----- 310
D54280 ACAAGCCACGCGCCTTGAACCGTTTGGCAGTCTGTATGAATAGAGCAGAGCCTGATGC 4201
QY 311 PheGly----- 312
D54280 TTCGGGTTGGATGCCCTTCAAGGAACGAGGATGTCAAAACCCCATCTTTCGGAGGAC 4141
QY 313 ---Pro-----Gly----- 314
D54140 GTGACTGAGCCTTGGCCGGTGGTTCAGAGATAAAATTTATCTGCTCTGTACCGAACCC 4081
QY 315 ---Ala---Val----- 316
D54080 AGTCTGCAATTAGCAGTCACGTTTGGCAGCACCGGTGAACAATTTGCCCGAATTCAGCTTCA 4021
QY 317 Ser-----Glu----- 318
D54020 TCAGTATGCGGATGACATCATCCCAAAATCGCGAGGCGATGAATAATACAGGCGTAGGCA 3961
QY 319 Val-----Ser-----Asn----- 321
D53960 GTCTAGGTAATTCGACAAGAAATCCCGAGGTAGCCCATGGATGCCGCTGTTCTCTCACAC 3901
QY 322 ---Gly-----Thr-----SerArg----- 325
D53900 TCCTAATGTGTGCAATTCGTCTATGTGTGAGTAACCTCGTCACTTCAAGCGCTGACCC 3941
QY 326 ---ArgAla-----Gly-----Cys----- 329
D53840 ATTGTCGAGCCTTCCCGGAGGGGTCTCGTGTGTCAAAAGGATGAATGTAGTCAGCGT 3781
QY 330 ---Val-----Trp-----LeuLeu---Pro----- 334
D53780 CTTCAATCGGCTTAGTGTGCGAAGGTTTGTATATCTTTGGCCCTTTGGCCAGGTTTCAG 3721
QY 335 Leu----- 336
D53720 CTAGACCTTTCGTAGCTTGGGCCATTTTGACCCCATTTTGTGAGTGTGTTTTCAAACAAGAGT 3661
QY 337 Val-----Leu---His-----LeuLeu---Leu----- 342
D53660 GTTGGCCGCTTTTCATATAATCAGGACTGAACCTTCTTCAGCTCCACAGGAGTGTCTAG 3601
QY 343 -----Lys-----Phe 344
D53600 GCTCGTTCTCAAGATGACCTCGAGAACCGCTTGTGTTT 3562

RESULT 20

US-08-222-617A-26

; Sequence 26, Application US/08222617A

; Patent No. 5882879

; GENERAL INFORMATION:

; APPLICANT: Veenstra, Annemarie E.

; APPLICANT: Martin, Juan F.

; APPLICANT: Garcia, Bruno D.

; APPLICANT: Gutierrez, Santiago

; APPLICANT: Barredo, Jose L.

; APPLICANT: Von Doehren, Hans

; APPLICANT: Palissa, Harriet

; APPLICANT: Van Liempt, Henk

; APPLICANT: Montenegro, Eduardo P.

; TITLE OF INVENTION: A Method for Influencing Beta-Lactam

; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large

; TITLE OF INVENTION: Quantities of ACV Synthetase

; NUMBER OF SEQUENCES: 27

Qy	1	Met-----LysThrile	4
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Db	1059	CTCTTCAACGAGGAGACGATATGCAATTTTACCGATGCCCTAAACATCTTGTCTGCGGAA	1118
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Db	1119	GCAGTGATAGGAAGAGTGACCCCGTTGCGGATATCGAACTACTATCCGCGGACGAAG	1178
Qy	5	--Gln-----Lys-----MetHis 9	
Db	1179	CAGCAGCTGGAAGTGGAAACAACACGGATGGCGAGTACCCCTTCATCAAAAGCACTGCAC	1238
Qy	9	-----	9
Db	1239	CATCTCATTGAAGAGGTGTTGAACGCGATGAAGACAAATAGCCGTTGCTCGACGAG	1298
Qy	10	-----AsnSer-----	11
Db	1299	CGAGAGCTCACTTACGCGGAGCTCAATGCCCAAGCGAACAGCCTCGCACGCTATCTCCGT	1358
Qy	12	-----Ile-----Ser-----	13
Db	1359	TCCATTGGTATCTCCCGAGAGCTAGTCGCATTTGTTCTAGATAAGCGAGAAGCTC	1418
Qy	14	-----Tyr-----	14
Db	1419	ATTGTTACCATCTCGCGCGTGTGAAATCGGCGCGCCCTACGTGCCCATCGACCCGACT	1478
Qy	15	-----AlaIle-----	16
Db	1479	TATCCGAGTACGAGTGGCGCTTCGTGCTGATGACACCAAGGACCGGCCATCATCGCC	1538
Qy	16	-----	16
Db	1539	AGTAATCAACAVTGGAGAGGCTCCAGCGAGAGGTCATCGCGGATAGAAACCTTCATTC	1598

Db 2679 CTGCCTCGATACATGATTCACGCGGTTGGTACAGCTGTCCAGATCCCAAGTGAATGTG 2738
QY 61 Asn-----Arg-----Val-----Thr----- 64
Db 2739 AACGGGAAGCGGACCTACGCGCTTGGCGCGCTGCGATATCTCOAATTCACGAGGTG 2798
QY 65 -----ValAla-----Tip-----Leu 69
Db 2799 CGTTCGACCTTCGAGGGGATACGGAATCGCCCTCGGGGAAATCTGGCGCGAGTGTG 2858
QY 70 -----Asn-----Arg-----Ser 72
Db 2859 GGAGCCGCCAGAGATCGCTCTCTCGCAACAGCAACTTCTTCGCGCTAGGAGGCACAGC 2918
QY 73 -----Thr-----Ile 74
Db 2919 ATCACTGCATCCAACTGATCGCTCGCATCCGACAAAGCAAGCACTCTCGTCAAGATC 2978
QY 74 ----- 74
Db 2979 TCCGTGAAGATGTTTGTCAACAAGGACACTGTGAGCGCATGGCAGACCTTCTACAGAAC 3038
QY 75 -----Leu----- 75
Db 3039 AAGCAGAGGAGAAATGCGACAAACCCCATGAGCGCGCGACAGAGCTGCTTGAAGAGAAAT 3098
QY 76 -----Tyr-----Ala-----Gly----- 78
Db 3099 GCAGCAACGGACAAATATCTATCTGCGAAACAGTCTTCAGCAGGCTTCGTCTACCATAC 3158
QY 79 -----Asn----- 79
Db 3159 CTCAGAGCATGGAACAATCCGACGCTATGTAATGCACTCGCTTCTTCGGTACACACACC 3218
QY 80 -----Asp----- 80
Db 3219 ACATTGCTCCAGATCTGTTTCAGAGAGCCCTGGAAGCATGACAGCAGTCTTTCACGCG 3278
QY 81 -----Lys----- 81
Db 3279 CTGCGGCTCGGTTCTCATGSGAAAGAGAGGTTTTCACACTGCTCGATCAGATCCACCA 3338
QY 82 -----Trp----- 82
Db 3339 TTGAGCTGGCGTTTCTCTACTTCACCGACGTTCCCGGGTGTCTGTCGAGGACCGGAAA 3398
QY 82 ----- 82
Db 3399 TTGGAAGACTTGGCGGCCAAGACCTTACGAGAGATTCAGCTGGATGTTGGCAGACTG 3458
QY 83 -----CysLeu----- 84
Db 3459 TTCCGCGTCTATCTGATTAAACACAGCGAGAATCGCTTCAGCTGCTTTTCAGCTGCCAT 3518
QY 84 ----- 84
Db 3519 CATGCAATCTCGATGGTTGGAGTCTGCCACTCTTGTTCGAAAAGGTTCAAGACCTAC 3578
QY 85 -----AspPro----- 86
Db 3579 CTGCAACTGCTGCATGGGACAACTCACTTCGTCCATGATGACCTTACCTCGCACC 3638
QY 87 -----Arg-----ValVal----- 89
Db 3639 CAGCGGTATCTCCAGCTCACCGTGAAGATCACCTCGACTTTTGGCGGCTGTGTTCAA 3698
QY 90 -----LeuLeuSerAsn----- 93
Db 3699 AAGATCAACGACGCTGTGATATGAACGCTTGTGTG-----AACGAGCCGACGCTTACAAA 3755
QY 94 -----Thr----- 94

Db 3756 GTCCAGCTGCAGACTATGACCAAGTGCAGAGCAGCGACACGTCGCAATTTGCTCTCTCT 3815
QY 95 -----GlnThr----- 96
Db 3816 GGAGACGATGGCTAGCAGACCTTCGTTCAGACCTGCTCCGCCAGGATATTACCTACAT 3875
QY 97 -----Gln-----Tyr----- 98
Db 3876 TCGATTCTCCAAATTTGTTTGGCAGCGCGTCTGCACGCTTATGGCGGTGGACCCACACC 3935
QY 99 -----Ser-----IleGlu----- 101
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QY 101 ----- 101
Db 3996 GGTCCGTATATCAACACTTACCGCTGGTACTCGATCAATTCGACGTTCAAGGATAGACA 4055
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Db 4056 ATCATGGAGCCCATCGAGGATGTCCAGGCCAAGGTAAACGTCATGAACAGCCGCGGCAAT 4115
QY 105 Val-----Asp----- 106
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QY 107 Val-----Tyr-----Asp----- 109
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QY 110 -----GluGly-----Pro----- 112
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QY 113 -----TyrThr-----Cys----- 115
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152 QY ---Asn---IleSer---Leu--- 155
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183 QY ---Asp---Glu--- 184
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6633 DB GAGATAGCCAGTCTATCCAGCATGTTTTCCGCTCGATGATGAATGCTCTGGGAGGCC 6692
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6693 DB CGCATCTTAAACTCGAATCCCGGCGCTGTATCTCATTTCTGGCGTTCCACCATACCTGC 6752
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195 QY ---Gln---SerGlyAsp--- 198
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198 QY --- 198
6933 DB CGAAACTCATTTGGCTTGGAACTTGCAGTGTACGGAACCGGCCACGCTCTGTGCAAA 6992
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QY 294 -----Thr----- 294
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Db 10593 GTCAACTACTGGGCCAGCTCGCCCCCAAGCAATCGAAGCAAGATGGGTCTCTCGCG 10652
QY 328 -----Gly----- 328
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RESULT 21

US-08-222-617A-1
; Sequence 1, Application US/08222617A
; Patent No. 5882879
; GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Santiago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palisa, Harriet
; APPLICANT: Van Liempt, Henk

APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE:
NAME/KEY: CDS
LOCATION: 264..11600
OTHER INFORMATION: /function= "enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
US-08-222-617A-1

Alignment Scores:
Pred. No.: 5.75e-25 Length: 12364
Score: 1718.20 Matches: 300
Percent Similarity: 10.03% Conservative: 40
Best Local Similarity: 8.85% Mismatches: 2
Query Match: 71.35% Indels: 3048
DB: 2 Gaps: 257

US-10-017-084A-523 (1-344) x US-08-222-617A-1 (1-12364)

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QY	4	-----	4
DB	1119	GCAGTATAGGAGAGTGACCCCGTTGCGGATATCGAACTACTATCCGCGGAGCGAAG	1178
QY	5	---Gln-----Pro-----Lys---MetHis	9
DB	1179	CAGCAGCTGGAAGAGTGAACACACGAGTGGCGAGTACCCTTCATCAAGCGACTGCAC	1238
QY	9	-----	9
DB	1239	CATCTCATTGAAGAGGTGTTGAACGCGCATGAACAAAAATACCGCTTGCTCGGACGAG	1298
QY	10	-----AsnSer-----	11
DB	1299	CGAGAGCTCATTTACGGCGAGTCAATGCGCAAGGCAACAGACCTCGCAGCTATCTCGT	1358
QY	12	-----Ile-----Ser-----	13

DB	1359	TCATTGGTATCTCTGCCCGAGCAGCTAGTCGCATTTGTTCTAGATAAGAGCGAGAGCTC	1418
QY	14	-----Trp-----	14
DB	1419	ATGTGTACCATCTCTGGCGGTGTGGAATCCGGCGCGCCTACGTGCCCATCGACCCGACT	1478
QY	15	-----AlaIle-----	16
DB	1479	TATCCGGATGAGCGAGTGGCTTCGTGCTGGATGACACCAAGGCGCGCCCATCATCGCC	1538
QY	16	-----	16
DB	1539	AGTAATCAATGTGTGGAGAGGCTCCAGCGAGAGTTCATCGCGATAGAAACCTATGCAAT	1598
QY	17	-----Phe-----	17
DB	1599	ATCCGCTCGAGGCCCTTGTGTGGCCTCCCTTGTCTCAGGATTCCTCAAAATCCCGCGCAT	1658
QY	17	-----	17
DB	1659	AACTTGGACGACCTACCCCTCAAGACGAGCTGCGCTATGTGACTTACACCTCTGGG	1718
QY	18	-----ThrGly-----	19
DB	1719	ACCACTGGTTTCCAAAGGCGCATATTTAAACAACACACCAATGTGGTGAACAGTATACC	1778
QY	20	---Leu-----Ala-----Ala-----Leu-----	23
DB	1779	GACCTGTCTGCAAGGTACGGGTGGCGGGGAGCAGCAGCAAGCCATCTGTTTTCTCG	1838
QY	24	---CysLeuPhe-----Gln-----Gly-----	28
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QY	44	-----AsnVal-----	45
DB	2199	GGGAGACCGGTGCGCAACGCTCAAGTCTACATCTCAATCCATCCCTTAAACGTGTCCCG	2258
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DB	2259	ATTGGAGCTACGGGTGAGTTGCATATCGAGGGTTGGCGATTTCCAGGGATACCTCAAC	2318
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DB	2319	CGCCCGAACTCAGCCCGCAGCGCTTCATTCACCAACCCCTCCCAACCGGATTCGAGAG	2378
QY	45	-----	46
DB	2379	CAGCTCGGATCAACAGCTTGATGTACAAGACCGGTGACCTGGCCCGCTTCCGAAC	2438
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DB	2439	GGCGAGTTGAGTATCTCGGACGCGCATTTCCAGATCAAACTCGGAGGTATTCGAAT	2498

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QY 57 -----Cys-----ThrIle-----Asp----- 60
Db 2619 TATGTTTGTGATAGCGCTCAGTGTCCGAGGACAGCTGCTGTCAATTTTAGAGAGAAA 2678
QY 60 ----- 60
Db 2679 CTGCCTCGATACATGATTTCCACGCGGTTGGTATACAGCTGTGCAGATCCCACTGAATGTG 2738
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Db 2859 GGAGCCGCCAGAGATCGGTCTCTCGCAACGACAACTTCTTCGCGCTAGGAGGCGACAGC 2918
QY 73 -----Thr-----Ile 74
Db 2919 ATCACTGCATCCAACTGATCGCTCGCATCCGACAAACGAACTCTCGGTGAGCATC 2978
QY 74 ----- 74
Db 2979 TCCGTGAAGATGTTTTTGCAACAGGACACTTGAGCGCATGGCAGACCTTCTACAGAAC 3038
QY 75 -----Leu----- 75
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Db 3816 GGAGACCATGGCTAGCAGACCTTTCGTACAGACCTGCTCCGCCAGGGTATTACCTTACAT 3875
QY 37 -----Gln-----Tyr----- 98
Db 3876 TCGATTCTCCAAATTTGTTGSCACGCCGTGTGCACGCTTATGGCGGTGGCACCCACACC 3935
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Db 4893 TTGCCTGCCAATCCGATTCGAAGTGAGCGGTATCGAACCCCTTCACGTTGAGTCGGAGC 4952
QY 136 - - - - -ProLys- - - - -Ile- - - - - 138
Db 4953 ACGGACTTAGCTTATATCATCTATACCTCTGGAACGACAGGTCCGCCCAAGGGGCTCACG 5012
QY 139 ValGlu- - - - -IleSer- - - - - 143
Db 5013 GTAGAGCATCATGAGTGCTCAACTGCGAGGTGCTGCTATCCAAAGTATTTCGAGCTACGG 5072
QY 144 - - - - -Ile- - - - -SerIle- - - - -Asn- - - - -Glu- - - - - 149
Db 5073 GATACGACGACGAGGTAATCTCTCTCTTTCCAACTATGTGTCGACCATTCGTCGAG 5132
QY 150 - - - - -Gly- - - - -Asn- - - - - 151
Db 5133 CAGATGACGACGCCATTCATATGCGCAAAACCCCTCTGCTCTCAACGATGGAATGCGC 5192
QY 152 - - - - -Asn- - - - -IleSer- - - - -Leu- - - - - 155
Db 5193 GGGGACAAAGAGCTCTACAGATACATTGAGNAGAACGAGTGACCTACTTGTCTGGC 5252
QY 156 Thr- - - - - 156
Db 5253 ACCCCATCCGTGCTCCATGATACGATTTAGCCGTTCAAGGACCATCTACGCCGTGTG 5312
QY 157 - - - - -CysIle- - - - -Ala- - - - -Thr- - - - - 160
Db 5313 GACTGCTGGGGAGGCGTTTCAGCGAACCGGTCTTCGACAAGATCCGCGAAACGTTCCAT 5372
QY 161 - - - - -Gly- - - - -Arg- - - - - 162
Db 5373 GGCCTGTTATCAACGGCTACGGCCCACTGAAGTTTCCATACCACCACCAAGCGGCTC 5432
QY 163 - - - - -ProGlu- - - - - 164
Db 5433 TATCATTTCCAGAGCGCGGAATGGACAAAGTATTGGCCAAAGGTTCACAAATAGCACG 5492
QY 165 - - - - -Pro- - - - - 165
Db 5493 AGCTATGCTGAACGAGGACATGAAGCGCACCCCATAGGGGCTGTCCGCGAGCTCTAC 5552
QY 166 - - - - -Thr- - - - - 166
Db 5553 CTGGGTGTTGAAGGTGTTACGGGATATCACATCGCGCAGNATGTGACCGCGGAGCGT 5612
QY 167 - - - - -Val- - - - - 167
Db 5613 TTTATTCCTTAATCCATTCAGTCGGAAGAGATAAGCGAAGGTGCTAACTCCCGTTG 5672
QY 168 - - - - -Thr- - - - - 169
Db 5673 TACAGACCGGTGACCTGGTACCGTGGATTCCTGGAAAGCAGCGGGAGGTGCGAGTATCTA 5732
QY 170 - - - - -Arg- - - - - 170

Db 5733 GGTCTGAATGACTTCCAGGTCAAGATTTCGGGACTCGCATCGAAGTAGCGAGATTGAG 5792
QY 171 - - - - -His- - - - - 171
Db 5793 GCCATCTCTATCGTCTTATCACGGAATCAAAACAGTCTGTGGTATTGCCAAGGATTGACA 5852
QY 171 - - - - - 171
Db 5853 GAAGGGGCCAGAAATTCCTGGTTGGTTACTATGTCCCGCATCGAGGCTGCCGTCGGCT 5912
QY 172 - - - - -Ile- - - - - 172
Db 5913 GCCATTTCGGGCTTTCATGACAGTCTCGGCTCCCTGGCTACATGTGTCCTCTCTCTCAT 5972
QY 173 - - - - -Ser- - - - -Pro- - - - -Lysala- - - - - 176
Db 5973 CTCGTAGCAAGTTCCTCGGTCACTCTCTAGTGGAATAATAGACACCAAGGCTTTGCCGCCA 6032
QY 177 - - - - -Val- - - - - 177
Db 6033 GCCAGAGAGAGAGCGAGATTGACGTGGTGGCCGCGTAGTGAATCGAACGCTCCTTG 6092
QY 177 - - - - - 177
Db 6093 TGTGACATCTGGGCGGAACCTACTCGAGATGCACCCAGAGAGATCGGCATTTACAGCAT 6152
QY 178 - - - - -Gly- - - - - 178
Db 6153 TTCTTCAGCTGGAGGTGACAGCCTAAAGAGACAAAGCTTTCCTTCATGATTCAGGAG 6212
QY 179 - - - - -Phe- - - - -ValSer- - - - -Glu- - - - - 182
Db 6213 TCCTTTAAACCGGCCCTCTCAGTCAGCGGCCCTTTCTGTACCGGACAGTTGAAGCCAG 6272
QY 183 - - - - -Asp- - - - -Glu- - - - - 184
Db 6273 ACGCACTTGATCTGTGAACGATGTCAGATGTGACGAAATTAATCCCATAGATTGCAAT 6332
QY 184 - - - - - 184
Db 6333 GATACGAGATGATTCCTCGTGTCCCGTCCAGGAGCGACTCTCTTCATCCACGATTT 6392
QY 185 - - - - -Tyr- - - - - 185
Db 6393 GAGATGGCAGCAATGATACAAATATCGACGCTGCATTTGAATGCTGCTGCTGCTGAC 6452
QY 186 - - - - -LeuGlu- - - - - 187
Db 6453 GCGTCTCTTCGAGCAGCGGCTGCTGGAAACCTTGCTCGACATGAGCGTTGAGAACT 6512
QY 188 - - - - -Ile- - - - - 188
Db 6513 TTACTGCTCAAGGATCACGCAACCGGCATCTATCTTCAGAAGTATTGATCCCGATGAA 6572
QY 189 - - - - -GlnGly- - - - - 190
Db 6573 GCCAGGCGATGTTCTTCGTCACCTGAGGACACAGCCAGCAGGTGGAGCGGCTGGACAC 6632
QY 190 - - - - - 190
Db 6633 GAGATAGCAGTCTATCCAGCATGTTTTCGCTCGATGATGAATGCTGTTGGAGGCGC 6692
QY 191 - - - - -Ile- - - - -Thr- - - - - 192
Db 6693 CGCATCTTAAATCGAATCCGGCGCTGTATCTCATTTCTGGCGTTCACCATCTGTC 6752
QY 193 - - - - -Arg- - - - - 193
Db 6753 TTGATGATGTCATGAAAGTCTTCGAGCAAGAGCTTCGGGCGCTTGTACGACGCGTC 6812
QY 194 - - - - -Glu- - - - - 194
Db 6813 CAGAAACCAAAAGTGACGCAACTTACAGCCCTCAAGCGCAGTACAAAGGAATACGCG 6872

Db 9033 GTTCAGAACGTCCTCACTTCAAGTCCGGTGTCCGGAGGGTGCAGTCGTGTCACAGTAT 9092
QY 288 -----His----- 288
Db 9093 GAGAACACGATACCTATTCCCGACCGCTCACTCTCTGTGCGTTACTATACACGGAC 9152
QY 289 -----Asp-----Tyr 290
Db 9153 AATGAACAGATATCGAAGCGGATATTCTCACTTTTCATGAAAGCAAGGCTTCCACAGTAC 9212
QY 291 -----Gly----- 291
Db 9213 ATGTCGCAAGCCACCTCTGCTGTCTGGAAGGGCACTGCTGTGACGATTAACGGAAG 9272
QY 292 -----Asn-----Tyr 293
Db 9273 CTCGACGTCGGAGATTGCGGAGATTATCAACGACTCCGGCGAGTCTCTGTACAGCCCA 9332
QY 293 ----- 293
Db 9333 CCAAGAACATAATCGAGGCCAAGATGTGCAGACTGTGGGAATCCCGCTTGGGAATGGAG 9392
QY 294 -----Thr----- 294
Db 9393 CGATGCGGTATCGACGACGACTGTTCAAACTGGGTGGCGACAGCATCATCTTTGCAT 9452
QY 295 -----Cys-----Val----- 296
Db 9453 CTGTGCGCCAGATTCAACACAGGTGGTGTGCAAGATCACCGTTCGGGATATATTGAA 9512
QY 297 -----Ala-----SerAsn 299
Db 9513 CATGTTACCGCCGAGCCCTCCATGATFCACGTCTTCATGAAGACTCCCGACCGAGTAAT 9572
QY 300 -----Lys-----LeuGly----- 302
Db 9573 GTGACTCAGTTCGAAACCGAACAGGGCCGGTCATCGGCGAGGGCCCTTACTGCGGATT 9632
QY 303 -----HisThr----- 304
Db 9633 CAAGACTGGTTTTGTCAAAGGCTCTGCAGCATCCGATGATTGGAAATCACACTTTCTAC 9692
QY 304 ----- 304
Db 9693 GTCCGAACGCGAGCTGGATGTTGATTCTTAAGCGCTGCTGTCAAGGACTTSCAACAG 9752
QY 304 ----- 304
Db 9753 TATCAGATGTTTTCCGATGCGACTCAAGCGCGAGGAACTCGGATTCGTGCACTCTTT 9812
QY 305 -----Asn----- 305
Db 9813 GCTGAGGACTTCTCTCTGCCAGCTTCGGGTGCTGAACGTAAGATGTTGACGGGTCC 9872
QY 306 -----Ala----- 306
Db 9873 GCGGCCGTCAACGAGATATTGGATGGTGGCACTCTGGCTTCAACTTGAAGACGGACCC 9932
QY 307 -----SerIle----- 308
Db 9933 ATTGGTTCCATTGGCTACCTACATGGGTATGAAGACCGATCCCGCGAGTCTGTTCTCC 9992
QY 309 -----Met----- 309
Db 9993 GTTCACATATGSCATTGACACCGTACGTGGCAGATCCTTGTCCGTGACCTGCAGACG 10052
QY 310 -----Leu-----Phe----- 311
Db 10053 CTGTACGGAATGGAAGCCTCGAAGCAAGGGCAGCAGTTTCCGGCAGTGGGTGAAGCC 10112
QY 311 ----- 311

Db 10113 ATCCAAATTAAGGCGTCAGACTCTGAGAGGAACCATTTGAATAAGCTCGTCAATGAA 10172
QY 312 -----Gly----- 312
Db 10173 ACAGTCTCAGCANATCCGATTCGCTACGTCAACCGGTTTCGCGGTGCGCTGAGCAGA 10232
QY 313 -----Pro----- 313
Db 10233 AGTTTGAGCCCTCAGAAGACAGCCTCACTGATCCAAAGGAGGAATCGATCGACAGGATGTC 10292
QY 314 -----Gly-----Ala----- 315
Db 10293 TCCGTGTACGACTCCCTCTCTGACTTCAGTTGGATGGCGCTCCAAATATCGTCTCAACC 10352
QY 315 ----- 315
Db 10353 GGCCCAAGTATGGTTACGATCGAGGACATGCGCGTGAAGAAGTGGATCAGACACTGGAT 10412
QY 316 ValSer-----GluVal-----Ser 320
Db 10413 GTGAGCCGCACCATGGGTTGTTTCCACCACATGTATCCATTGTTGAAATTCCTCCGCTCAGC 10472
QY 321 -----Asn-----Gly-----ThrSer----- 324
Db 10473 ACCGAAACATTTCAAGGAGTCTGCTGTGAGCGAACCGTTTCAGACAGGTGCTCGCC 10532
QY 325 Arg----- 325
Db 10533 CGTGGCTCGGTATGGAACCTTTACGCTATATCTAACACCCGCTGCCCGAGGTGACC 10592
QY 326 -----Arg-----Ala 327
Db 10593 GTCAACTACTCGGCCAGCTCGCCGCAAGCAATCGAAGCCAAAGAAATGGGTCTCTCGCG 10652
QY 328 -----Gly----- 328
Db 10653 GTGGGCGCAACGAATTTGAATACCGACTCATGACTAGCCAGAGCAAAAGACCGGAGC 10712
QY 329 -----Cys-----Val----- 330
Db 10713 TCTTCTGCGTCGACGTCACGGCCGTGTGTATTGAGCGCACTATGATCATCATGTGTGGAC 10772
QY 331 -----Trp----- 331
Db 10773 AGTGTCTTGAGCCTTGAGGAGACGAGCAATTCATCTCGAGCATCGAGGAGGACTGAAC 10832
QY 331 ----- 331
Db 10833 AAGATCTCGACGGCAGGGCAAGTCAAGAACTCGCGATTCGCGATGTTCTCTCAACCG 10892
QY 331 ----- 331
Db 10893 GCGGAGACATATACCGCTATTTCGAGTATCTGGAACCTCCACGACAGGACCGAGCTG 10952
QY 332 ---LeuLeuPro-----Leu----- 335
Db 10953 TTCTCTGCTGCGCCGCGGAGAGGCGCGAGAGTTACTTCAACAACATCGTCAAGCGC 11012
QY 336 Leu-----Val-----LeuHis----- 339
Db 11013 CTGCGTCAGACAAATATGGTGTCTTCAACAATACTACTTGTGCACAGCAACGCTCGGC 11072
QY 340 -----Leu----- 340
Db 11073 AGTTCGAGGAGCTGGCGGAATGTATCTCGACCAAGTACGGGCATCCAAACCAACAGCA 11132
QY 341 -----Leu----- 341
Db 11133 CGGTACCACTTCATCGGATGGAGCTTCGAGGAATTTCTCGCAATGGAATGTGCGGGAGA 11192
QY 342 Leu-----Lys-----Phe 344
Db 11193 CTGGTAGCTCGGACGAGAAGATTGGCTTC 11222

RESULT 22

US-08-859-694-1
; Sequence 1, Application US/08859694A
; Patent No. 6001613
; GENERAL INFORMATION:
; APPLICANT: Donis, Ruben O.
; APPLICANT: Vassilev, Ventsislav B.
; TITLE OF INVENTION: A plasmid bearing a cDNA copy of the genome of bovine
; TITLE OF INVENTION: viral diarrhea virus, chimeric derivations thereof, and
; TITLE OF INVENTION: method of producing an infectious bovine viral diarrhea
; TITLE OF INVENTION: virus using said plasmid
; FILE REFERENCE: UNVNS1110
; CURRENT APPLICATION NUMBER: US/08/859,694A
; CURRENT FILING DATE: 1997-05-21
; EARLIER APPLICATION NUMBER: 60/018,246
; EARLIER FILING DATE: 1996-05-24
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14578
; TYPE: DNA
; ORGANISM: bovine viral diarrhea virus
US-08-859-694-1

Alignment Scores:

Pred. No.: 1.21e-24 Length: 14578
Score: 1717.50 Matches: 293
Percent Similarity: 10.79% Conservative: 44
Best Local Similarity: 9.38% Mismatches: 7
Query Match: 71.32% Indels: 2780
DB: 3 Gaps: 248

US-10-017-084A-523 (1-344) x US-08-859-694-1 (1-14578)

QY	1	MetLys-----ThrIle-----Gln---	5
DB	169	ATGAGGGGGTAGCAACAGCGTGGTGGTGGTGAAGCCCTGAGTACAGGGTA	228
QY	6	-----Pro-----Lys-----Met-----His	9
DB	229	GTCTGAGTGGTTCGACGCGCTTGGAAATAAGGTCCTCGAGATGCCACGTGGACGGGSCAT	288
QY	9	-----Pro-----Lys-----Met-----His	9
DB	289	GCCAAAGCACATCTTAACCTGAGCGGGGTGCCAGGTAAAGACAGTCTTAACCGACT	348
QY	10	-----AsnSer-----Ile-----	12
DB	349	GTTACGANTACAGCCTGATAGGTGCTGCAGAGCCCACTGTATTGTCTATAAAATCTC	408
QY	13	-----SerTrp-----	14
DB	409	TGCTGTACATGGCACATGGAGTTGATCACAATGAACTTTTATACAAAACATACAAACAA	468
QY	15	-----Ala-----IlePhe-----	17
DB	469	AAACCCGTGGGTGGAGAACCTGTTTATGATCAGGCGGTGATCCCTTATTGTTGAA	528
QY	18	-----Thr-----Gly-----	19
DB	529	AGGGAGCAGTCCACCTCAATCGACGCTAAAGCTCCACACAGAGAGGGGAACGGAT	588
QY	20	-----LeuAlaLeu-----Cys-----	24
DB	589	GTTCCAAACCACTGGCATCTTACCACAAAGAGGTGACTGCAGGTGGGTAAATAGCAGA	648
QY	25	-----LeuPhe-----Gln-----	28
DB	649	GGACCTGTGAGCGGGATCTACCTGAAGCCAGGCGCCACTATTATCCAGGACTATAAAGGT	708
QY	29	-----Val-----Pro-----	30

DB	709	CCGCTCTATCACAGGGCCCGCTGGAGCTCTTTGAGGAGGGATCCATGTGTGAACGACT	768
QY	31	-----Val---Arg-----Ser---Gly-----	34
DB	769	AAACGGATAGGGAGAGTAAGTGAAGTGCAGGAAAGCTGTACACATTTATGTGTGATA	828
QY	35	Asp-----AlaThr-----Phe-----	38
DB	829	GATGGATGATATAATAATAAAAGTGCACACAGAGTTTACCAGAGGGTGTTCAGGTGGTC	888
QY	39	-----Pro-----Lys-----	40
DB	889	CATAATAGGCTTGACTGCCCTCTATGGGTCAAGTTGCTCAGACACGAAAGAGAGGGA	948
QY	41	Ala-----Met-----	42
DB	949	GCAACAAAAGAAAACACAGAAACCCGACAGACTAGAAAGGGGAAAATAAATAGTG	1008
QY	43	-----Asp-----AsnValThr-----	46
DB	1009	CCCAAGAAATCTGAAAAGACACGAAACCTAAACCTCCGGATGCTACAATAGTGGTGA	1068
QY	47	-----ValArg-----Gln-----	50
DB	1069	GGAGTCAAAATACCAGGTGAGGAAAGGAAACCAAGAGTAAACACACTCAGGACGGC	1128
QY	51	-----GluSer-----	52
DB	1129	TTGTACCATAAACAAACAACTCAGGAATACGCAAGAACTGGAAGAAAGCATTTTG	1188
QY	53	-----Ala-----Thr-----	54
DB	1189	GCCTGGCAATAATAGCTATAGTTTGTTCAGTTTACATGCGGAGAAACATAACACAG	1248
QY	55	-----Leu-----	55
DB	1249	TGAACTTACAGAAATAGGACGGAAGGATACAAAGGCAATGTTCCAAGGGGTGTG	1308
QY	56	-----Arg-----Cys-----	57
DB	1309	AATAGAGTTTACATGGATCTGGCCAGAGAAAATCTGTACTGGCTCCCTCCCATCTA	1368
QY	58	-----ThrIle-----Asp-----	61
DB	1369	GCCACCGATATAGAACTAAACAAATTCATGTTGATGATGATGATGATGATGATGATG	1428
QY	62	-----ArgValThrArg-----	65
DB	1429	TACACGTGTTGCAGACTTCAACGCCATGATGATGATGATGATGATGATGATGATGATG	1488
QY	66	-----ValAla-----	68
DB	1489	AATATTGAACCTGGATTCTAGTCATGAATAGAACCAAGCCAACTCTCACTGAGGACAA	1548
QY	69	-----LeuAsn-----	70
DB	1549	CCACCAAGGAGTGCAGCTCACTTGTAGTATGATGATGATGATGATGATGATGATGATG	1608
QY	71	-----Arg---Ser-----Thr-----	73
DB	1609	ACAAAGCTAGAGTAGCCCCACACCCCTTAACAGGTTGCAAGAAAGAAAGAACTTCTCC	1668
QY	73	-----	73
DB	1669	TTTGAGGCATATTGATGGGGGCCCTGCAACTTTTGAATAGCTCAAGTGAATGATTA	1728
QY	74	-----Ile-----LeuTyr-----	76
DB	1729	TACAAAGAACATGAACGCATTAGTATGTTACAGGATCTAACTCTTTACCTTGTGACGG	1788
QY	77	-----Ala-----	77
DB	1789	TTGACCAACTCCTTAGAGGTGCCAGAACGAAACCGCTAAACTGACAACTGGTTAGGC	1848

QY 78 -----Gly-----Asn----- 79
Db 1849 AAGCAGCTCGGATACCTAGGAAAAAGCTTGGAAAAAGAGTAAGACGTGGTTGGAGCA 1908
QY 80 -----Asp-----Lys-----Trp----- 82
Db 1909 TAGCTGCTCCCTTACTGTGATGTGCTGCGCAAAATTTGGCTACATATGCTATACAAA 1968
QY 83 -----CysLeu----- 84
Db 1969 AATTGCAACCTCGCTGCTTACCCCAAGAACACAAAAATTTGCGCCCTGGGAAATTTGAC 2028
QY 84 ----- 84
Db 2029 ACCAATGCAGGACGGCAAGATATTACATGATGGGGGTCACTTGTGCGAGGTACTA 2088
QY 84 ----- 84
Db 2089 CTACTTTCTTTAGTGTGCTGTCGACTTCGCACCGGAAACAGCTAGTGTAAATGTACCTA 2148
QY 85 -----Asp----- 85
Db 2149 ATCTACATTTTCCATCCCAAAAGTCACGTTGATGTATGATGTTGTGATAGAGCCAG 2208
QY 86 -----Pro----- 86
Db 2209 TTGAACCTCAGTGGAGCTGCAACACAGCTGAAGTAATACTCGGTGCTCGAATCTA 2268
QY 87 -----Arg-----ValValLeu----- 90
Db 2269 GGCAATATGTATGTATAGACCAAAATTTGGTGGCTTATGAGACAACCTGTAGTTGGCA 2328
QY 91 -----LeuSer----- 92
Db 2329 TTTGAAGAGGTAGCCAGGTGGTGAAGTTAGTTGTGAGGSCACTCAGAGATTTAACACGC 2388
QY 93 -----Asn-----Thr----- 94
Db 2389 ATTGGAAGCTGCAACAACTACTGCTTTTTTAGTATGCTTGTGAAGATAGTCAGGGGC 2448
QY 95 -----Gln-----Thr----- 96
Db 2449 CAGATGTACAGGCACTCTGTGGTACTATTGATAACGGGTACAGGGGCATTGGAT 2508
QY 97 -----Gln----- 97
Db 2509 TGCAAACTGAATTCCTGATGCCATAGCAAGGAGCAAAAGAAATTTGCTCAACTGGGGCT 2568
QY 98 -----TyrSer----- 99
Db 2569 GAAGGCTTACCACCTTGGAAAGGAATCTACCTGGAATGAAGCTGGAAGACACAATG 2628
QY 100 -----Ile-----Glu----- 101
Db 2629 GTCAATTTGGTGGAGAGTGGAAAGTTAATGTAACCTCCAAGATGCACAGAGAAACC 2688
QY 102 -----Ile----- 102
Db 2689 AGATATCTCGCAATCTTGCAACAGAGGCTTCCGACCACTGTGTATTTCAAAAACTC 2748
QY 103 -----Gln-----Asn----- 104
Db 2749 TTTGATGGGGAAAGCAAGAGGATGTAGTGAATGAACGACAACCTTTGAAATTTGGACTC 2808
QY 104 ----- 104
Db 2809 TGCCCATGTATGCCAAACCCATAGTAGAGGGAAGTTCAATACACGCTGTGTAACGCA 2868
QY 105 -----Val----- 105
Db 2869 CCGGCTTCCAGATGTATGCCCATAGGATGAGCAGGGACTGTAAGCTGTACGTCAATC 2928

QY 106 -----Asp-----Val-----Tyr----- 108
Db 2929 AATATGGACACCTTAGCCCACTGTGGTACCGACATATAGAAGTCTAAACCATTCCT 2988
QY 108 ----- 108
Db 2989 CATAGGAAGGCTGTATATCCCAAAAGAAATCTGGGGAGGATCTCCATAACTGCATCCT 3048
QY 109 -----Asp----- 109
Db 3049 GGAGGAATTTGACCTTGTGTGCTGGAGACCAACTACTATACAAAGGGGCTCTATTGAA 3108
QY 110 -----GluGly-----Pro----- 112
Db 3109 TCTTGCAAGTGGTGGCTATCAATTTAAAGAGAGTGGAGGACTACCACACTACCCCAT 3168
QY 113 -----Tyr----- 113
Db 3169 GGCAAGTGTAAATTTGGAGAACGAGACTGTTTACAGGCTAGTAGACACTCTTGTCAAT 3228
QY 113 ----- 113
Db 3229 AGAAGGTGTGGCCATAGTACACAGGACATTAAGTGCAGATAGAAAAACAAC 3288
QY 114 -----Thr-----Cys----- 115
Db 3289 GTACAGTCTATAGTATGATACCAAACTCGGACCTATGCTTTCAGAGACCATATGAATC 3348
QY 116 -----Ser-----Val----- 117
Db 3349 ATATCAAGTGTAGGGGCTGTAGAAAAGACAGCGTGTACTTTCAACTTACACTAAGACATTA 3408
QY 117 ----- 117
Db 3409 AAAAATAGTATTTTGCAGCCAGACAGCACTACTTTCAGCAATATACATGCTAAAAGAGAG 3468
QY 118 -----Gln-----ThrAsp----- 120
Db 3469 TATCAACTACTGTTTGAACCTGAGGTGACTGACCATCACCGGATTTACTTCGTGAGTCC 3528
QY 120 ----- 120
Db 3529 ATATTAGTGTGTAGTAGCCCTCTTGGGTGGCAGATATGTACTTTGGTTACTGGTTACA 3588
QY 120 ----- 120
Db 3589 TACATGGTCTTATCAGAACAGAGGCTTAGGATTCAGTATGATCAGGGGAAGTGGT 3648
QY 121 -----Asn----- 121
Db 3649 ATGATGGGCACTTGTCTAAACCCATAAATATTTGAAGTGGTGACATCTTCTTGTCTGTG 3708
QY 121 ----- 121
Db 3709 TACCTACTGCTGAGGAGGAGAGCGCTAAGAAAGTGGTCTTACTCTTATACCATCTTA 3768
QY 122 -----HisPro----- 123
Db 3769 GTGGTACACCCCAATCAATCTGTAATTTGTATCTCTACTGATGATGTTGGGATGTGTAAG 3828
QY 124 -----Lys-----ThrSer----- 126
Db 3829 GCCGATTCAGGGGCCAAGAGTACTTGGGGAATAATAGACCTCTGTGTTTACAACAGTAGTA 3888
QY 126 ----- 126
Db 3889 CTAATCGTCATAGTTTAAATCATAGCTAGGCGTGACCACTATAGTCCACTGTAAACA 3948
QY 127 -----ArgVal-----His----- 129
Db 3949 ATAATGGCAGCACTGAGGGTCACTGAACTGACCCACAGCCCTGGAGTTGACATCGCTGTG 4008
QY 129 ----- 129

Db	4009	GCAGTCAAGACTATAACCCCTACTGATGGTATGCTATGTGACAGATTATTTAGATATAA	4068	Db	5089	AGTGCCAGATACTGTGCTGAGTGTAAATAGGCTGCATCCTGCTGAGGAAGGTGACTTTTGG	5148
Qy	129	-----	129	Qy	166	-----	166
Db	4069	AAATGGTTACAGTGCATTCACAGCCTGGTATCTCGGGTGTCTTGATGAAGAGCCTAATA	4128	Db	5149	GCAGAGTCGAGCATGTTGGCCCTCAAAATCACCTACTTTTGGCGCTGATGATGAAAGGTG	5208
Qy	129	-----	129	Qy	167	-----	170
Db	4129	TACCTAGGTAGATCGAGATGCCAGAGTAACCTATCCAAACTGGAGACCACTAATCTTA	4188	Db	5209	TATGATATCACAGAGTGGCGTGGATGCCAGCGTGTGGGAATCTCCCGAGATACCCACAGA	5268
Qy	130	-----	132	Qy	171	-----	176
Db	4189	ATACTATTATTTGATCTCAACAACAAATTGTACGAGGTGGAGTTGACGTGGCTGC	4248	Db	5269	GTCCCTTGTACATCTCATTTGGTTCACGATGCCCTTCAGGAGGAATAAATATGAGGCTTT	5328
Qy	133	-----	135	Qy	177	Val	179
Db	4249	CTATTGTGCAATGTGTGCCTATCTTATTGTCTGTCTACAACCTTGTGGCGGACTTCTTA	4308	Db	5329	GTACAAATATACCGCTAGGGGGCACTATTCTCTGAGAACTTGCCCGTACTGGCACTAAA	5388
Qy	136	-----	137	Qy	179	-----	179
Db	4309	ACCTAATACTGATCCTGCCTACCTATGAATTTGTTAAATATATCTATCTGAAACTGTT	4368	Db	5389	GTAAAAATGCTCATGTAGGCAACCTTGGAGAGAAATTTGGTAATCTGGAAACATCTTGGG	5448
Qy	138	-----	138	Qy	180	-----	182
Db	4369	AGGACTGATACAGAAAGATTGGCTAGGGGGGATAGACTATACAGAGTTGACTCCATC	4428	Db	5449	TGGATCCTAAGGGGGCTGCCGTGTGTAAAGAGATCACAGAGCACGAAAAATGCCACATT	5508
Qy	139	-----	140	Qy	183	-----	185
Db	4429	TACGACGTGTAGAGTGGAGGGCGGTATATCTTTTCCATCAAGGCAGAAAGCACAG	4488	Db	5509	AATATACTGATAAACTAACCAGCATTTTCGGGATCATGCCAAGGGGACTACACCCAGA	5568
Qy	141	-----	142	Qy	186	-----	188
Db	4489	GGGAATTTTCTATPACTTTGCCCTTATCAAGCAACACTGATAAGTTGCGTCAGCAGT	4548	Db	5569	GCCCCGTGAGGTTCCTCTAGAGCTTACTAAAGTGAGGAGGGTCTGGAGACTGCGTGG	5628
Qy	143	-----	144	Qy	189	-----	191
Db	4549	AAATGGCAGCTAATATACATGAGTTACTTAACCTTTGGACTTTATGTACTACATGACAGG	4608	Db	5629	GCTTACACACACCAGCGGGGATAGTTTCAAGTCAAGTGTACCGATGTAACCGCCGGAAGATCTA	5688
Qy	145	-----	146	Qy	192	-----	195
Db	4609	AAAGTTATAGAGAGATCTCAGGAGGTACCAACATAATATCCAGTTAGTGGCAGACTC	4668	Db	5689	CTGGTCTGTGACAGCATGGGAGCACTAGAGTGGTTTGCCAAAGCAACACAGATTGACC	5748
Qy	147	Ile	149	Qy	196	-----	199
Db	4669	ATAGAGCTGAATGGTCCATGGAAGAAGAGAGAGCAAGGCTTAAAGAAAGTTTATCTA	4728	Db	5749	GATGACAGAGTATGCGCTCAAGACTGACTCAGGTGCCAGCGTCCAGACGCTGCAGATGTTAT	5808
Qy	150	-----	152	Qy	199	-----	199
Db	4729	TTGTCTGGAAGTTGAGAAACCTTAATAAATAAATAGGTAGGAATGACCGTGGCT	4788	Db	5809	GTGTTAAATCCAGAGCGCGTTAATATATCAGGATCCAAAGGGGCGAGTCGTTCACTCCAA	5868
Qy	153	-----	153	Qy	200	-----	201
Db	4789	TCTTGGTACGGGAGGAGGAAGTCTACGGTATGCCAAAGATCATGACTATAATCAAGGCC	4848	Db	5869	AAGACAGGTGGAGAAATTCAGCTGTGTCAACGATCAGGCACACCGGCTTCTTCGACCTA	5928
Qy	154	Ser	162	Qy	202	-----	204
Db	4849	AGTACATGAGTAAGACAGCAGCACTGCATAATATGCACTGTATGTGAGGGCCGAGAGTGG	4908	Db	5929	AAAAACTTGAAGAGTGGTCAAGCTTTCCTATATTTGAAGCCTCCAGCGGAGGCGTGT	5988
Qy	163	-----	163	Qy	204	-----	204
Db	4909	AAAGGTGGCACCTGCCAAATGTGGAGCGCATCGGAAGCGGATAACGTGTGGATGTGG	4968	Db	5989	GGCAGAGTCAAGTAGGGAAGATGAAGAGTCTAAACCTTACAAAAATATATGATGGGAATC	6048
Qy	163	-----	163	Qy	205	-----	207
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Qy	164	-----	165	Qy	208	-----	209
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Qy	165	-----	165	Qy	210	Pro	215
Db				Db	6169	CCAAAAGCAGTTATAGAGGAGATAGGAAGACACAGAGAGTATTAGTTCTTATACCTTAA	6228

QY 216 -----Lys-----ValThrVal 219
Db 6229 AGGCAGCGGAGAGTCAAGTCTACAGTATATGAGATTGAACACACCCCAAGCATCTCTTT 6288
QY 220 Asn----- 220
Db 6289 AACCTAAGGATAGGGGACATGAAGAGGGGACATGGCAACCGGATPAACCTATGCATCA 6348
QY 221 -----Tyr-----Pro----- 223
Db 6349 TACGGGTACTTCTGCCAAATGCCTCAACCAAGCTCAGAGCTGTATGGTAGAATCTCA 6408
QY 224 Tyrlle----- 225
Db 6409 TACATATTTCTTAGATGAATACCAATTGTGCCACTCTTGAACAACTGGCAATTATCGGGAAG 6468
QY 226 -----SerGlu-----AlaLys-----Gly----- 230
Db 6469 ATCCACAGATTTTCAGAGAGTATAAGGGTTGTGCCATGACTGCCAGCCAGCAGGGTGG 6528
QY 231 -----ThrGly-----Val-----Pro-----Val----- 235
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QY 236 -----Gly-----Gln----- 237
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QY 240 ----- 240
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QY 241 Leu-----Gln----- 242
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QY 243 -----CysGlu----- 244
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QY 249 -----Pro----- 249
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QY 260 -----Lys----- 260
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QY 267 -----Lys-----Gly-----Vallys----- 270
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QY 290 -----Tyr-----GlyAsn----- 292
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QY 293 -----TyrThrCys-----Val-----Ala----- 297

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Qy 299 Asn -----Lys 300
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Qy 300 -----
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Qy 301 LeuGly-----HisThr-----Asn 305
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Qy 306 Ala-----Ile-----
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Qy 309 MetLeu-----PheGly-----Pro-----
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Qy 314 ---GlyAla---Val---Ser-----Glu 318
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Qy 321 -----
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Qy 322 -----GlyThrSer-----
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Qy 342 -----LeuLys-----
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; Sequence 1, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 1
; LENGTH: 11272
; TYPE: DNA
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: nucleic acid sequence of rat cubilin
US-09-341-461-1
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Pred. No.: 4,1e-25 Length: 11272
Score: 1717.20 Matches: 283
Percent Similarity: 11.96% Conservative: 46
Best Local Similarity: 10.29% Mismatches: 12
Query Match: 71.31% Indels: 2409
Gaps: 4
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Qy 6 -----Pro-----
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Qy 7 ---LysMet-----His-----Asn 10
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Qy 11 -----SerIle-----
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Qy 13 -----Ser---Trp-----
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Qy 15 -----AlaIle-----PheThr-----
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Qy 18 -----
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Qy 19 -----Gly-----
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Qy 20 -----Leu-----AlaIleLeu-----
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Db 9226 ATAATAATTAGTTCAATGATTTTCGATGTGGCTCTCTTCCAACTTTGTGCAATGATTC 9285
Qy 252 ---Glu---Phe--- 253
Db 9286 CTGGAGGTGTTGATGGTCCCAGCATTTGGAATTCGATCTCTTTGGAAAGTTCTGTGTGTTCC 9345
Qy 254 ---Gln--- 254
Db 9346 ACGCGTCCACAAACTGTTAAGAGCACCATAAGCAGCCTGACCTGTGTTCAGACAGAT 9405
Qy 255 ---Trp--- 255
Db 9406 TCTTCTCAACACAGAGAGGTTGGAAATAATTTTCCGGAGACAATAGGGCCACAGCAG 9465
Qy 256 ---Tyr---LysAsp---AspLys 260
Db 9466 GGATGTGGTGATACCTGACCGAGGACACACAGAGCTTTGTGTCTCTGATTTCTGATTCG 9525
Qy 261 ---Arg---LeuIle--- 263
Db 9526 AATGGACGTATGACAAAGGTTCTCAGTGCATATGGTACATAGTTGCACCTGAAACAAA 9585
Qy 264 ---GluGlyLys---LysGly--- 268
Db 9586 CTGGTTAAGCTCACCTTCAATGTGTTCCTCTGGAGGAGCCATCTGTCAGCTGGAGCTGC 9645
Qy 269 Val---LysValGlu---Asn--- 273
Db 9645 GTCTATGATTAATGTGCAGATAGCAGATGGCGCAACATAACTCATATTTAGTGGAAAA 9705
Qy 274 ---Arg---ProPheLeuSerLys---LeuIlePhe--- 282
Db 9705 TTCTGTGCTCCGTATGCTGCTGCCCATTTATCTCTCCGGTACTTCTTACGTTTTCAG 9765
Qy 283 ---PheAsn---Val--- 285
Db 9765 TTTGTCTCTGAGTAACTGTTGAATGAGGGGATTTAATGCAACATATACCTTTTGTGGAC 9825
Qy 285 ---SerGluHis 288
Db 9826 ATGCCTTGGGGGAAACATATAACCAACCTCGACACCTCAAAATCGCTCATCCTCAT 9885
Qy 288 --- 288
Db 9886 TTATCCAAATCGGAGCGCCATCTTCCACCTGTACTTGGGTCTATCGCAGCTCCGCCACAG 9945
Qy 289 ---Asp--- 289
Db 9946 CAGCAGGTTCAAGTAACCTGTGTGGGACTTACAGTGTGCCCTCACAAAGACTGTCTCAAAAGC 10005

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QY 290 Tyr-----Gly 291
Db 10006 TACTTTAGAACTTCAGGATTCAGTACAGACTGGTGGAAACCGGGTCACTAGTCTCTCGCGT 10065
QY 292 --AenTyrThr-----294
Db 10066 GCGAACTATACAACTTCCAGAGTGTTCACCTCAATGAGCACTGGCGGTGTCTGTTTTTC 10125
QY 295 -----Cys-----ValAl 297
Db 10126 AAGCTCGAGTTATAAACAAGAACTCGCAAGTGAATTCCTCTATCAGATTGCAGATTGC 10185
QY 297 aSer---Aen-----Lys-----LeuGly-----302
Db 10186 AACAGAGATACAAACCAACGTTTGGCAATCTGAAGAGTCTCTGGTGGCTCAGAACTAT 10245
QY 302 -----302
Db 10246 GACATAACCTGGACTGCACCATCATCTCTCAGAGCCCGGAGACCAAGCACTTCCTC 10305
QY 302 -----302
Db 10306 TTTTCTATTGGTTTCAGCTGGAAGATTCAAGACAATGCATGAATGATTTCTTGGAGTA 10365
QY 303 -----His-----303
Db 10366 AGAAACGGCGGAGCAGCAGCACCCTCACCAGCTGTTGACAAGTACTGTAGCAACCTGTCGCC 10425
QY 304 -----ThrAsn-----Ala-----307
Db 10426 AACCGGTCTTCTCTCAGAGCAACGAAGTGTATCTGCACATTTTCAGCGACCACTCAGTC 10485
QY 307 r-----IleMet-----LeuPheGlyPro-----Gly-----314
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QY 315 ---Ala-----ValSerGlu-----ValSer-----320
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QY 327 -----Ala-----Gly-----CysVal-----Tr 331
Db 10846 GGGTTTGAATAATGTGGAGCAGCTGAATCAGGAGAGCTGTGTATACCCAGGACTCTG 10905
QY 331 p-----Leu-----LeuPro-----334
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QY 335 -----Leu-----336
Db 10966 CGTCTCTGCTGCTCATCAACATGAGTCTGAGCTTCTTACAGCCTTGACGAGAAAGTG 11025
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QY 338 -----Leu-----HisLeuLeu-----LeuLys-----343
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QY 344 -----Phe 344
Db 11146 TTATCTGGCACATTTGATGACGGTTTT 11173
RESULT 24
US-09-873-404-3/c
; Sequence 3, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(63588)
; OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3
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Alignment Scores:
Pred. No.: 6.63e-22 Length: 63588
Score: 1717.20 Matches: 303
Percent Similarity: 9.50% Conservatives: 34
Best Local Similarity: 8.63% Mismatches: 4
Query Match: 71.31% Indels: 3168
DB: 242

US-10-017-084a-523 (1-344) x US-09-873-404-3 (1-63588)

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QY 3 -----ThrIle-----4
Db 46928 TCATCCAGACCACTCTGGGCGCAGAGAGGCATCTGAGTTTTTAAAGTTCTGGTAAAA 46869
QY 5 -----Gln-----5
Db 46868 GCGGTGGCTCATGCTTATAATCCAGCATTTTAGGAGCGGAGGCTGGTGATCAGAG 46809
QY 6 -----Pro-----6
Db 46808 GTCAGAGATAAAGACCCTCTGSCCAACATGTGAAATCTCTCTACTAAAAATACA 46749
QY 7 Lys-----Met-----8
Db 46748 AATAATAGTGGGCATGGTGGCGCATGCCCTGTAGTCCCAGCTACTCGGAGCGCTGAAGCA 46689
QY 9 -----His---Asn-----10
Db 46688 GGAATCACTTGAACCCAGGAGCAGACACTGCAGTGGCCAGATCGCACGACTGCAC 46629
QY 11 -----Ser-----11
Db 46628 CCAACTGGCGCAGAGTGAAGTCCGTCTCTAGAAAAAAGTTCCCTACGTG 46569
QY 11 -----11
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QY 14 Trp----- 14
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QY 14 ---- 14
Db 46388 TTTAACAACAATTATACACAGTCAACAGATGGTCTGAGTGAAGCTACTT 46329
QY 15 ----AlaIle----- 16
Db 46328 GGCTGATGCGGATCAATGATGAATGGCTGGACAGAACCTTTTATAGCTCCTTTTCC 46269
QY 16 ---- 16
Db 46268 CCGCCACAGCTTCAGTATTTCCCAATCTTCTCCATAGCCTCTGTAGAAATGTCTGAT 46209
QY 17 ----Phe-----Thr----- 18
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QY 19 ----Gly---LeuAlaIleLeu-----CysLeu 25
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QY 25 ---- 25
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QY 26 Phe-----GlnGly-----Val-----ProVal 31
Db 46028 TTTTAGTAGACAGAGGTTTCACTGTGTAGCAGGATGATCTCGATCTCCCGACT--- 45972
QY 32 Arg-----Ser---GlyAsp----- 35
Db 45971 CGTGATCCGCCACCTCAGCCTCCCAAGTGTGGGATTTACAGGCGTGAGCTACCGCGC 45912
QY 36 AlaThr-----Phe-----Pro----- 39
Db 45911 CTGACCAATGTCTGCTATCACTTTTTCAGGGCTCAGGCTGCCATCCAGATCAGCCTT 45852
QY 40 ----LysAla----- 41
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QY 42 ----Met--- 42
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QY 42 ---- 42
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QY 43 ----Asp-----Asn----- 44
Db 45611 CACCTACAGGCTTACTCTATGATTTTATGTTTATACATGTCTCGTCATTTCCAAACATTTA 45552
QY 45 ----ValThr-----Val----- 47
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QY 48 ----Arg----- 48
Db 45491 GGACAGGGCTCCCTCTGTGTGCCAGGCTGGAGTGCAGTGGGAAAATCACAGTTCCACAGC 45432
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QY 53 ----Ala--- 53
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QY 54 ----ThrLeu 55
Db 45251 ATTACAGGCATGAACATGATAGTAGGGTTTGTAGATCAGATTTTCAATTTTACTTTA 45192
QY 56 ----Arg-----Cys-----ThrIle----- 59
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QY 59 ---- 59
Db 45131 CTCACCTGCAGCCTTTAGCTCCTAGCTCAAGCAATCCTTCTGCTTTAGCCTCCCAAGTAGC 45072
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Db 44891 GGCTCTCAAACTCTAGGCTCAAGCAATCCTCCACCTCAGCCTTTCAAATTCGTGGATT 44832
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Db 44831 ACAGCATGAGTACCGTGCAGCCTAGAGTACAGATTTAAATTAATTTTCGTCTGCTTTG 44772
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QY 73 ----

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QY	193	Arg-----	193
Db	40934	CGGGCCAGGTGCAGTGGCTCAGTCTGTGTAAACCCAGCACTTTGGGAGGCCTAGTGGGTG	40875
QY	193	-----	193
Db	40874	GATCACCCGAGATCAGGAGTTGAGNACCAAGCTGGACACATGGTGAACCCCTGTCTCTA	40815
QY	193	-----Ser-----	193
Db	40814	CTAAAAATACAGAAATTAGCTGGGGGTGGTGGCGCCTGTATATCCAGCTACTCAGG	40755
QY	194	-----Glu-----	194
Db	40754	AGGCTGGGGAAGAGAAATTGCTTGAACCTGGGAGGAGGTTGCAGTGAAGCCAGATCA	40695
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QY	199	-----	198
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QY	199	-----Tyr-----GluCysSerAla	203
Db	40454	TGAGCTTCAAAATTTCTGTAAGTACTCAGCAGGCCTTAGAAAAATAAGAAATGTTCACT	40395
QY	204	-----SerAsn-----	205
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Db	40214	CAAGTGGGATACAGSAGAGGATTAACAGAAAAATATTTCTATCCAGTGATTTTCTTC	40155
QY	206	-----	206
Db	40154	AGGACAAGATTCAGTCTTCCATCTCTATAATATGTTGGGGAGGAAAAACAGACCCAC	40095
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QY 216 -----Lys-----ValThrVal-----Asn----- 220
Db 39914 TCTGCTAAAAAATTAAGTGGGGGTGGTGGTGGCACCTGTATCCAGCTACTGGGA 39855
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Db 39854 GGCTGACGAGGAGCAGAGGTTGACGTAAGCCAAATCGCACCTGCACTCCAGCGTG 39795
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Db 39794 AGTCAGAGTGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAA 39735
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Db 39734 AGAATGCTCATATCTGTTCTCGCACCACTACTGAGCTCCCTGAGAGCAGAAATGTGT 39675
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Db 39554 AACAAATTTCAAGTTTATCTACATTTATATGATCTTTTTTTTGGCAGAAATTTCTGTGA 39495
QY 224 -----Tyr-----IleSer----- 226
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QY 227 -----Glu-----AlaLys----- 229
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QY 230 -----GlyThr-----Gly 232
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QY 240 -----Thr-----Leu-----Gln-----Cys----- 243
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QY 305 Asn-----AlaSer-----Ile-----MetLeuPhe----- 311
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QY 312 -----Gly----- 312
Db 37334 TGGAAATRAAACAAATCTTTCTAACAAAAAAGAAAGAGCGTGGGAATAGTGG 37275
QY 313 -----Pro-----GlyAlaValSer-----GluVal 319
Db 37274 CTCTTGCTGTAGTCCAGCACTTTAGGAGGCCAAGGCAGGTGGA--TCACATGAGGTC 37218
QY 320 Ser-----Asn----- 321
Db 37217 AGTGGCTGCTGGTAGAGGGTACCTGAGATTTGAAGAACCACAACTAACCAAGCAGGTATA 37158
QY 322 -----GlyThr-----Ser 324
Db 37157 GGGCTGACATAGAAGAAGGACTACATGCGCAGCATGGTGGCTGCTGCTGTAATCC 37098
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Db 37097 CAGCACTTTGGAGGCTGAGCGGGCGAGATCACCTGAGTCAAGAGTTCAAGATCAGGTT 37038
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Db 36917 GGCAGAGGTTGAGTGAGTGTAGATTTGCCCCAGCACTCTAGCCCTAGGCATCAGAGTGA 36858
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Db 36857 GACTGCTACAAAAGCAACAAAGAAAGAGTCAAGGAATATGTGTTAAATGAAG 36798
QY 330 ValTrp-----LeuLeu----- 333
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QY 333 ----- 333
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QY 334 -----Pro----- 334

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QY 335 Leu-----LeuVal----- 338
Db 36617 CTTGAGGAATAGGTGATATAACTTTGGTTTGTGGCTCTCCTCCTCAGATATCAAGTTGAG 36558
QY 339 -----His----- 342
Db 36557 CATATAATAATCAATAATGTCACACAGACAGCAATTTTGGGTCTTCTCTATCATTTT 36498
QY 343 -----Lys-----Phe 344
Db 36497 TCTGAAGAAACAGAGGGGATGTTT 36471
RESULT 25
US-09-453-702B-242
; Sequence 242, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31880
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-702B-242
Alignment Scores:
Pred. No.: 3,97e-23 Length: 31880
Score: 1714.90 Matches: 304
Percent Similarity: 11.31% Conservative: 34
Best Local Similarity: 10.17% Mismatches: 3
Query Match: 71.22% Indels: 2648
DB: 4 Gaps: 256
US-10-017-084A-523 (1-344) x US-09-453-702B-242 (1-31880)

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Qy	61	-----Asn-----	64	-----Val-----Thr----	
Db	20498	TTAAAGTTTGTATGGAACACATCTGGCCACCGTTCTCGATTAAATAGTATCGCACTCAT	20557		
Qy	65	-----ArgVal-----	68	-----AlaTrp-----	
Db	20558	GAGCTAGATTATTTGCTCGTCTATATGACAGGAAGAAACCCAGCCTGGCAGGCACGT	20617		
Qy	69	-----Leu-----	69	-----	
Db	20618	TTGCCAGCCTTACATGCTAAACAACTTGTGTCTGTACTTGGAAAAAGTTTGTAAATCAGCG	20677		
Qy	70	AsnArg-----SerThrIleLeu-----Tyr	76		
Db	20678	AATGATTTAGTGTATTTGCAGGGCGAGTATTTTCAACGGTTATCTTCGATCAACAACATAT	20737		
Qy	77	Ala-----	77	-----	
Db	20738	GCTCAGAGGATGGGACAATTTACGGCAGACTCAATTCCTCAAGATTCATCAATGG	20797		
Qy	78	-----Gly-----	78	-----	
Db	20798	GTACTGTCTGGCCCTCATTTCTTGTGTGGAGCGGCTTCTACAGACTCCGGCGAAAAAC	20857		
Qy	78	-----	78	-----	
Db	20858	TGTACGTTAAACAGCGAATTATGACTGCCTGGAGTTGCTAACTCTGCCTGACGACTATCTG	20917		
Qy	79	-----Asn-----Asp-----Lys----	81		
Db	20918	CCGGCAGCTAACTACATTCGGCGATGTGATGCACAGGAGTATGCAAAACGTACTCCATGC	20977		
Qy	82	-----Trp-----	82	-----	
Db	20978	GTTACATGGACTGAACCTGCTGAAGATGAACCGAAGAGGTAAACAGATTATTCGCTTA	21037		
Qy	82	-----	82	-----	
Db	21038	GCTATCAGAGCCATGTTGGCTCAATCGGGGGAACGACACTAAATTAGTGTATTATCCG	21097		
Qy	82	-----	82	-----	
Db	21093	CCGAAATAAGTCACATGAACCGCAGTACGTTCTTACTGCTATAGCTCAGAAATCTGTTA	21157		
Qy	83	-----Cys-----	83	-----	
Db	21153	CTCGAACATTCAGGTATGTTTTTTTCTTACCTTTTGATTTTATTTGTAATCTACTGGC	21217		
Qy	84	-----LeuAsp-----ProArg-----	87		
Db	21218	AAGGCAACTTACATCAGATGCTTGATGTTTCTCATACGTATTATTCAATCCGAGACAA	21277		
Qy	88	-----Val-----ValLeu-----	90	-----	
Db	21278	AAGGCATTTATTAATGCTTAGTATATCAATAAATCTGTAAAATGATGATATGCTGGC	21337		
Qy	91	Leu-----Ser-----AsnThrGln-----	95		
Db	21338	CTTTGGCAATCTGCTACACCCGACCTTCAACACCCAGCGTTGGAGCGGGATCTCCCG	21397		
Qy	96	-----Thr-----Gln-----	97	-----	

Db 21398 CAGCTCCCCAGGATTTCTTCCGCAAACTGACCCAGAGTGGCAGCGTAATCGCTTTA 21457
Qy 98 -----TyrSer-----Ile----- 100
Db 21458 CGCTCTGACTACAGTCTGTCAGGCGCTGTCGAAATCGACGTATTGGTGGCGCAGCG 21517
Qy 101 -----Glu-----Ile----- 102
Db 21518 CTGGGGTTAACTCTCGAAGAGCTGCTTACCATTATTCGCGTTTCAGTTCCCGGTGATGCGC 21577
Qy 103 -----Gln----- 103
Db 21578 CAGTACGAGCGGATACCTGCTAGCATCAAAACGGTCGCAATTATCTTTACCCCAAGCAAA 21637
Qy 103 ----- 103
Db 21638 GGGCTGGTGGCGTTGGCTTTCCTCGCAGCGCGTAAAGCTGACCTGAAAAACGGCTTT 21697
Qy 104 -----AsnValAsp----- 106
Db 21698 GTCTTTAACTGACAGCCCGGAGTGAGCCGGCGGTGACTGTCACCGATCAAGCTATCGGT 21757
Qy 107 -----Val-----Tyr----- 108
Db 21758 TGGGATGATGCAAAACATCTTAAACCGGTACCGTCAGCGTCACCTTTGATGATTATACC 21817
Qy 109 -----AspGluGly----- 111
Db 21818 CGCAGCGAAGAGTGAGCGCGTACCGTCACCTGCGAGGCTCCGTTTATCAAGCCAGAT 21877
Qy 111 ----- 111
Db 21878 CGCGAAGATGACTACAAAGTGGCTGGCGTCTTTGGCAAGATGAAGAGCGCGCTGA 21937
Qy 112 -----Pro-----Tyr----- 113
Db 21938 TGTGTCCGTCCGTTGTCAGTGGCAGGTCCGCGACAGCGTTGCGGCTTTTACGGGCG 21997
Qy 114 -----Thr-----Cys-----SerVal-----Gln----- 118
Db 21998 CGTTCCCGCTAAACAGCCGCTGTTTAAACGGTGAGATTAACGATATGTCATGCTGG 22057
Qy 119 -----Thr-----AspAsnHis-----Pro----- 123
Db 22058 AGCAATTTCTGGCCAGCGCGAAACGCTGCTGAAAGGAC---CATACCTTCGCGCCAGT 22114
Qy 124 -----Lys-----Thr----- 126
Db 22115 TGCCGTTTCGTAAAAGTGACTTACCGCTGAAATTTTTCCTTAATCTGACGCTGCCGTTCC 22174
Qy 127 -----ArgVal-----HisLeu----- 130
Db 22175 CGCGCAGCGCATCAGGCCCGGCGATTTACGCTCTGGAAAGCGACGCGCCACAGCCGA 22234
Qy 131 -----Ile-----Val----- 132
Db 22235 CGCTGTCGCAACCGTACCGCTCCGCTCGGTAAACAGATGTTTATGTTCCGCTGTCTCA 22294
Qy 132 ----- 132
Db 22295 ACCACTGCGCGGCGCGTCAAAAGCGGGGTTAAAGCGATTATCATCTACCGATGAACG 22354
Qy 133 -----Gln-----ValSerProLys-----Ile----- 138
Db 22355 CCCTGGCAACCGATCAGGCCAGCCGCTTTCGCCAAACCAATCGCCAGCGATCCACAACCTGC 22414
Qy 138 ----- 138
Db 22415 ATGCAAGGTGACCTGCGGCTGTTTGTGCGGACAGCGAAATCGAACCCAGCAAAAAA 22474
Qy 139 -----Val----- 139
Db 22475 TGTGCGCAAAAAAGGTGATTACCTGTAAGCACACGCTCGCGGAAAGCGCGCGGACATCC 22534

Qy 140 -----Glu-----IleSer----- 142
Db 22535 TGTGTACCAACTACAAAATGCTCGACTACTGCTGATGCGCCCTGGCGATCAGCCGCTCT 22594
Qy 143 -----Ser----- 143
Db 22595 GGGTTTAAACACAGCCCGGTTTCATTGCGTTTACTGTCGTGATGAATTCATACGTTTG 22654
Qy 144 -----AspIle-----SerIle----- 147
Db 22655 ATGGCGCGCAAGGGTGGGATCTGGCGCTGCTGGTCGACGTTTGAAGCATCACATAGTG 22714
Qy 148 -----AsnGlu-----Gly-----Asn----- 151
Db 22715 TGGATAACCAAGATTCGCTCGCGGACATCAGCTACCGTCGCGGACGAACTGGGCG 22774
Qy 152 Asn-----Ile-----SerLeu----- 155
Db 22775 AACTGCTGATTACGCAAAAACAATCTTTGACCAGCGGTTTACCGATGACGCGTTATTTC 22834
Qy 156 -----ThrCys-----IleAla-----Thr----- 160
Db 22835 GCGAAGATCGTACACGCGCAGCGAGTACTTGCAGAAATTACGCCATTGCGTACAGTCAGT 22894
Qy 161 -----GlyArg-----Pro----- 163
Db 22895 ATCCGGGCGCGAGGTGCGTTCGGCCCTGGAGCCCGCAGAGTTACGCTACCCCGTAGCGT 22954
Qy 164 -----Glu-----ProThrValThr----- 168
Db 22955 ATCTTAAAGGCAAAATCCCTTTGTGTTCCCGCAGACGAGTTCGCACTCCCGGACGATC 23014
Qy 163 TrpArg-----His----- 171
Db 23015 TGGAGAGCGACGACGGCGGTGAAAAGCGTATTTGCGCTGGGGTCACTGTTCACGCGCCACA 23074
Qy 171 ----- 171
Db 23075 GCGTGATGATGCTTACTTCATGATCTGCAAGGCGGATCTCTCTGAACGAGAGTGTCT 23134
Qy 172 -----IleSer-----Pro-----Lys 175
Db 23135 TGGAAAATCTCCAGTCTATGCTGGCAGAAAGCGCGACCATGTCGCGACGCGTGTGCAA 23194
Qy 176 Ala----- 176
Db 23195 GCATTCGGCACTGATCGCGCAGGACGCTCTCGAAGTACCGGAAACGGAACACGATCGGC 23254
Qy 177 -----Val----- 177
Db 23255 AAAAAGCTCTCCAGCGAAGAAAGCGGTCGCGTGTGCTGCGGTTTGTGCACTGCGCTCC 23314
Qy 178 -----GlyPheValSer----- 181
Db 23315 AGTTGTGCTCTGTCGAG-ATGCGTGTCTGTCGCCAGCGTGGCGGAAAAACGCCGCGACTG 23373
Qy 182 -----GluAsp-----Glu-----Tyr----- 185
Db 23374 GTGTTTCCCGATGATGTGGCGGTGGAAAGATCGCGAACAATTTTGGCGGTTATCCACTGC 23433
Qy 186 -----LeuGlu 187
Db 23434 CGTGACTGCCACGCAACTGCTGGCGCAGCTGCGTTCATGGGCAAGCGTTTCAGTTGGAA 23493
Qy 188 -----Ile-----Gln-----Gly-----Ile----- 191
Db 23494 ACAGACTCGACCGCATTTTATCGCCAGTCTTTTGAAGAAAGGCGCTCCATCGTCTTGTCT 23553
Qy 192 -----Thr----- 192
Db 23554 TTCCCGGATAAACGNAAGGCGTTCAGTGGCGGCAACCCAGAAACTGTGTCTTACCTGT 23613

Qy 193 -----ArgGluGlnSer-----Gly----- 197
Db 23614 CTGAACGTAACCGA-----CAGTCAGCGCTCAGTGTGGACATTCGCGGTTCATACGGAACGTG 23670
Qy 198 -----Lys----- 200
Db 23671 TTGCAGGTACTGATCCCGGATATGCTCAAGAGCGGTAAAGACGAGCTGGAGTTTGCTAAT 23730
Qy 201 -----Cys----- 201
Db 23731 GAATGCCGCTACTGCAACAGCAAGAGGGGATTCGATTCTGGGTCAACGGCTGCCAGT 23790
Qy 202 -----SerAla----- 205
Db 23791 CTGTCCGCGGTGATGATCCAGCTTTATGGCAGCCGCGCATCGTCCAGCTTCTTACTGCCCGT 23850
Qy 206 -----Asp-----Val-----AlaAla----- 209
Db 23851 ATTACGTTTTCTGACTCGGTACAGAGCGCGCGCATCGTCCAGCTTCTTACTGCCCGT 23910
Qy 210 -----Pro-----Val----- 211
Db 23911 ACCTGCCGCTGATGATTCGTGGGCAATCGCCAGTGTCTTAGCGAAGAAAGACATTA 23970
Qy 212 -----Val-----Arg-----Arg----- 214
Db 23971 CCCTGGATCGTTCCGGCGCGGTGTTGCGCAACAAACGCGTGAACGTTCACCGGACGAT 24030
Qy 215 -----Val----- 215
Db 24031 GCTCATTTTCAGCAAAACGTTCATCGCACCACCAATATGAGTGGCTGGAATGATATCAGACG 24090
Qy 216 -----Lys----- 216
Db 24091 CTGAATAATGAAGCAAACTGGCGGAGAACTCCGATCTGCGGAGCTGGTTCCCTGCCG 24150
Qy 217 -----Val----- 217
Db 24151 CTCGACTGGAGGTGTACAGCAATTTACCTCGCGCGCGTATCGGAGTATCGGAGTGGAA 24210
Qy 218 -----Thr-----Val-----Asn----- 220
Db 24211 GCCACCGGTTATGCCGTTCCGCGAGTGGATAAAGATCGCTTCATCCGCAATACCGCC 24270
Qy 220 ----- 220
Db 24271 CTGCATCAACAGCTTTGTGAAGAGCTGGGTGATGAGATGCTGGTGTGAGCGTTCGAGCAG 24330
Qy 220 ----- 220
Db 24331 GTAGCGCACTCGCGCTGGGGTTATCTGGTATCAACGCGCAGCGCGGCGCTTATGCAAT 24390
Qy 220 ----- 220
Db 24391 CCGCGGTTTGAAGTTATCGCGGTGATGCGCAGCTTTATGATGACGCAAAAGAGCGT 24450
Qy 221 -----Tyr-----Pro----- 222
Db 24451 ACCTCGCGTATATGCTTCTATCGGTTCGAAAAACGCGTAAACCGGCTTATGCTGCTTT 24510
Qy 223 -----Pro-----Tyr----- 224
Db 24511 GAAAAAATTAATGTTTCCATCGCTGATTGGCGGAAGTCTAACCCGAGTTGTTATCAG 24570
Qy 225 -----IleSer-----Glu 227
Db 24571 CATTGGATCAATTCGACCGCTGAGTAACGCAATAATCTGTTTATCAGTAGCGTTTCGGAA 24630
Qy 228 -----Ala-----Lys-----Gly----- 230
Db 24631 ACAGTGTACGCGCTGTTTACGGCGTGAATAATAGCGGAGTAGTAAAGATTTTGAC 24690
Qy 231 Thr -----Gly-----ValPro-----ValGly----- 236

Db 24691 ACCAAAGGGCGTGAAGCTCGGACTGCTCGCTTCGGCGCTGGTGGAGCCGTGACGTC 24750
Qy 237 -----Gln-----Lys-----Gly----- 239
Db 24751 GTTCAGCTTAATTTGCTCATGTTGCCGTGAGGTGTCCGGCTCCGGCCGATCAAGGCTGG 24810
Qy 240 -----ThrLeuGlnCysGlu----- 244
Db 24811 CAGTGGGTAAATGCGGCTTGTCTCTCTTTACGTGTGAAGGTCTGTACCAAGAGTCGAC 24870
Qy 245 -----Ala----- 245
Db 24871 AATACGGCAGCTGGCGTTGGGAGAACATGACATCGCGCGGTACAGGGCGGAGAACAC 24930
Qy 245 ----- 245
Db 24931 ACGGGCTCTTAGCGTGAAGATCGGAAGTCAACGAAAAATCGTTCTACCGCGCAAC 24990
Qy 246 -----SerAla----- 247
Db 24991 CAACCGTGAATATCAACCTGTTGTCCGCAACACACGACGCTGGAGATGGGTATTGACGTT 25050
Qy 248 -----ValPro----- 249
Db 25051 GGGGATCTTTCCACCGTTTACTCTGTTCTGTCCACCTGCTCAGGCCAACTACTTGCAG 25110
Qy 250 -----Ser-----AlaGlu----- 252
Db 25111 CGTATTGTCGCGCGCTCGTAAAGATGTAACGCTTAAACATTACCGTGGCAGAAAGG 25170
Qy 252 ----- 252
Db 25171 AACCCGACGATCAGTTTTTCTTTTGAAGAACCACTGGAGATGATGAGGGCCAGGTGCAG 25230
Qy 253 -----Phe-----Gln----- 254
Db 25231 GCTCTGGCGTCTTCTTAAATGCAACGGCTATCTCGAAGCCAGCTGCGCAGCTTTTGT 25290
Qy 255 -----Trp----- 255
Db 25291 ATGGATAACTGGGTGAAAAACCGGTGTACAGAAATCCGCTATCTGTAAAAACGTCAAACAG 25350
Qy 255 ----- 255
Db 25351 ATGCTGGATGAGTGGAGTTCGGCGTAAATCGGGTTTTTCGGTATTAACCTACTGCGATAT 25410
Qy 255 ----- 255
Db 25411 ATCGAACAGCATCATGCGGAGATTGCTCGCAATTTACGGCAATCTTCCCGATCTTGCC 25470
Qy 256 -----Tyr----- 256
Db 25471 GCAGAACTCCCAACAGCTGTTGTCTTATCTTCAGGGCGCGCAGGACAACTGTCGCTG 25530
Qy 257 -----Lys----- 257
Db 25531 GTGCAGCGTATCGAAGAGCGTTAAACTGCTGCTGGAGAGATCGCAATCTTTGGGCTCA 25590
Qy 258 -----Asp-----AspLys----- 260
Db 25591 CGCATCGATAAATCAAGCGCAGTATCGATAAATCGGAGAACGCGCGCGGATCAAAAC 25650
Qy 261 -----Arg-----Leu----- 262
Db 25651 TTTGATAGCGATATGCGGAGTTAACTTCGGAAACGCGAGCGCTGATGGCGCTGTCAAT 25710
Qy 263 -----Ile-----GluGly----- 265
Db 25711 CAATCAACATAGCAACACGCTGAATTTCTCTCAGGATGAGGTCTGCTCCCTAACATAC 25770
Qy 266 -----LysLysGly----- 268

QY 335 -----LeuLeu----- 336
Db 27991 GAGACTGATGAGAGTTGGGCTGAGATTATTGAGTTTGGCTTAATAAGCGCTGAAGAGATC 28050
QY 336 ----- 336
Db 28051 GCGTGTCTCAGTCTCATTCTCTCTCTGCGCGGACTCTCGGCTACGAATTCGAAAATGAT 28110
QY 337 -----Val-----Leu-----His---Le 340
Db 28111 GAAGGTGAATATTGGGAAGCGGATCTCGCTGGCCATCACAATAATGGCAATTTGATT 28170
QY 340 uLeu-----LeuLys-----Phe 344
Db 28171 ATTGATAATCAAGAAATTTATTC 28192

RESULT 26

US-09-453-702B-50
Sequence 50, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <unknown>
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38584
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 50:

QY 1 Met-----LysThr-----Ile-----Gln----- 5
Db 26158 ATGCAGCAATGCTGAGCGGTGTAAAGTTCCGCAATAACGTCGGCAACTTTGCGCGCTT 26217
QY 6 Pro-----LysMet----- 8
Db 26218 CTTTTCCATTAAACAACTTTTCGACGTAATCCCATGACACAGACAGATCAGGATCTCG 26277
QY 9 ---His----- 9
Db 26278 GCGCAGCCCGCGGATGTGCGCAGCGAGTCTGCGGGCTTCTGTGTAAGCAGCGCGAG 26337
QY 10 -----Asn----- 10
Db 26338 GGGGAAAGATATTTCCCTCGCTGAATATCTCCGGTGAGCCGAGCGTAATTTCCGTATG 26397
QY 11 Ser-----Ile-----Ser 13
Db 26398 TCGCGGAAGACTGGCTGCAGGCAGAAATGCAAGGTGAGATTGTGCGCTGCTCCACGC 26457
QY 14 -----Trp-----Ala----- 15
Db 26458 CACCCCGGTGTCTGCGCTGGCTGAGTGAGGCGGACCGCGGCTGCAGGTGAGAGTAT 26517
QY 16 -----Ile-----Phe----- 17
Db 26518 TTGCGTGTGTGCTGTGCTGCGGGGAGGATTCATTAAGTTCCGTGTGTGCGCATCTC 26577
QY 18 ThrGly----- 19
Db 26578 ACCGGGCGCGCTTTGAGCAGCGGGTGAGGACTGTTACACGCTGTTCCGGATGCTTAT 26637
QY 20 ---LeuAla----- 21
Db 26638 CATCTGGCGGGGATGAGATGCGGATTTTCATCGAGGATGACTGTGGTGGCTCACGCT 26697
QY 21 ----- 21
Db 26698 CAGAACTCTATCTCGATTAATCTGGAGGCCACAGGGCTGTATCAGGTGCGCTTGTATCA 26757
QY 22 Ala-----LeuCysLeuPheGlnGly-----ValPro----- 30
Db 26758 GCACAAACCGCGGATGTGCTGTGCTGTGTTT---GGTTTCATCGTGTGCGGATCATGCC 26814
QY 31 -----Val----- 31
Db 26815 GCCATTACTGTGTGATGGCGAGCTGCTGCACCATATTTCTTGAAACAACAGTGAACAA 26874
QY 31 ----- 31
Db 26875 GAGAGGTATACGCAAAATGGCAGGCGACACACTCCCTCTGGCGGTACCGGCGATGG 26934
QY 32 Arg---Ser-----Gly-----Asp-----Ala---ThrPhe----- 38
Db 26935 CGCGCATCTGCTTTACGGGATTTGCAACGATTTGGCGCGCGCATCCACCTTCGTGTAA 26994
QY 39 -----ProLys----- 40
Db 26995 AAACGGGGCGCAAGCCATCCGGGCGCTGGCCATGCGAGATCCCGCGTTTCTGTCAGAA 27054
QY 41 -----Ala-----MetAspAsn 44
Db 27055 TGAGCGAGCGGTGTATCTGTACGGATTGCGGGCGGTGATACAGGTGAAAATG---AAT 27111
QY 45 -----Val-----Thr----- 46
Db 27112 TATCTGCGGCTTTAATGAGCGGCTGGCAATGTGCGGTGATCCACATCGTGGCGCGCC 27171
QY 47 -----ValArg----- 48
Db 27172 TGGCGGGTGTAAAGTGGCGGTGTGTTTCAGGCGAGTGTGTTTCAGGCGGTGCGGTGATTGGG 27231

Alignment Scores:
Pred. No.: 9,06e-23 Length: 38584
Score: 1714.70 Matches: 297
Percent Similarity: 10.1% Conservatism: 37
Best local Similarity: 9.04% Mismatches: 7
Query Match: 71.21% Indels: 2943
DB: 4 Gaps: 246

US-10-017-084A-523 (1-344) x US-09-453-702B-50 (1-38584)

Qy 48 ----- 48
Db 27232 TGGCATGGTGAACCTGTGGGCTGGCTGGGGCGCGGCTGTATCGGGTATGTATGCAG 27291
Qy 49 GlnGly----- 51
Db 27292 CAGGGCCAGTATGATCCTCGGTGGTGTGGCGCAGATGTGGCACCAGAAAGCCAGAACTC 27351
Qy 52 -----SerAla-----Thr 54
Db 27352 CCGGTACACAGACAAACGGATAACGGCAACAAACAAACACCTATTCTCTCTCACTGGATAACA 27411
Qy 55 ---Leu---Arg-----CysThrIle----- 59
Db 27412 TGGTTCGCCAGGGCAATGTTCTGCCCGTTCTGTACGGTGAATGATCGGTGGATCACGTG 27471
Qy 59 ----- 59
Db 27472 TGGTTCCTCAGGAGATCAGCAGCGCAGACGAAGGGAGCGGTGTGAGTTGTGGTGAATTG 27531
Qy 60 -----Asp-----AsnArg----- 62
Db 27532 GTCGCTGATGCAAAATGTTTATGTGAACCGCCTCGGGCGGTGTTGTGTTTATGGAG 27591
Qy 63 -----Val-----Thr 64
Db 27592 CATGACGAATGGTAAGGAGCAGTAAGGGGCATACCCCGCGCAAGCAAGGACAACCC 27651
Qy 65 -----Arg-----Val 66
Db 27652 TGAAGTCCACGACGTGCTGAGTGTGATCGATGCCATCAGCAGGAGACCGATTGAAGTTC 27711
Qy 67 -----Ala----- 67
Db 27712 CGGTGATGGATTAAAGCGTGTCTCTGAACAGTACGCGGTGTGGACAGTGAAGGTA 27771
Qy 68 -----Trp----- 68
Db 27772 ATACCAACATCTCCGGTGTCAAGTGGTGTTCGGGCGCGGTGAGCAGGAGCAGACACCGC 27831
Qy 69 -----LeuAsn----- 70
Db 27832 CGGAGGGATTTCGAATCTCCGGTCTGAGACGGTGTGGTACGGAGTGAATACGACA 27891
Qy 71 ---ArgSer-----Thr---Ile-----Leu----- 75
Db 27892 CGCCGATACCCCGCACCATCACGTGCGCAACATCGATCGTCTGCGCTTTACTTTTCGGTG 27951
Qy 75 ----- 75
Db 27952 TGCAGGCACTCGGGAAACCACTCAAGGGGGACCGGNAATCCGTGCGAAGTCCCGCTGC 28011
Qy 76 -----Tyr----- 76
Db 28012 TGGTTCAGATACAGGTAAATGTGTGGTGTGGTGAACGAAAGACATCACCATTAAAGGCA 28071
Qy 76 ----- 76
Db 28072 AAACCACTGCGAGTATCTGGCTCGTGGTGTGGTGAATACCTGCGCGCGCCCGTTTA 28131
Qy 77 -----AlaGly----- 78
Db 28132 ATATCCGATGCGCAGGATGACCGCGGACAGCAGCAGCAGACCAAGCTCAGCAACAAACG 28191
Qy 78 ----- 78
Db 28192 CTCTGGTGGTCAACCGGAAATCATCCATGTGTGAACAGTGTACCCGACAGCAGCA 28251
Qy 78 ----- 78
Db 28252 CTGGTTGGCGTGCAGGTGGATCTCGAGCAGGTTTGGAGTGTGAGCGGTGAGCGGTAATTAT 28311
Qy 79 -----Asn----- 79

Db 28312 CATCTTCGGCGGCGCATTTCTGCAGGTGCGCTCAAACTATGATCCGGAACACGACTTAC 28371
Qy 80 -----Asp-----Lys-----TrpCysLeu 84
Db 28372 AGCGGCATCTGGGACGGAACGTTAAACCGGCATACAGCAACACATGSCCTGTGTCTG 28431
Qy 85 ---Asp-----ProArg-----Val 88
Db 28432 TGGGATATGCTGACCCACCCCGCTACCGCATGGGGAACGCTTGTGGTGGCGGATGTG 28491
Qy 89 -----ValLeu-----Leu-----Ser----- 92
Db 28492 GATAAATGGCGCTGTATGTCTCATCGCCAGTACTGCGACCACTCAGTACCGGACGCTTT 28551
Qy 93 -----Asn-----ThrGln----- 95
Db 28552 GCGGCACGAGCCGCGCATCACTGTATGCTACCTGACCAACGCGCAAGCGGTGG 28611
Qy 95 ----- 95
Db 28612 GATGTGCTCAGTGATTTCTGCTCGGGATGCGCTGTATGCCGTATGGAAACGCGGAGAG 28671
Qy 96 ---Thr-----Gln----- 97
Db 28672 CTGACGTTCTGTCAGGACCGCGCGTCCGATAGGTGTGGACCTATAACCGCAGTAATGTG 28731
Qy 93 -----TyrSer----- 99
Db 28732 GTGATCGCGGATGATGGCGCGCGTTCGCTACAGCTTTAGCGCCCTGAAAGACCGCAT 28791
Qy 100 -----IleGluIle----- 102
Db 28792 AATGCCGTTGAGGTGAATCTGGACTACCGGCACACGCTGGGAGACCGGCAGAGTT 28851
Qy 103 ---Gln-----AsnVal----- 105
Db 28852 GTGGAGGACACCGCAGGCCATTTGCCGTTTACGCTGTACGTCACGATGATGGATGCTTT 28911
Qy 105 ----- 105
Db 28912 GGCTGTACCACTCGGGGGCAGGCAACCGTCCGGGCTGTGGCTGATTAAACCGGAAGT 28971
Qy 105 ----- 105
Db 28972 CTGAAACGCGACGCGTGACTTCAGCGTGGCGCAGAGGGCTTCGCCATGTACCGGCG 29031
Qy 106 AspVal----- 107
Db 29032 GATGTCAATTGAATCTGNGANGCCGANTNTCGGGGATCAGCATCGGTGGGAGTGTCTN 29091
Qy 108 ---TyrAsp----- 109
Db 29092 GCGGTGAACAGCCAGACCCGCAACGTCAGCTTCGACNGTGAATCAAGTCCCATCTCC 29151
Qy 110 -----Glu----- 110
Db 29152 GGCACACGCTGATAAGCTGTGTGACGGAAGTGGCAATCCGTCAGCGTGGAGTTCAG 29211
Qy 111 ---Gly-----Pro-----Tyr 113
Db 29212 TCCGTCAACCGAGTGAAGGTAAAGTGAAGCGGGTTCTCGACGGTGTGTGTAATAC 29271
Qy 114 ---Thr-----Cys---Ser--- 116
Db 29272 AGCGTGTGGGGCTGAAGCTGCCGACCTCGCCAGCGCTGTTCGCTCGGTGAGTATC 29331
Qy 117 -----ValGln----- 118
Db 29332 CGTGAGAACGACGACGACGATGATCCATCTGCTGCGGTGAGCATGTGCGGAGAAAGAG 29391
Qy 119 ---ThrAspAsn----- 121
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Db 29392 GGCATCGTGATACGGGGCGCACTTTGACGGTGACCGAGCAGCACGGTGAATGGTGTG 29451
Qy 122 -----His----- 122
Db 29452 ACGCCGCCAGCGGTGCAGACACCTGACCGCGAAGTCTCCGACAGACCGGGGAATATCAG 29511
Qy 123 -----ProLys----- 124
Db 29512 GTGCTGGCGGATGGGACACGCCGGAAGTGTGAAGGTGTGAGCTTCCTGTCTGGCTG 29571
Qy 124 ----- 124
Db 29572 ACGTGGCAGCGGATGACGGCAGTACGGCTGGTACGACGGCCCGGACGACGGAAC 29631
Qy 125 -----Thr----- 125
Db 29632 ACATACCGCTTCACGACGTGGCGCTGGGGAACCTACAGGCTGACAGTCCGGCGGTAAAT 29691
Qy 126 -----Ser---ArgVal----- 128
Db 29692 GCGTGGGACAGCAGGGCGATCCGGCGTGGTATCGTTCCGGATTCGGCAGCGGACGCG 29751
Qy 129 -----HisLeu--- 130
Db 29752 CGCTCACAGATTGAGCTGACACCGGCTATTTTCAGATACGCCACCGCGCATCTTCGG 29811
Qy 131 -----Val 132
Db 29812 GTTTATGATCCGAGGTACAGTTTGATTTCTGTTCTCGGAACGGGATTCGGATATC 29871
Qy 133 ---GlnVal-----Ser 135
Db 29872 AGCAGGTTGAACACAGCGCGGCTTATCTTGGTACGGCGTGTACTGGATAGCCGCACT 29931
Qy 136 -----Pro----- 136
Db 29932 ATCAATATCAACCGGCCATGATTATTACTTTTATATCCGAGTGTGAACCGTGTGGC 29991
Qy 137 Lys-----Val-----Glu----- 140
Db 29992 AAATCGGCATTCGTGAGGCCGTGGTTCGGCGAGCGATGATGCGAAGTTTATCTGGAT 30051
Qy 141 -----Ile----- 141
Db 30052 TTTTTCAAAGGCAAGTAAACCAATCTCATCTCGGCAAGAGCTGCTGGAAAAAGTCGAT 30111
Qy 142 -----Ser----- 143
Db 30112 CTGACGGAGGATAACCCAGCAGACTGGATGAGTTTTCGAAAGATGGAGACGCTAAC 30171
Qy 144 -----Asp----- 144
Db 30172 GATAAATGAATGCCATGTGGGGCGTCAAAATGACAGACCAAGACGGCAACATAT 30231
Qy 145 -----Ile-----Ser----- 146
Db 30232 GTCGGGGTATTCGCTCAGCATGAGGACACGGAGGAGGCAAGCTGAGCCAGTTTCG 30291
Qy 147 -----Ile-----AsnGlu----- 149
Db 30292 GTTGCCGCAATCGTATCGCGTTTATGACCGGCAACGGGAATGAACGCCGATGTTT 30351
Qy 150 -----GlyAsn-----Asn----- 152
Db 30352 GTGGCGCAGGCAACAGATATTCATGAACGAGTGTTCCTGAAGCGCTGACGCCCC 30411
Qy 153 -----Ile-----SerLeuThr----- 156
Db 30412 ACCATTACAGCGGTGGAATCCACCGGTATTTTCCCTGACATCAGACGGAAGCTGACC 30471
Qy 156 ----- 156
Db 30472 GCTAAAAATGCGGATATCAGTGGCAGTGTGAATCGGAATCGGAACCTCGGGACGCTCAACACGTC 30531

Qy 157 -----Cys---Ile-----AlaThr----- 160
Db 30532 ACGTAAATGAAAACTGTACGATTAAAGGCGCATCTGGAGCGCACTCAGGTGAGAGTGAC 30591
Qy 160 ----- 160
Db 30592 TTCGTTAAAGCTGTATCCAAATCATTTCCGAAACAGGCTGGTACGTGGGGTAAACACGGA 30651
Qy 161 -----Gly-----Arg----- 162
Db 30652 ACACCAACCGGACCGGTTACAGTCACCATCAGCGATGATCAATACTTTGACCGTCAATC 30711
Qy 162 ----- 162
Db 30712 ATTTATCCGCCCATTAATCTTTTAACGGAATAGCGTATAGCGATCCGGAAAGTGTATAAC 30771
Qy 163 Pro----- 163
Db 30772 CCGGAGGTACAAGATACACGGGTTATGGTTTGAAGTTCCGAAAACCGGTGATTAAATC 30831
Qy 164 -----Glu-----Pro 165
Db 30832 GCATCCAGAGAACTAAAGGGCCATTCCCGGTAGCTACAGTGGCTTATTGATATGCG 30891
Qy 165 ----- 165
Db 30892 AGTGGCAGGGGAAGCGTCACTCTGGAGTTTAAAGTTTCCATAAAGGAATCAGCGGCA 30951
Qy 166 -----Thr---ValThr----- 168
Db 30952 GGTAATATCACCGACTGACGGTGTATGTGACCAAAAGACGGCTTCCGGCATCAGTATC 31011
Qy 167 -----TrpArg----- 170
Db 31012 CGTTGAAATATTTAACCCTAATAACGGCGCCAGAAATGCGGCTTTTATTGACGA 31071
Qy 170 ----- 170
Db 31072 AAATCGGAGGTAAATTATGCGTAAAGTTTGTGACGAATTTGTCCGAGCAATTTGTCT 31131
Qy 171 -----His-----Ile 172
Db 31132 GSCCGTATCCGTGTGCTGATGGCGCTCTGAGCATCAGTCCAGCTGAGCGCAGGATA 31191
Qy 173 Ser----- 173
Db 31192 TCTTCATGCCAGTACGACGCTCCCGCAGCGCATGATCTGAACGGGATTAACGTTGAATA 31251
Qy 174 Pro----- 174
Db 31252 CGTTATGAGTTTACGACACACTGGGGCTGATTACGTCCTTACGTTATGCAACGCGGA 31311
Qy 175 -----Lys----- 175
Db 31312 AGATGACAAAACCGCATTAACGATACCGGTGCGCATGAGGATACGTGCGTAAACCG 31371
Qy 176 -----AlaVal----- 177
Db 31372 CTGTTACGCTGATGCGAGGGCGCTCTGTGCGTGTGAATGATGTTTACGTTGCGTATGC 31431
Qy 178 ---Gly-----Phe----- 179
Db 31432 GATGCGGGTGTGCTTACAGCCGCTGTGCGACTTTTCCGGGGAATTTATTTCCGCGTAAC 31491
Qy 179 ----- 179
Db 31492 TGACAACAGAGGAAACGACGAGTGTCTGACCGGAAGTGAACGCTCGCTACAGCA 31551
Qy 179 ----- 179
Db 31552 CACATCTCTGCGGTGGGGGCTGGCGTGCAGTTTAAACCGACCGAATCAGTGGCGGTGA 31611

QY 179 ----- 179
Db 31612 TGTGCTTATGAAAGCTCCGGCAGCGGTGACTGCGCAGCTGACGGTTTCATCGTGGGTGT 31671
QY 179 ----- 179
Db 31672 CGGTTATAAATTTTGTATTAGTAACAACAGCGTTTATGACAGCCCGCGGTTTCAGCGCGGCT 31731
QY 179 ----- 179
Db 31732 TTTTGTGGANTGGGTATGGCAGCANTACAAATATCANGCGTCTGAAGANGGTGCGNGA 31791
QY 179 ----- 179
Db 31792 AAACCAATACAGAACTGCNCNTTCAACTGAAGCCAGAGCTAAACAGCACCANGGTGGTG 31851
QY 180 -----Val---SerGlu---Asp---Glu 184
31852 GTGAACACCGTGGCCTCTGAAATATCCGATGAGCGAGCGGCTTANAGNATGGACGTGCGAG 31911
QY 185 Tyr---Leu---Glu--- 187
31912 TATGGTCAGTACAGCTCACTCTGTTGGTGGAGGGATTCCCGCCATCATGCGCGGACC 31971
QY 188 Ile---Gln---Gly---Ilethr 192
31972 ATCTCGTGTATGAAGATTCTCAACCGGCTAGCTGAATGATTTCTCGGTGCCATGAGC 32031
QY 193 -----Arg---GluGln--- 195
32032 GAGGATGATGCCGTCGCGAGGCACTGCGTCTGTTTGAACAGATGGTGAAGAGCAGCG 32091
QY 196 -----Ser--- 196
32092 CGTCACGAGAGGCGGAAGAAGATGCCGAGAAGCAGACGCTCCCGAGGATGCC 32151
QY 197 Gly---Asp 198
32152 GGCATATCAGCCAGTAAGCGGGAAGCGAGCGCGCAAAATGCTGATACITTCAGCAGAGGAT 32211
QY 198 ----- 198
32212 GCATCGAGTCAGCCCGGCGGCGGAGAAAGTCAGCCTCTGCAAGAAGTCAGAGAA 32271
QY 199 -----Tyr--- 199
32272 CGGTCTCTGCTCAGCCTCTGAGGCGGCTCAAAAAGCCAGTGAAGTATCAAAAGTCA 32331
QY 200 -----GluCysSer---Ala---Ser---Asn--- 206
32332 ACAGATGCGGATTTGTCAAAAAGACCGGAGAAAGTCAGCGCGGTAATGTCAGCCAGGAT 32391
QY 206 ----- 206
32392 GCAACGACTCAACAGAAAAAGCCCGGATCAGCAGAAAGCGCACAGTCAGCGGAACA 32451
QY 207 -----ValAlaAla---Pro---ValVal--- 212
32452 AGCAGAATAGCGGCGGAAGACGCGGTAAACAGAAATTCACCGGTGGTGGGCGCTCCCGA 32511
QY 212 ----- 212
32512 CCAAGGGGGAACCGGTCCCGCGGTCCTCAGGGGCGGAAGGGAGATAAAGGAGAGCGT 32571
QY 213 -----Arg--- 213
32572 GGAGACACCGGTCCCGCAGGCGCAACCGGTGAACCGGGAACCGGGAGGATACAGGTCCG 32631
QY 214 -----Arg--- 214
32632 GCAGTCCGACGGGCGGAANGCNACANGGACANCGGGANAGACCGGTCTGACGGGA 32691
QY 215 -----Val--- 215

Db 32692 AATGCAAGTCCACAGGGTCCAAAGGGAGACACCCGGGGCAGCAGGCGCGCCACAG 32751
QY 215 -----Lys---Val--- 217
32752 GGACCGAAAGAGAGAAACAGGTGCGGCTGCGCGGTGGGGCAACCGGACCTCAGGGNGC 32811
QY 213 -----Thr---Val--- 219
32812 AAGGCGACCCCGGGGAGACACAAATACGGTTCCTGCTGGGGCCGATGAGAATTATTGAG 32871
QY 220 ---Asn---Tyr--- 221
32872 ACAAACAGCTATGGTGGTTCCTCGGGTACAGATGGTGGCTCATCACCGGACTGACCTTT 32931
QY 222 ---Pro--- 222
32932 CTTGACCCCAAGATGCCAGGATGTTAAGGGAAGTGGAGTGGGAGTATACAGGCAGA 32991
QY 223 ---Pro--- 223
32992 GGTGACGGCCATGCCAGGATGTTTGAAGGAAGCTTATGCAGAGCTGTGCGGTTCGGGAAA 33051
QY 223 ----- 223
33052 ACTGGAGATGACATGATATTTTGAAGAAAGCTTATGCAGAGCTGTGCGGTTCGGGAAA 33111
QY 224 -----Tyr---Ile--- 225
33112 GCATGATGACTGTGAAGAACGACGCTCACTTACAGACAAATTCGACATTCGGACTGGGACCGCAGA 33171
QY 226 ---Ser---Glu---Ala---LysGly--- 230
33172 CATCTGGAGTCAGATGAGAATGCAATTTATTCGGAGCAGCAGCAGGGTAAATCACACAGT 33231
QY 231 ---ThrGly---Val---Pro 234
33232 GGTGATCTGATGCAGATAAAAGCAGATACAGTGTGTGTAAGACCGCTGCAATCCT 33291
QY 235 ---ValGly---Gln---Lys 238
33292 GCCTGCTGACGGGACGCTGGGAAAAATATTGGCAAAATGAAGTAACCCGACAGCTTCACAAA 33351
QY 239 ---GlyThr---LeuGln---Cys--- 243
33352 ACCGGAGTCCGACTCCGGTTTGTGTATGTCCGGTGGATGTTGTAGGAAAGCAAA 33411
QY 244 ---Glu---Ala--- 245
33412 GATGGCAAAACTGCTGGAGGTTTGTGTGATGAGTATGCCAATATAATTAATAGATTAAAG 33471
QY 245 ----- 245
33472 AGTTAGTTGTGAAGAAATATGGATAAACAGGACGCAATGCTTTCACCGATAAGGACA 33531
QY 246 ---SerAla---Val---Pro---Ser---Ala 251
33532 ACTTTCATTAACACTCAGTAAATATAGTGCAGAGTTCACCTGTCAACCGTTTCTTTTGA 33591
QY 252 ---Glu---PheGlnTyr--- 255
33592 GGAAGGAATATGAGTTAAAGTTCATTGATGAAAAAAGCGCTATTCTTTTTCAGTGGTTT 33651
QY 256 ---TyrLys--- 257
33652 GAACCTAATCCTGAACGATATAAGAAAGATGAGGTTCCAAATAGTTAATACTAAGCAGCAT 33711
QY 257 ----- 257
33712 CCCTATTAGATAATGTCACAAAATGCGGAGGATAGAGAGTATCGTATGATAGGTATT 33771
QY 257 ----- 257


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Db 8179 GGTCTTTGGTCAGCAGAGCTGAGATGAGACATTGCTCAATGGCCCGAGTCGTTCTGATC 8120
Qy 67 ---Ala---TyrLeu---Asn-----70
|||
Db 8119 CAGCCCGTCATGCTTGGCTGCCACAGCGGAGGAGTGGCATCTCTTTAGCATCAGG 8060
Qy 71 Arg-----Ser-----ThrIleLeu-----Tyr-----76
|||
Db 8059 AGGAGGAAGATATTCACAAATCCGGCTTACTGTACTGCTCATAGAAAATCTCCATGAG 8000
Qy 77 ---Ala---GlyAsn---Asp-----Lys-----81
|||
Db 7999 CAGTCCAGGTAATGCTCCATTCAGATATTCAGAGAACACCTTGGTTACGGTT 7940
Qy 82 ---TyrCys-----LeuAsp-----85
|||
Db 7939 GTTTGGTGAATCAGGCACCCATCATGAATGAATAAATGGATGAATCAGCATTAGTGAG 7880
Qy 86 -----Pro-----86
|||
Db 7879 GTTTAGATCCACAGTGAATTAATCGACTACAAACCCCACTGAAATGGAGAGCCATTC 7820
Qy 87 ---Arg-----87
|||
Db 7819 CGAGGCCAGGCTCCACACTGTACTCAATTCCTCCGTTCCAGTCAAGCCAGTTCTG 7760
Qy 88 -----ValVal-----89
|||
Db 7759 ACTGGATGAGCTCGATTGAAGTTGTTTGGTTGGAAGAGAGGTCTCGGGGTC 7700
Qy 89 -----89
|||
Db 7699 ATCAGATACAGGCCACCCACCTGTTTCATCAGAGCCAGATTTCCTGGATGCATCCTCC 7640
Qy 89 -----89
|||
Db 7639 ATGGCCACTGCATGCTCTATGAGCCATCCCGATATAGACATTAATCTATTGCCCATGT 7580
Qy 90 ---LeuLeu---Ser-----Asn---Thr-----94
|||
Db 7579 CTGCTGCTTTCAAAGAGAGCTGGTTGATGATCCAAACGAAACGATGGCTTGGACCTGT 7520
Qy 95 -----Gln-----95
|||
Db 7519 ATAAGAGGAGAGCGAGTGAATCTAGTCCACTTGTGTAAGTGTCTGACACCCAGGAT 7460
Qy 96 -----Thr-----Gln-----Tyr-----98
|||
Db 7459 CCGTTGCAGATGATAGCGACTCATTCACATTGGTAGGCACACAGTCCCTTACCAATGG 7400
Qy 99 -----SerIleGluile-----Gln---Asn-----Val 105
|||
Db 7399 GTGCCATGACAATCC---AAGATCTACTGATGATTCCAAATTCATCGCATACAAGAGTC 7343
Qy 106 ---Asp-----ValTyr-----108
|||
Db 7342 TGTGACTGAGCAGGAGGAGCGAAGTCTATCTGTAGGAAGGAATCCTCATTCACGGCAAC 7283
Qy 109 -----Asp-----Glu-----110
|||
Db 7282 GTCTGTGCTGACCGTAACGGGTGCTGGCCCTTTTCAATGAAGACCGGCGATCACCAGT 7223
Qy 111 -----Gly-----ProTyr---Thr-----114
|||
Db 7222 AGAGCCACACAGGCGATCTTGGTGCTCTCTGGTGAAGACGCCATTTCTACTATCAAG 7163
Qy 115 ---CysSerVal-----Gln-----Thr-----119
|||
Db 7162 GGTGTGAATCATCTTCCAGACCGTATTAACAGAAATATTTCTCCAAATGAATCTG 7103
Qy 120 ---AspAsn-----121
|||
Db 7102 ATCGATAACCCAGGGGCTGTAGAGTGCCCATCTCTCAGAGGTTGCCACCGAGGCG 7043
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Qy 122 -----His-----122
|||
Db 7042 AGTAGAACCAAGACGGGCTTTCAAGGTATCTCCAGGGCAATGATACCTGCCACATGTCT 6983
Qy 123 -----Lys---Thr---SerArg---127
|||
Db 6982 GGAATTGCTGAAAAGGAACCTCTGGAAGAGACTCCACAGAGAGGCCACCGTTGAGAGATA 6923
Qy 128 -----Val-----His 129
|||
Db 6922 CTGTAGGACACGGGTTGACTCCTGGGGTCAGGAAGCCCTTTACCACATCCCACTCTCAT 6863
Qy 130 -----Leu---Ile---Val-----Gln 133
|||
Db 6862 GAAGAACTGCACAAATCTAGCATGTGATTAATCCAGGTCTCGTGTCTCAACATGCGCAA 6803
Qy 134 -----ValSer-----135
|||
Db 6802 GCCATCTTCATTGAAAAGAGAGGTGTGTTTCCACTAGAAAGGATTCACACTTTGAGATGG 6743
Qy 136 ---Pro-----LysIleVal---139
|||
Db 6742 TTTCCCACTCATTAATAAGAAATCTATCAGATCTAGCTGACCTTCGAAATCATCTTT 6683
Qy 140 Glu---Ile-----141
|||
Db 6682 GAGAAATCAGGATTTTGGTCTTATTTTACAGTTGGAACCTGAGTAGCCAGGGTCACA 6623
Qy 142 ---Ser---Ser---Asp-----IleSerIleAsnGlu---Gly 150
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Db 6622 TATACATTTGGTTCCATTGATACAGCTCCCTGTCTCCATTACACATCTCTCACATGGG 6563
Qy 151 Asn-----Asn---Ile---Ser 154
|||
Db 6562 ACCGATGATAGACATTAATCAATGGCCCATGTCTACTGGCTGAGAGCGGAGGTTAAATCC 6503
Qy 155 Leu-----Thr-----156
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Db 6502 CTGGTACCATCTGAACCGACAGATCCAAAGGTGACGTTCCCAAAGTGCAACGCTC 6443
Qy 157 -----CysIle-----158
|||
Db 6442 CTTCTCCAGCCCTCATGCTGCTCTGTCTAGTAGTGTCTGGGGTGTGCTCGGTGGA 6383
Qy 159 -----AlaThr-----Gly 161
|||
Db 6382 GCATTAAGAGCTGAGTGGTGTCTGTGTGTAGCAGAGGGGACAGAGAAGTGCAGGT 6323
Qy 162 ArgProGlu---Pro-----165
|||
Db 6322 CGCCCGAAGTCCCTTGAAATTCAGTCTCAGTGTCTGATCCGGGATGAGCTATCAGTGA 6263
Qy 166 Thr-----ValThr---168
|||
Db 6262 ACAGCAACGTTGATCTCAAATTGTATGATGGTGTCTCTTCAATTCACATTTAGTCAAGGT 6203
Qy 168 -----168
|||
Db 6202 GGTAAATGGAATGTCACCAACTTCATTTTGAAACAAACACCATAGCTGAATCTTCTTCAGG 6143
Qy 169 -----Tyr---Arg-----170
|||
Db 6142 TGCCTCTTTGAAGAAATATGACAAATAAGAACCGATGTACCACCGATAGAAAACCA 6083
Qy 171 -----His-----171
|||
Db 6082 ATTGTCTTCTGCGGCCCAAAATCAAATGTATCCAGAGCATCACAGGTTGTTTACATT 6023
Qy 172 IleSer-----173
|||
Db 6022 ATTTCATCGAATGAAGTCAATCAACATCCAGATTTCTTTTCTTACCGTTATTATA 5963
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QY 174 -----ProLys-----AlaVal-----Gly----- 178
Db 5962 AGSTTGCAGAGCTGTAATCTTGTAGCATTTGGTGGCAGTGTATGCCAAGGGAACATT 5903
QY 179 -----Phe-----Val-----SerGlu 182
Db 5902 GATCAAAAGTATATTCGTTGTTGAGGAAAGTAAATTCATCCATCAGGTGCCAAGTGAT 5943
QY 183 -----Asp-----Glu----- 184
Db 5842 TCCTCCACTGATGGAGAATTGTAACAGAAATAGAGTGAGATCTCTCTGGGGTACTTTTGGC 5783
QY 185 Tyr----- 185
Db 5782 TATAAATCTAAGTGAAACCTGGACATACATTTGTTGTACAAATAGATCTCTTGAAT 5723
QY 185 ----- 185
Db 5722 AAGCATCTTAGTCTTCCCTTTAAATATAGAGATGTTCCAGATTTGATGTTTCCACG 5663
QY 186 -----Leu----- 186
Db 5662 ATTCAATTCCTCTCTCTGCAACATACACTTCAGGCCAAAGTCCAGGATGTAATTTCCC 5603
QY 187 -----Gluile-----Gly----- 190
Db 5602 ATTGAATCGTCTTTAAGAAATCAGGGCAGAGGAAACAACAGGAAACAATAGGGTCCACC 5543
QY 191 -----IleThr----- 192
Db 5542 AAAGCCCGGTCAACACACAGCGTCCAGATCACAAATCCCTCGTCTGAGCACATCCA 5483
QY 192 ----- 192
Db 5482 AGGGCACCTGAGCGCCAGTACAAATTAATTCGCCAGGAATCAGCCCCCAGTGTGTA 5423
QY 193 -----Arg----- 193
Db 5422 GTTGGCTGAATCCATCTGAACCGGGTCTGGGAGAAATGGTGGAGTGGAGGTAGAC 5363
QY 194 -----Glu----- 194
Db 5362 AGTGATTCGGTTCCTCAATTCCTGAATCTTTCGAGGTGTAATTTGAACCTTCGTTGTAATG 5303
QY 195 GlnSer-----GlyAsp----- 198
Db 5302 CAGACAGCAATGGTTGAGGAAACACATCTTTCGGGTGACAAGATCCAGTCTTGCCTT 5243
QY 199 -----Tyr-----Glu----- 200
Db 5242 GTTCAGAGAACTACTGGAGCTGTACACTGTGGAGTTGCTGAAGGCTTGCTACAGCCCAT 5183
QY 201 -----Cys----- 201
Db 5182 GCTCATTTCAAACTGCAAAAGGTAGATGCTGACACATGAAAAATCCCAGGTCTCAGCATA 5123
QY 202 -----Ser-----AlaSer-----Asn 205
Db 5122 ACGAGTTTTCCTATGTTTTCAGTGAATATCAGAGCAGTATCCATAGAGACAGTCAAT 5063
QY 206 -----Asp-----Val-----Ala----- 208
Db 5062 ATCAACTTGACCTCTCTGGATTTCGATACCAAGTTGGCTTGCCTGCAAAATCTATAGAGCCATCAA 5003
QY 209 -----Ala----- 209
Db 5002 TTTGTCTTGAATCCAGTTTCAGAGCTGTCTATCTTATTAAGAAATCATCATCCAAAGC 4943
QY 209 ----- 209
Db 4942 CCACCTGGGCTGAATGCTTCCCATGTTGGGTGGCCATCCAAATGCGTTGAGGTGT 4883
QY 209 ----- 209

Db 4882 CTTCCGGTCTCTGTGGCAGGTCAATGGAATGATCTCTGGTTCAGGAAGGACATGAAGTC 4823
QY 210 -----ProValVal----- 212
Db 4822 CAACTCTCGAAGCAATGCCAGAGTATCCCATTTGTCATTTGATCTGAACATAAGCCC 4763
QY 212 ----- 212
Db 4762 TTCAATTTCTAGTTCTTGGTTTGTGATGCAGGTAATGCCCTGAAGTTTCTCTTCCAAATTTGTAT 4703
QY 213 -----Arg----- 213
Db 4702 ATAAATTTGAAACAAGTCTGATATTCTGTGTCTCCAGAGGACCGTCCGGGCTTCCCTTTT 4643
QY 214 -----Arg-----Valys-----Val-----ThrVal-----Asn 220
Db 4642 CCCAGGGCCATTGAAGTAGAGAGATTGCGATCGTTTAAGTGTTCACACAGCCAGTCCCAAC 4583
QY 221 -----Tyr-----Pro----- 222
Db 4582 CTGGGCACCTGTTATCTTGTACCAAGAGGGCTGAGCTTCCCTCAAACTATCGAAT 4523
QY 222 ----- 222
Db 4522 CTCAATTTGTTGGGACATTTGACACACAGATTTCTTGTGTCAGCAGTATATCCCGAGTC 4463
QY 223 -----Pro----- 223
Db 4462 ACAGAAACACACTCTCTGAATGTCAGTCCCTCCCTGCGCACTGCAAGTAACTGGGACAGGCTC 4403
QY 224 -----Ile----- 225
Db 4402 GGATATGTACACTCCATCTAAACCAATGGAGGACGTTTCTGTGAGTCTCTCTCTG 4343
QY 226 -----SerGlu-----Ala----- 228
Db 4342 GATCCATCGGAATCTGGTCTTGTGTCGTCAGAGACCTTGGAAATACAAATGGTGTATCT 4283
QY 229 -----Lys-----Gly-----Thr-----GlyVal 233
Db 4282 TGTCCATTTCTCAAAGTCCCTGTGTGATACATGGTGGCTCACTTAGTCTCTGAGATT 4223
QY 234 -----Pro----- 234
Db 4222 TCCTTGGCATCTTTCCTGTCAGAGCGGGTAACAGCTTCTTCCAGAAACCCAGGA 4163
QY 234 ----- 234
Db 4162 CATACAGCATCATGAGAGTACTGAAGAAGAACTGGAGCAGTACTGCTGATTTGATTGGC 4103
QY 235 -----Val-----GlyGln----- 237
Db 4102 ACAACCTATGTTAGTTGAACTGTAGCACATATCCAGGTTTCAGGGTCAAAATCTCGAGT 4043
QY 238 -----Lys----- 238
Db 4042 TACTGCAAAATCGATCTCCATCTGATTTTCCAAATATCATTTGCTGATGGTGGCAGCACA 3983
QY 239 -----Gly-----Thr----- 240
Db 3982 GAAGGTTTCAATTTTAAACCATTCCTTCATTAGCCAAACATCAACACACACTCATCTGATT 3923
QY 240 ----- 240
Db 3922 CATAGGTAATCAAAGCTGGCTTCTCATAAAGTTCTGAGGTAAGTTGGATTGATAAC 3863
QY 241 -----Leu-----Gln-----Cys----- 243
Db 3862 TGGGATGATCTGCTTCTGCTTCTCGSACAGATGATGATGTCATCGACTGCCACTGGTC 3803
QY 244 -----Glu-----Ala----- 245

Db 3802 ATAGTCCTCCCTGAGAACAGGGCTGCCACAGCGGAACCTGTGTGAAGGGTCTTGGC 3743
QY 246 -----Ser-----Ala----- 247
Db 3742 AGCAGCTGGAAGCTCCAGATAGACAAATCTGGGTTTGTCTGAAGTCTGAAAGTACATCTC 3683
QY 248 -----ValPro----- 249
Db 3682 TGCTAGCAGGTGCCACTGGATGCCCCCATTTGTCTGTACTGTGAAGGAGGACGCCCTCCTC 3623
QY 250 -----SerAla-----Glu----- 252
Db 3622 TCTGTCTCAGGCTGTGTGCATGAAGCACTCTCTCCGCTATCTGTGGATGTAGAAGTGTGAC 3563
QY 253 -----Phe----- 253
Db 3562 AAAGTCCACCAAGAAGTATCCAGTCCCAACTCACCAGCTGTCTTTTCCAGGCTTGGCT 3503
QY 254 -----Gln----- 254
Db 3502 GAAGTACAGAGATATCCAGAGAAGATGACACCAACACCCCTTGTCTGTGTTTACAATTC 3443
QY 254 ----- 254
Db 3442 TCCCCCAATAACTTCTTCCAGTCAGACTCCAGCCATTCTGGTTCTCAAAATCTGACAT 3383
QY 255 -----Trp----- 255
Db 3382 AATTGTGACGGAAGGCAAGCTTCTGGGTGGCAATTCAGTGCCTTGGTACCCCTGGTCACA 3323
QY 256 -----Tyr----- 256
Db 3322 CCTGCATATGCCATGATCGCATGAGCCATGCCCACTGCACATGTTGGGGCACTGCTGCC 3263
QY 256 ----- 256
Db 3262 AATGTAAATGCTGTCCAAAGCCCACTCGTCTTGAGTGTGTATAGTCTTGGCTCCAGCG 3203
QY 257 -----Lys-----Asp----- 258
Db 3202 GAAACGGGTAGCACTGGACCAAGTTTCTGGGAGGAGCACTATGACTCTCTCCACTG 3143
QY 258 ----- 258
Db 3142 TGTAAACTCACTGCATGGTAATACCTTGTGTATGTAAATTCCTGCAACTTGGCATACT 3083
QY 259 -----Asp-----Lys-----Arg 261
Db 3082 TGGAGGCAATCTTCTTGGACGAGGTGCCAGGTAAAGCCGTGGTGGTTGAGTACTCCAG 3023
QY 262 Leu-----Ile-----Glu 264
Db 3022 CTTCACTGGTGTCCATGTGGGGTGTATTTCTGGCCACATCCCATCACCAGAACTGAA 2963
QY 264 ----- 264
Db 2962 CTGAATCATAGATGCTCCTATCTGCATGTGATGTGTGTTCACATAGGCGCATCTGA 2903
QY 265 GlyLys-----LysGly-----Val----- 269
Db 2902 GGCAAGTTTAGAATCTCTGTAAACAAAGGGTCCAGTGTGGCCACAGTATGGCTGAC 2843
QY 270 -----LysValGlu----- 272
Db 2842 AITTCAGGTAGAATCCCAAGACTGAGTGCCTCCACAGATTGGTAAAGTCAAGACT 2783
QY 273 Asn-----Arg-----Pro-----Phe----- 276
Db 2782 AATGCTGTTGAAGACACAGATGTATGATATCTCATCAATAGCCCATCATCTTCTCT 2723
QY 277 -----Leu-----SerLys----- 279
Db 2722 CTGGGAAGATGATAGGGTTGCCACCATCTGAAGTGAATTCCAAACTGCTTTGTCATACC 2663

QY 279 ----- 279
Db 2662 TGGTAGTTCTACGAGATTAATCTGGGCTCATGATAGCTGAGATATGAATAATGCTCCAG 2603
QY 280 -----Leu 280
Db 2602 GAGTTTCCAAAGTTATCCCATTAATCATGAAGATATGACGCAAAACTCCTTCCAGGCTG 2543
QY 281 Ile----- 281
Db 2542 ATCAGGGGCTCTGCACGTGCTCAGAACAGATTTGCTCCCAAGTCTCAGTGTGAAGTGGAG 2483
QY 282 -----PhePhe----- 283
Db 2482 AAACCTGGATTGTGAGCTGTCAAGAAAGATGTAATTAGCTGTGACGCCGCTTCTTTGTT 2423
QY 283 ----- 283
Db 2422 GAAACCCAGGGCCTTACCCTGCGGCAAGACACACCAACCAAGCTGACTTCAGACCAAG 2363
QY 284 -----Asn----- 284
Db 2362 GATAGATAAAGTTATGTATGAGAGAGAGCTGTGAAGTCCCAAGCTTTTCAGAAATPAA 2303
QY 285 -----Val----- 285
Db 2302 CATTTGGGAATGTCTGGGATGCCATCTCACAAAGCTGGGCCAGAAAAATCCAGGGTCAACAT 2243
QY 286 -----Ser-----Glu----- 287
Db 2242 GCAACCATGTCTAGTGCATGCTCTGTCCAGAACAGAAATTTGAGACATGACGGGCAAT 2183
QY 288 -----His-----Asp----- 289
Db 2182 ATAAACATTAATCAATTTGCCACATGTTTCCAGGAATGGTCTGTGTCTCCAGGCAAT 2123
QY 290 -----Tyr----- 290
Db 2122 CCTGGTGTCCGGGTAGTGTGCTGTGAGGAGGGAATGTTTATTTCCGTTCCACCCACT 2063
QY 290 ----- 290
Db 2062 GTAGTTTTCAGAGGAGTACACAGTGTCTGTGGGAGGCTGGGTCCAGACAGATCTCAGG 2003
QY 290 ----- 290
Db 2002 TAAGCATTCAGTGTGAAGGAGGACCCAGGAGGCCCATGGTTGGTAGAAAAATTCCAAGCT 1943
QY 291 -----Gly----- 291
Db 1942 GACACTGTTACCAGGCTGATGGTTCCATCCAGATGTGAGAAAACTGTATCATGTG 1883
QY 292 -----Asn-----Tyr----- 293
Db 1882 AGACATTGTAGAAGGAGAGAACAGGCAAGACATGGAAGTCTACAGCCACACATTCCT 1823
QY 294 -----Thr----- 294
Db 1822 ATTATGTCCTTGAATGGTTCTTTTGTCCCTGAGACAAAAATTTGGTAGCAGGAGTCTGAATTC 1763
QY 294 ----- 294
Db 1763 AGGATTGATGACCACAGAAACCAAGACGGAACCTTATATAGGAAATAGGAAGGATATC 1703
QY 295 -----CysValAla----- 297
Db 1702 CAGTGTATATGCTCTTTCTCTCTCTCAATTTTGTGCATACAGGATATGTCAATTTTCATG 1643
QY 296 -----Ser-----Asn-----Lys-----Leu----- 301
Db 1642 AGAATTTCCAGGGTCACAAAATTCCTCCCATCACAAAGTAAACCTCAGGTTCCCATACC 1583

QY 302 -----Gly-----His--- 303
Db 1582 GGTAGTGTCCATGGAGTGCATAATTTCTCTCCATCTTTGAGGAAGACCAATTGA 1523
QY 304 -----ThrAsn---AlaSer-----Ile----- 308
Db 1522 TAAGCTGATCTATCTGTTCCACATCTGTACCACTGACAGCTCCCAAGACATCCCATCC 1463
QY 309 -----MetLeu-----Phe---Gly----- 312
Db 1462 TGTAGGTGGCTCTCAAAATCTCTGACCAATGCTCTTGAATATCTCTGTGGAAGATC 1403
QY 313 -----ProGly-----Ala---ValSer---Glu----- 318
Db 1402 TACATCCCTGGTGGTGCAGAAATGAATGAACTGCTGCTTCAATTCATGGAATAAATGA 1343
QY 319 Val-----Ser----- 320
Db 1342 GTTCCCATCTGACTGACAGCTATCTTAATCTAGTCTCTGGGAAGAAAGCCAGTTGCC 1283
QY 321 -----Asn----- 321
Db 1282 TGTGTCCACTGGTTCGAGACTATCTTAAAGCACTTGTCTGTGAGCTGAATTGATGAT 1223
QY 322 -----Gly-----Thr----- 323
Db 1222 CAAGATGTTATCTAAGCCCGAGGCTTCATACATTCACCTACAGAGATTTTCCTG 1163
QY 323 ----- 323
Db 1162 CTTCCTCAATGAATGGACATCTCCCTTTGGGCTCTCAGGAAGTAGAGATATGAT 1103
QY 324 -----Ser-----ArgArg----- 326
Db 1102 GATTGTGCTGACATGGAAGGGCTCTAAATTTCTCTAGCTGAATCCAGTCCGACAGTT 1043
QY 327 -----AlaGly----- 328
Db 1042 ATTCTTGGCATATAACACGATGATGCTGGGTCTGAATACTAAAGCGACATGAACCTGA 983
QY 329 -----Cys----- 329
Db 982 CCCAATGGAATAATTGGAGACAGAGCTGTGTGTATTAAAGCCCTGTGTATCAGTTC 923
QY 330 -----ValTrp-----Leu 332
Db 922 TCGTGGCCCATATGTTTACAGAGGTGACGCGATGCGCATTAATCGCCACACTG 863
QY 333 -----Leu-----Pro-----Leu---LeuVal 337
Db 862 TTCTCCAGTCTCACAGTTGTTACATTCACCCATATATTGGAATTAATTGAGTTGGTG 803
QY 338 -----Leu----- 338
Db 802 GTAGAGTCAAAGTCATCTCTCAGGATATGCTGTCACTATGATTTTCACTAGATGTTGG 743
QY 339 -----His-----Leu-----LeuLeu-----Lys---Phe 344
Db 742 GTGCACAGTGACATCTGTGGAGCTCTTGTTCACAACTGCTGGGTAAAGCATCTTT 683

RESULT 28

US-08-471-119A-1/c
; Sequence 1, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Leitner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoerendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation

STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kassenhoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 46899 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tolypocladium niveum
STRAIN: ATCC 34921
US-08-471-119A-1

Alignment Scores:
Pred. No.: 2,348-22 Length: 46899
Score: 1712.70 Matches: 291
Percent Similarity: 11.34% Conservative: 45
Best Local Similarity: 9.82% Mismatches: 5
Query Match: 71.13% Indels: 2623
DB: 1 Gaps: 249
US-10-017-084A-523 (1-344) x US-08-471-119A-1 (1-46899)
QY 5 MetLys-----Thr-----Ile----- 4
Db 14957 TTGAAGTGTGCGGTGAGTGTAGTGAAGTATCACGGATGGCAGCAATCGATGCGC 14898
QY 5 -----Gln-----Pro--- 6
Db 14897 CGCTTCCTGAAGCTTGGCGGGGTAAAGTTTGGCCCGCAGCAGGATGAGCTGTTCCCGG 14838
QY 6 ----- 6
Db 14837 TAGCAGCATATAATGGCATCAATCGCGGAGAGAGCTTGACATCCAGAGGTAGGTA 14778
QY 7 ---Lys----- 7
Db 14777 GCGAAGTTTGCCTTGAGGATTCGAGGAACGGATGATCGTCTCGAAGACCGTGGCGC 14718
QY 7 ----- 7
Db 14717 CAACACCGCATTAACGTGTGCGGAGCTGAAGAAGCGGTGAGGAGCCAGCGGACCCCT 14658
QY 7 ----- 7
Db 14657 GTCAGATTCCTCTGAGCTGGGCTGAGCTTCTCGAGCCATGATATCAGTGCAT 14598
QY 8 -----Met---His---Asn----- 10
Db 14597 GGAATCGGGTGTATCGAGAGCTGCTCATGGAACACATCAACCAAGGAATCAGAGG 14538

QY 11 -----Serile--- 12
Db 14537 ATATTCGGTCTTCTGACATCCAAACAGGCCCTCTCTTTGTAGTGCAGCATTCCTCTG 14478
QY 13 SerTrp----- 14
Db 14477 AAGTGGTGGGTGCTGATGGGACGTCGGACCGTTCAACCCCGGGCGAGAAATTCCTG 14418
QY 14 ----- 14
Db 14417 GAATACTGAAGAAGACTTTGGACCGAGACTGCTTGAAGAGATCGTTGAATAGAGAT 14358
QY 15 --Ala----- 16
Db 14357 GGAGCCCTCAGCTTGTGATCTTTGCTGGAACAGGTGGAATTCAAATCGAACCGGTCGT 14298
QY 17 -----Phe----- 17
Db 14297 GATCTCCGTGGGAACAACCTCGCTGTGAGCGTTTTCAGCTTCAGCTCACCAGGTTCTT 14238
QY 18 -----Thr 18
Db 14237 CTGCGAATGACCGCAACATGAGCTGCACAAGTGGGTTTCGGGATGCATCTCGAGAACC 14178
QY 19 Gly----- 19
Db 14177 GGGCAAAAGATAGACAGCATCTTCTCGAACGGGACGTCCTGATGGCGAATGCAGCTGT 14118
QY 20 -----Leu----- 20
Db 14117 CGCCGTTGACCGGACCTGCTGCTGACTAGTCAAGGTCTCGTCTCTGTTGACGGTAAT 14058
QY 21 Ala-----Leu----- 23
Db 14057 GCGTATACATTCGATTGACGAAGAGCGGATATCTGCTCAAGTTCAGGTTCGGTTAGC 13998
QY 24 -----CysLeuPhe----- 26
Db 13997 ATTGGGATTGGTGTCCCTATAGTTGCTTCGTCCTCGGAACTGCTGAGCGGAAATATGGGCTGC 13938
QY 27 -----Gln-----Gly----- 28
Db 13937 GCGTAGGCGCGCAAGCAGTACCACGAAGAGGTAAACGGATGACCGCGAGAAATTCCTC 13878
QY 29 -----Val----- 29
Db 13877 CAAATTCTGTATAGTCTCTCTCGATCGTGACCGACATCTCCCGAGCGTGCAGAGAG 13818
QY 30 -----Pro-----ValArgSer-----Gly----- 34
Db 13817 GATCGAAGCGCGCGCAGATCGGTGATAGTCTCGCGCGGGGCACTATCTACAAAGTTGCTC 13758
QY 35 Asp-----Ala-----Thr-----Phe-----Pro----- 39
Db 13757 GACCCAGTATTGCAGCTCAGCTCGCTGTTGCTTTCTTGGGTTGGCTTCTTCTCGCCACAG 13698
QY 40 --Lys--Ala--MetAsp----- 43
Db 13697 AGCAAAATCGGATATGATCGGAGGGGTGTGTCTGCGATAGGGGATCGTGGCCTTT 13638
QY 44 -----AsnVal-----ThrVal 47
Db 13637 GACAGCCGTGGATAGAACTGCCCCAGCTCTTGGAAAGAGACATCCACAGACCGCCGTC 13578
QY 48 -----Arg-----Gln--- 49
Db 13577 GGAATGATGATGATCATCAGCAGATGAAGATGATGCTGCTGCGCGCGGCGCAGTAG 13518
QY 50 -----Gly-----Glu-----SerAla-----ThrLeuArg 56
Db 13517 AGCCAGCGCCATCCGGGCTCGGTTTCAGGTGGAAACGGAGCGATTGCTCTCTCTTCTTCAA 13458
QY 57 Cys-----Thr-----Ile-----Asp 60

Db 13457 TGTGGGAGATAGTTCGCGCTGCGCGTTCGAGAGATCAATGATCCTCAGGGTCTCGGTGAC 13398
QY 61 Asn-----Arg----- 62
Db 13397 AACTGATTGACCTTTTGCATACCGACGCGTTTGTTCGTAGAACGTGTGCGGAGAG 13338
QY 63 --ValThr-----Arg-----Val----- 66
Db 13337 CTCGTGACGCTCTCGAGGGCCCAACAGCCCGGTGAAGAGCATGAACGTTTCATGSCACC 13278
QY 67 -----Ala----- 67
Db 13277 GCGAAGACGAGCGCAAGGGCATGAGATACCATGTTGGCCCAAAAGTTTGAGCTGGTCGAG 13218
QY 68 -----Trp----- 68
Db 13217 GAACCAAGACGACCTGGGCAACGACTGAGGCACTGCGCCGCTGTATTGTCGAAAC 13158
QY 69 -----Leu-----Asn-----Arg 71
Db 13157 GATGGGTCATGAGGGGCTGATCCCTGTCTGTACTATGAGAACAGATCGCAGACTCGCG 13098
QY 72 -----Ser----- 72
Db 13097 ATGGTCAAAGATCTCTTTCGACGAGACGTGAGTCTCTAGTCGGCGCTGATCGGTGCGC 13038
QY 73 -----Thr-----Ile-----Leu-----Tyr----- 76
Db 13037 TAGCTTTGTTGCCATGAGGAGTGGCCACCGAGATCGAAGAAGTTTTCATATATCCCGAT 12978
QY 77 -----Ala----- 77
Db 12977 ATCAACCCCTAGGACGTGCGAGAACTCTCGCAGAGCACCTTTTCGATCTCTGTGCGGG 12918
QY 78 -----Gly----- 78
Db 12917 GGGCACAGAGCAGACACTTGTCTGGCCTTGGGTACCGTCTGGGCGCGTTGGTCAACTG 12858
QY 79 -----Asn----- 79
Db 12857 CTTCCGTCGACCTTTTCATTCGCGTTGAGAGGTAGTGTTCGAAGAACCATGATCTGGC 12798
QY 80 -----Asp----- 80
Db 12797 CGGATCATGTAGCGCGCAGAGAGTCTGGAGTCTCTCGGATCTCGCTCTCGACGG 12738
QY 80 ----- 80
Db 12737 TCGAGACTGTCTCGGTGACGCGGTGGTTCGTGAGGCTTCTTCTGTGTCGACCTTGGTG 12678
QY 81 -----Lys-----Trp----- 82
Db 12677 GTCGTCAAGAAGTCAATCAACATGAGACACTGTGTGTATGGCCAAAGTGGTGGAA 12618
QY 82 ----- 82
Db 12617 TACGGCGTCCAAACGCGCATCTCGAGACCACTGCGCGCGCAGCTGATCTCGACCCGAA 12558
QY 83 --CysLeu-----Asp----- 85
Db 12557 GCCTGCTCTTGTGCAATATCAACGAGATCGATCGCGAGAGGAAGCCACTTTCACGGC 12498
QY 86 -----Pro-----Arg----- 87
Db 12497 ATTCGATCGAGCAGCCGAAGCCATGAGACTCTGCTGTTGAGTCTTTGGGCTTCGCC 12438
QY 88 --ValVal-----Leu-----LeuSer----- 92
Db 12437 AAGTCTGTAACCGATTGCGAGATGGTTCGTCGACGATTGTCTTGTGTGGGAATATT 12378
QY 93 -----Asn-----Thr-----Gln----- 95

Db 12377 GCGATTGCAATGTGGTCGGAAATTTTGGTGCCCTGAGCAGACGGATCAGGCATCGCG 12318
Qy 96 -----Thr----- 96
Db 12317 ATCCATCTTGGTCGGGCAAAATCAACCCAGGCGCCAGGACTGACTTTTGTGTCGGGTTT 12258
Qy 97 --Gln-----Tyr-----SerIleGluLeu-----Gln----- 103
Db 12257 CGCCAGATCATTCAGTGGTGCAGAAACAGCAGCATACCGATACGACTCAGCTCGTTCTGGC 12198
Qy 104 -----Aen-----Val-----AspVal-----Tyr----- 108
Db 12197 TCGCATTCTCTTGGGAGATCTCCAGCTGCTTGATATCTCTACTTGGTCTCAGGGA 12138
Qy 108 ----- 108
Db 12137 GGTGA AAAAGCCGGATCAACGAGCAGTTCTGCTTCAGACTCTTCATTCGAAACAACCTC 12078
Qy 109 ----- 109
Db 12077 CCGTTGAACTCGGCCCTTTGTTCGCCCTATCGCCAGTGCATGAACCTGCGCGAGCGACAAG 12018
Qy 110 Glu-----Gly-----Pro----- 112
Db 12017 GAAATCCTCTTGTATGGCGTGGACCTCATATCAACCAAGAGATACGCTCCACGCCAG 11958
Qy 113 ----- 113
Db 11957 GACCTTGGTAAGATCTCTGACCAACTGGCGAGATAGTCTTGACTCGGGAAGTATGAGC 11898
Qy 114 -----ThrCysSerValGln----- 118
Db 11897 GACCGAGTTGACGACGACAAAGACTGC-----GTGCAGATCGTCTCCAGCCGGTCCGATATC 11841
Qy 118 ----- 118
Db 11840 AGTTGTGTTTCCAACCTCAACCGGATCCTATCTCAAGCCAGGGAATGACTTGGCGGC 11781
Qy 119 ---ThrAsp----- 120
Db 11780 CTTGTTGACAAACGGGTTTGGCGATGGCGATGGCTCTAGGCCAACGATGCTTTGACAGCC 11721
Qy 121 -----AsnHis-----Pro-----Lys----- 124
Db 11720 CCCTTCTCTGCGAGGTTGAACAGAACCATGCCAGTCCCTGTACCAACTTCGAGTACGTG 11661
Qy 125 ThrSerArg-----Val-----His 129
Db 11660 ACC---AGGGGCTGGGAATCCAGAGTGACCGCATGGTGTCTATCGAGCCACTCTCTGCAT 11604
Qy 130 Leu-----IleVal-----GlnValSerPro 136
Db 11603 CTGGCTCTTGTATCAGGCTGCCATGTATCATGGAGGTCCATGATGAAAGTC---CCG 11547
Qy 137 ---Lys-----Ile-----ValGlu----- 140
Db 11546 TCCAAGGCTTTGCTGATCGATTGTGTGATATCTCGTATGCGATGCTGTGCAAGTGTG 11487
Qy 141 -----IleSer----- 142
Db 11486 CTGCCATTCTTGGACCTGTTGCTGGACTCATCTCTCTAAACATCAGCGACTCGGGCGGC 11427
Qy 142 ----- 142
Db 11426 CACGAATCCAACTCTCCAGTCTTGATTTTCTTGAGATGGGTGAGCACTGCCGCATC 11367
Qy 143 SerAsp----- 144
Db 11366 AGTGACAGGTGCTGGCTTAGAAGACATACCTCGACCTCAGCTGTTGATGCGGTGCCC 11307
Qy 144 ----- 144
Db 11306 GCGGATCTTGACCTGGTATCGATACGGCCGAGAAATTCGATCTGGAGGTCTTTTGGTGC 11247

Qy 145 -----IleSer-----IleAsn----- 148
Db 11246 GTAGCGCACTCGATCTCTGTGCGGTATGCCCTGACTTGTCTGCCATCGATATCAAGTT 11187
Qy 148 ----- 148
Db 11186 GATAAATCGACCACTGTTGAGAGAGGAAGTAGTAGCTTCGAGCAGACCGTCTCCAGT 11127
Qy 148 ----- 148
Db 11126 CAGATGAGTTCTCCATTGCAACAGGGGGGGTGTATTTGCTGATTCTGTCCATGACAAA 11067
Qy 149 -----Glu-----Gly 150
Db 11065 AGCTCCCGAGTTACTGACAGCATGACCGATGGGCACACCATTTGATGAAGGGGTCTTCGSC 11007
Qy 151 Asn----- 151
Db 11005 AATGGATAGATTGTCTCATGACTGTGTTTCCGTTGGGCCGTAGCATTTGAAAGCTTG 10947
Qy 152 -----Asn 152
Db 10945 CCGTGGACGACCCCTTGTCTTGGCAGCATCAGAGCATCTAGCCTATCACCACCAAT 10887
Qy 153 Ile----- 153
Db 10886 ATAGAGAACGTGAGAGTTTGTACCCAGAGCGGTGAGTTGTCAAGGCACGTGTTTCAGCAA 10827
Qy 154 -----Ser----- 154
Db 10826 GCGTGGAGGACGACAGCAACATTGACCGTTGTGCGAAGAACCTTCTCGAGCGCTGT 10767
Qy 155 ---Leu-----Thr----- 156
Db 10766 GCTCTCCAAGAGATGAATAATAGTCGATACACCAACGTCCTCCATTGAGAAGCGTGT 10707
Qy 156 ----- 156
Db 10706 GAACACTTCCACACGAGGATCGAAGGCAAGATTGATATGTGGGCCATGTGGAAGA 10647
Qy 157 -----Cys----- 157
Db 10646 CTCTGGCAGTTGATGTGATGTTGTTGCTGTCTTTGTAAGACGAACGATTCGCGATGCTC 10587
Qy 158 -----Ile-----Ala 159
Db 10586 GACCATGACGCCCTTTGGTGCACCACTCGATCCAGACGTAAGATCACAATACGCAAGCT 10527
Qy 160 -----Thr-----Gly----- 161
Db 10526 TGCTGCAGTGGGCTGACTCTCGCGGCAGCCCGTTGATGTGTCGCTTCTGCGTGGCGAG 10467
Qy 162 -----Arg-----Pro----- 163
Db 10466 AATCTCGTGTATCCGATCGCTCTCCGCTTTCAGCATCCCTCCGGAATCGGGGTCTCTGC 10407
Qy 164 -----GluPro----- 165
Db 10406 GCCCAAGGACCAACATCGATCCGACACCTCGAAGGATGGCTCGAGCCGGGACGC 10347
Qy 166 ---Thr-----Val-----Thr----- 168
Db 10346 AGGAACATTTGACATCAAGAGCAGATATCAAGTTTGGCTTCAACACCGAGGATGGC 10287
Qy 169 -----Tyr-----ArgHis-----Ile----- 172
Db 10286 CACGATTTCTCGACGAGCGTGTGTCAGGATCGCCACGACGATCTCTCAGAGCGATACC 10227
Qy 173 SerPro-----LysAla-----ValGly----- 178
Db 10226 TCSCGAGATAGCCAGCAACCCACTTGTATCCGACTCCGATCCAGTCCGCGCATAGCTCAG 10167

8006 TCCATCGATTGAGCTATGTGTATCATCGCCGCTGTGGTCTATCGGCCAAGACTTGGCGAT 7947
267 -----Lys-----Gly--- 268
7946 GTGCCGTTCCAGATAGTCTTGTCTAAGGATGTGAACACACGATATTTCCGGCATC 7887
269 -----Val-----Glu--- 272
7886 TTTGTTCTCTTTCAACAGCCTAGCAAGACCTGTCTATCCATCTGGCTTGGAGCGAAGTC 7827
273 -----AsnArgPro----- 275
7826 GATCCAGGACTCTGCAATTGATCTTGTGATCGACTCTTGTGATTCTGTTGTTGTTACG 7767
275 ----- 275
7766 GATGTGCAGAACCGCGCTACCGGATATGAGTCTGTTGTTTCACTTCACTGTTCTT 7707
276 -----PheLeu---Ser--- 278
7706 CGCAGGATCTCAACATGCTCTATTCTTCGATAGAGATTCCTTGAGACTTCTGAAGAA 7647
279 -----Lys-----Phe----- 282
7646 GGCAGGTCGACAAAGCAATTCCTCTCCAGTCTCTAACCAGGCGCCACCTCTCTGTTGCAC 7587
283 Phe-----Asn----- 284
7586 TTTAGATCTGTCACCTGCTCCGTTTGTGTGACCGCCGCTGCAACAAAGGAAGTCTTT 7527
285 -----ValSerGlu----- 287
7526 GTGGTGGCATAGTTCTCATGCTCTCGAAGAGATACCGGCAACCCCTGGAAATCCGGAC 7467
287 ----- 287
7466 CAGGGCTCAACACCTCGCGAGGATTTCTCGGCTCGGAAATCTGGGCCACCGAGTT 7407
288 -----His-----Asp 289
7406 GATGAGGATCAGATCGGGCTCAAGCGCTGAGCGCGCCGCTATCCATCGCGTGCAGAC 7347
290 -----Tyr----- 290
7346 ATGTACTTGGGCTTTCCCTCAAGCCCTGGAAAGTTGGGCTGCTGTTGACGAATG 7287
291 -----Gly-----TyrThr----- 294
7286 AACCGGATTTGGGAAGGTTCCAGTCAATGTAGCTCTTACGCCAGCTTGACCGAGATT 7227
295 -----Cys-----Val 296
7226 GAATAGAACCATACCGTTCGGGTACCGATTTCAAGCAAGTGGGCCAGCTGTTGACCGTC 7167
297 -----Ala---Ser-----AsnLys--- 300
7166 AAGGAAGTGGGCATAGTATCGTTCGAGCAATTCCTGCATCTCCCTCTTGTCAATAAGCGT 7107
300 ----- 300
7106 TCCATCGTACATAGAGTTCAGGATGTAAAGTCTCGCGCGAGCGTGTTCATCAATGGC 7047
300 ----- 300
7046 CGTGATGTCGCGTAGCGGCTGTCTGAATGCTCTCCCAATTCCTGGACTTGGTGTCT 6987
301 -----LeuGly-----His----- 303
6986 CGACTGTCTTCTCGAGAGTCTGTTGCTTGTGGCGGTGATGAAGCCACCATCTGCAC 6927
304 Thr-----Asn-----Ala 306
6926 TCCCTGATTGTTCTCTCGGAGTTTGAACGACAAACGCGCATCTGTGCACACCGGCACTGCT 6867

307 -----SerIleMetLeuPheGly----- 312
5866 TAACAAGCGTGTCTTACTTCGCGGAGCTCGATGCGTGCCTTCGGACCTTGACCTGGTG 6807
313 -----Pro-----Gly----- 314
5806 ATCCATCCGACCAAGAACTCAACCTGGCCATCTTGGCCGGTAAAGAGCTCGGTGCGC 6747
315 -----AlaVal-----Ser-----Glu----- 318
6746 TGTGCGATAGGCCCTCGAAGTTGGCTCGAGCAATGACATCCACGACCGGTGCGAATC 6687
319 -----Val-----Ser----- 320
6686 AAGAGCGGGTGTGTAGCCAGACCAAAACATCTCCAGTGACTACAGGCTCTCCCAT 6627
321 -----Asn 321
6626 CACGCCAACGCGACAGCTGCTGATTCTGTGTCATCAGTAGACCCAGAGTTGCTAAG 6567
322 Gly-----Thr-----Ser 324
6566 GGTCTTCCAAATTGGCACACCAATTAAACAAATCGTCTGTGTGTCAGCAATCGAGTATAAAGT 6507
325 -----Arg-----Ala----- 327
6505 GCTCATGACCGTATTTTCGTTGGCCGTAGGCAATTGAGACTCTGACTTGACCAGAGC 6447
323 -----Gly-----CysVal----- 330
6445 TTTGGCCAGAGCTGCGTCCGCTGTCTTAAACCGGCTCTCTTACGTATAGAGAGTCAAG 6387
331 -----Tyr----- 331
6386 AGACTGTAGTGTAGCAGTGTGATCGTGAGGCAATTGCTTCAACAGGGCGGTGGGAACAG 6327
332 -----LeuLeuPro-----Leu----- 336
6326 TGCAATATTGATGTCTCTCTGAGGAATAGTGCTTCAACCGTTGAGCATCCAAAGATGCT 6267
337 -----Val-----Leu----- 338
6266 AAACCTGTCAATGATCATACAGAGAGCTCGTTCAGAAAGGCGCGTGAAGACCTCCCATAT 6207
339 -----His-----Leu----- 340
6206 CGATGCATCGAACCAAGGTTGGACATGTGAGCCATTCGGAAGGCTCTGCGCCGGGGTAG 6147
341 -----LeuLeu---Lys----- 343
6146 ACTGGATAGAATGTGTCTGCTTCAACAGGCGCAAGACTCCGCGGTGCTGATCATCAC 6087
344 -----Phe 344
6086 ACCCTTGGGTTT 6075

RESULT 29

US-08-646-695-1/c

; Sequence 1, Application US/08646695

; Patent No. 6168943

; GENERAL INFORMATION:

; APPLICANT: Rose, John K.

; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR

; TITLE OF INVENTION: USES

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

QY 49 ---Gln----- 49
Db 8597 TCACAATCAATCATCCAATTCCTATGATACATTTTCTTAAGAGGATTCGGAATAGTAC 8538
QY 49 ----- 49
Db 8537 GAGAAATTTGAAATAGACTGATGAGCCGGTCTGCGGACTCCCAAAAAGTCCCTGATTGA 8478
QY 50 ---Gly---Glu---Ser-----Ala--- 53
Db 8477 ATTCACTTAAATACTAGGGAACAGAGGATTTATTGACCATAGAARACTTCTGAGCGAT 8418
QY 53 ----- 53
Db 8417 CTTCTTCATGATACAAATATATGTTGTCATCTTAATCACTCGTTCTGATGTTGTC 8358
QY 54 -----Thr-----Leu----- 55
Db 8357 TTGATTCGATTAGCATTTTAACTCAGTCTTTAAACAAGTTGGCTGGACTCATTTCCCA 8298
QY 56 ---ArgCys-----Thr 58
Db 8297 TAGCGATGTTTCAGAGAGTTGGATCTTCTACTAGCTTGTCTATGTGATTTATTCGAAC 8238
QY 58 ----- 58
Db 8237 TGGCTATCTCGGGTTTCCAAATAGTCACTCATCTCTTCAGATGCTCACTTCGAGCAT 8178
QY 59 -----Ile-----Asp----- 60
Db 8177 GTACATGGATGAATCTCCAGATGAGAGACTTTCCTTACGGGATCTGGAAGGCTCTAA 8118
QY 61 -----Asn----- 61
Db 8117 TCMAAACTGGCAAGAAGATGCCCCGACACTCTCCAATGGAAGGTCCTCAATACAA 8058
QY 62 ---Arg-----Val----- 63
Db 8057 TGGCGTATTGAAAGTAGAAGTGTGCAAGCCGGTATCTTATCTTGAACTTCATACAATG 7998
QY 64 -----ThrArg----- 65
Db 7997 ATTGACGAAGACAGGATCATGATCATCAACAGAGCTAGCAATGTCCTCAAAATAT 7938
QY 66 ---ValalaTrp-----Leu-----Asn-----Arg----- 71
Db 7937 TGTACTGTATCATGGCAATGATGGTTCTCAGCAAAATGAGCTACGGTGTGAGAGCATTTG 7878
QY 72 ----- 72
Db 7877 TGGAACTGAGCTATATATTAGCAAGTGGGTATTGTTGTCATGTTGATGACACAAGTCA 7818
QY 73 ---ThrIle----- 74
Db 7817 CTCGTGACCATCTCTTGGTCTCTAACCCTTAATCACTCCAGGAAATCGSTATTTTTC 7758
QY 74 ----- 74
Db 7757 CATAAATCAAGTAATCTGAGATGTCATAGTCTCATCGTCAATTTATCAAAAGTCCCTACT 7698
QY 74 ----- 74
Db 7697 TCCCTGCTCCTATTGATTGTCAGTCATAATTTCTCATATTATAGAAACCAATTTGATTGA 7638
QY 74 ----- 74
Db 7637 GAGCACTCTGTAATCTTACAACGTTTCTCGATTTCTCGATTTTCTCGTTTATACGTGTGCAATAA 7578
QY 75 Leu---Tyr----- 76
Db 7577 CTTGATTATCACTTGTGCCAAGACTTGTGACAGCAGTGTCTCGATTTTAGCCTCTCTTT 7518

QY 76 ----- 76
Db 7517 GAATAACCAAGTAGAATTGAGGATAGTCCATCTTTTTCGCTAGACCTTCCAGTCCACCT 7458
QY 77 ---Ala-----Gly---Asn----- 79
Db 7457 CTTGTCTCTTGGCAACAACTCGTTGGAGGTTGAATTTGATCAGTGTGTGTGTGAACAC 7398
QY 80 -----Asp-----Lys----- 81
Db 7397 GCATCAAGTCTGTCTTCCATTGTAGTATATAAGACTTTTCTCAAAAATTTCTAGTATC 7338
QY 81 ----- 81
Db 7337 TCTCGATTAAAGTAGATTAACCTAAGAACTGGCCCAATACTCGGAACACTGGGCGCTTTG 7278
QY 82 -----Trp---Cys----- 83
Db 7277 ATAACCTTCTTGGTGTATTTCCTATTTTTCGTAATCAATGTGATTTGGCTATGCAATG 7218
QY 83 ----- 83
Db 7217 CCTCATATGACTTCAATCCTTGGCCGGATGAGGAATCTAACATCTTTTAAATGACTGCG 7158
QY 84 LeuAsp-----Pro----- 86
Db 7157 TTAGATCGTCCGCAATGTGAGCCCTTTAAACATAGGACGAAATGAGTCTTTATCAAT 7098
QY 87 -----Arg---Val----- 88
Db 7097 ATTGGTAATTACAAAGTATTCTCGCAATTTCCAAGACATTAGGAGAGAAATCTACCTG 7038
QY 89 ---Val----- 89
Db 7037 CCAACTTCAGTTCCTCTCTTTTAAAGAACCAATTAATAGATCATCATCTAAAGC 6978
QY 90 ---Leu-----LeuSerAsn----- 93
Db 6977 CTTCTCATCAATCTCTTTAAGAAATCTTTTCCAATTTGGTAGCCTTTGTGTCACACATG 6918
QY 93 ----- 93
Db 6917 TCTGCAACACCTTTTACTAGGATAGGAGTGTTCGGATTTCATTCGGACATGTTTCAACA 6858
QY 94 ---Thr-----GlnThr----- 96
Db 6857 CCTCTGACCTATTCTTGAATGACTTTTGTGAGAGTATATTATCGATGGGTCTAGTAAGT 6798
QY 96 ----- 96
Db 6797 CGGTATTTCAAAACATTTAATCAGCGGAAGTTTCATGCCATTTATCTCCAAAATCTTGAA 6738
QY 97 ---Gln-----Tyr----- 98
Db 6737 CTTGAGCAGCTGTGGCCATGATATTCTTTTAAATGACATGACATTTTAAAGGATGATCAG 6678
QY 99 ---Ser-----IleGlu----- 101
Db 6677 GGACAAAGTCTCCATTCACGACCACTTTTATGATCATTTGAACTGTGAATAGAACAA 6618
QY 101 ----- 101
Db 6617 TCCGAGTAAATCACTTGCAGTGTCTTTTGCATATGACATCAATATCTTTCTTCATGG 6558
QY 102 ---Ile-----Gln-----Asn 104
Db 6557 TTACTGGGAATGTAATTTTCTAGTCCAGTGTATAATACTATAAAGGATGACCCCAAT 6498
QY 105 Val----- 106
Db 6497 GTCTGAACGATCCATAATCACCAGTGTGAGTCCACTGTTTTCACACTCATTTATCTGAT 6438
QY 107 ---Val-----Tyr 108

Db 6437 CATGAGGAATCTTATACCTCGGTCAATTTTGGCCCTTTCATCAACAGAGTCTTGATAT 6378
Qy 109 Asp-----GluGly-----
Db 6377 GATTTTCAAAATGAGGAAATTTGGGACTAAAGCCCTTGATCTCTTGCTAAATTCATCA 6318
Qy 111-----
Db 6317 GCTTCAAGTTCATATCGGTTCCACCATTTTAAATCAAGTCATAGAAAAATTTCCCTGCC 6258
Qy 112---Pro-----Tyr-----
Db 6257 TCTCCACAAATTTATCTCCAAATCTGTAGATATTTAGAGGAGAGATGCTTGTGCTG 6198
Qy 114---Thr---Cys-----
Db 6197 AGACAGGTTGTCTATTTCTACATACCATGATAGCACCCTTTCATCTCCCTATATCA 6138
Qy 116-----Ser-----ValGln-----Thr--- 119
Db 6137 CATCTTGACCATTAACAGAAAGTTTCGGTCCATTAGATATCAAGTTTCTTGAAGTAAG 6078
Qy 120-----Asp-----
Db 6077 CCATCTCTCTGAATAAAAGTAGACCCCAAGCTGGAAACCCTAATCTCGCATATGTTG 6018
Qy 121-----Asn-----
Db 6017 TTCCATGAGAAATCTTCTGACTTTGCTTTGAAAGTCTCGCCAAAGTTGAGCAATCCA 5958
Qy 122-----His-----ProLysThr----- 125
Db 5957 CCTCAGAGACGATTTAAGATTAATGTCAACTTGTGTAGTCCAAAAAATTTTGACACA 5898
Qy 125-----
Db 5897 AATAAGGAGAAATTTGAATGAGTCAGTCCATCTTCTCTTTTGTGATGATCAATGGTT 5838
Qy 126-----SerArg-----
Db 5837 TGTGTCGCCAGCGCGGATGAGGTCTCCACCAGTCAAAATGTTATTTCTGCTCTTTGT 5778
Qy 128-----Val-----His-----Leu----- 130
Db 5777 CCATCTCATGTAATAAACTATACCTTGTGATGATGATATCAGACATTAACCAAC 5718
Qy 131-----Ile-----
Db 5717 TTCCCATCCATTTATGATCTGAGATGTTGAGATGGATTTGGCTTGACATGATGTTAACA 5658
Qy 131-----
Db 5657 TCTCAAGAACTCCATCCAGTTCTTACTATCCACATCGAGGGAATCGGAGAGAAATGA 5598
Qy 132 Val-----Gln 133
Db 5597 ATTTCTGTGATCAAAATGTCAATATCATCACTAATAGAGGAGAAATCAAAATGTAATCAG 5538
Qy 134-----Val-----
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Qy 135-----Ser-----Pro----- 136
Db 5477 CTTCAATGAAATCATGTAACCTCGTGTCTCAAAATCGTGGACTTCCCATGATGCTGTTA 5418
Qy 137-----Lys-----IleValGlu-----IleSer----- 143
Db 5417 GTTTTTTTCATAAAAAATTAATAAATTAATGAGGCTCTTTGAGCATGTTATCA 5358
Qy 144-----Asp-----Ile-----
Db 5357 CAAGTTGATTTGGTCCAAACATGAAGAATCTGCTAGCAGGATTTGAGTTACTTTCCAG 5298
Qy 146 Ser-----IleAsn----- 148
Db 5297 TCGGTTTCATCTCTATGCTGTATATAAATCTCTCTTTTCTTGGTGTGCTTTAATTAATGCA 5238
Qy 149-----Glu 149
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Db 5177 AAAAGAGGCAATAGAGCTTTTCCAACTACTGAACCAACTTCTACAAGCTCGATGGAAT 5118
Qy 151-----
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Qy 152-----Asn-----Ile----- 153
Db 5057 GTCTTGAATGTGAGGATGTTTCGAACACCTGAGCCTTTGAGCTTAAGATGAAGATCGGAGTC 4998
Qy 154-----Ser-----Leu-----Thr----- 156
Db 4997 CAACATACCATGTCCAATCATGTATAAAGAAATCTTATATCTCTGAACTGGTCTCTCAGAAC 4938
Qy 157-----Cys-----Ile----- 158
Db 4937 TCCATTTGGGTCCAAATTTCCACGCTTTCATATGTTGCCAGTCAATCCACAGTTTCCCTTTC 4878
Qy 158-----
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Qy 159-----Ala---Thr 160
Db 4817 TCTGATGATCTGGTCTCAAAGTATTTTAGGGTACCATTGATTATGTTGTAAGCAGGACC 4758
Qy 161 Gly-----Arg 162
Db 4757 GGTCTCTGGTCTTTTAGGAGCAAGATAGCTGAGATCCACTGGAGAGATTTGGAAGACCCGC 4698
Qy 163-----Pro-----Glu-----Pro----- 165
Db 4697 TCTGATTTTGTCTCAGGTTTCTTGGCAGAGGGAATTAATCCAAGATCCCTCTCAAGCTCTG 4638
Qy 165-----Thr---Val-----Thr-----Trp----- 169
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Qy 170---Arg-----HisIle----- 172
Db 4577 TTCAGGGAATCTGGCTGCAGCAAGAGATCCTTATCAGCCATCTCGAACCCAGACACCTGA 4518
Qy 173-----SerProLys---AlaVal-----Gly-----Phe 179
Db 4517 TGGGAGTCTGACTCCCAATGCTTGCAATTTGCAATTTTGCAGGCTTGGCTCCAGTTTC 4458
Qy 180 ValSer----- 181
Db 4457 ATAAGCAAGTAGTACTTCTGAACCCCTGTGCTCTTCTCCAGGATGATAGCTCTCC 4398
Qy 182-----Glu---Asp-----Glu----- 184
Db 4397 GTCCTCTGAGAGAGAGTGTCTCCATGGAATGAGTTAGATATCAATAGCCCTTTGAC 4338
Qy 185-----Tyr----- 185
Db 4337 CTTATAGTCAGAAATGCCAGGTTGTAGAGTTATGACAGTGGGCAATATGTAATTTGCTCA 4278
Qy 186 Leu-----Glu-----Ile---Gln----- 189
Db 4277 TTTTCCGTTGATGAATCTGTGAATCAACCCATCTCTCTGTGTATTTCATCAACACGACATG 4218

Db 5357 CAAGTTGATTTGGTCCAAACATGAAGAATCTGCTAGCAGGATTTGAGTTACTTTCCAG 5298
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Db 5297 TCGGTTTCATCTCTATGCTGTATATAAATCTCTCTTTTCTTGGTGTGCTTTAATTAATGCA 5238
Qy 149-----Glu 149
Db 5237 AAGATGGATACCACTCGGAGAACCAAGAAATAGTCCATGATTAACCCATGATAAAGAA 5178
Qy 150-----GlyAsn----- 151
Db 5177 AAAAGAGGCAATAGAGCTTTTCCAACTACTGAACCAACTTCTACAAGCTCGATGGAAT 5118
Qy 151-----
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Db 4817 TCTGATGATCTGGTCTCAAAGTATTTTAGGGTACCATTGATTATGTTGTAAGCAGGACC 4758
Qy 161 Gly-----Arg 162
Db 4757 GGTCTCTGGTCTTTTAGGAGCAAGATAGCTGAGATCCACTGGAGAGATTTGGAAGACCCGC 4698
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Qy 180 ValSer----- 181
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Db 4337 CTTATAGTCAGAAATGCCAGGTTGTAGAGTTATGACAGTGGGCAATATGTAATTTGCTCA 4278
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QY 190 -----GlyTle-----Thr 192
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QY 193 -----ArgGlu-----Gln----- 195
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QY 205 -----Asn-----Asp-----ValAla 208
Db 3980 TTGAATAGCCTTGTGACTCTTGGGCATTTTGTATGGCTGTGCTTATTAAGTCATT 3921
QY 209 AlaPro-----ValValArgArg-----Val-----Lys 216
Db 3920 ATGCCAAATTAATCTGAGCTTGACGGCAATAATGTAATTAAGAGAACATTTTCCA 3861
QY 217 ValThr-----Val-----AsnTyr----- 221
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QY 222 -----Pro----- 222
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QY 224 -----TyrIle-----SerGluAla-----Lys-----GlyThrGly----- 232
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QY 233 -----Val-----Pro-----Val----- 235
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QY 236 -----Gly-----GlnLys----- 238
Db 3320 ATCTGCCAATACCGCTGGAGTGGCTTTAGATTAGAGAACCCCAAAAGCAAGATTTT 3261
QY 239 -----GlyThr-----Leu----- 241
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QY 242 -----Gln-----Cys----- 243
Db 3200 TGCCACATCTGAGTATGTTCTGAAGCGGACGATTAGATCTAAACCGTCACTTTCACTGTAAA 3141

QY 244 -----Glu----- 244
Db 3140 GAAGAATTTCTCATATCTTAATGTATCGGATCATAGGTGTCATCTCGTCAACTCAAA 3081
QY 245 -----Ala-----Ser-----Ala-----Val----- 248
Db 3080 ATAGGATTTGTCAATTTGGAGCGCTCGGAGCACTATCCATAGTGTCTCTTTCATAAGG 3021
QY 249 -----Pro-----SerAlaGluPhe-----Gln----- 254
Db 3020 GGGTGTGCGATCCCTTAATTTCTTAGATTCTTACC-----TTTCCCTTCAGACCGAG 2967
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QY 256 Tyr----- 256
Db 2845 TATCTAGCCCGAGCAGGATGGCTCTTTATGAGACATTCGTCCGTCACTCCGACAGAG 2787
QY 257 -----LysAsp----- 258
Db 2785 ATGAACCTCTCTCTAGATGAGAACAAATTCATCCAAGGATATGGTGAGAGGCTGAAGACTT 2727
QY 259 -----Asp-----LysArg----- 261
Db 2726 GCTTTCTTTGGTTGGAAGTCAATGATGCTTTGAGAGAGACCAAAACATCTGATACTGT 2667
QY 261 ----- 261
Db 2666 TCTGATTGGAGGATGTGTGTTTATCACTGAGTGAACCTTATATACATCCGGATTATC 2607
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QY 265 -----Gly-----Lys----- 266
Db 2486 CCACTTAAACCTCTGGGATGTCAACGTHAAGTCTTTTCCATGCTCGTCAGATTCAAGC 2427
QY 266 ----- 266
Db 2426 TCAGGCTGTTTCCAGTCCGAAGTAAATACAAATCCACTTCTCATCTGCATAGTCACT 2367
QY 267 LysGly-----ValLys----- 270
Db 2366 AAGGCCCTGTATAAAGCCTTCAACTGCTCAGCTTCTGGATCTGGATCGATACAAACCT 2307
QY 271 -----Val----- 271
Db 2306 TGATTGTCTCAATTTCTGGTTGAGATTCTGTGTGAGAAATCATCTGCTGCTGAAATAA 2247
QY 272 Glu-----Asn----- 273
Db 2246 GAGGGCTTAGTATGCTCTTCCATCCATCTCTTGGAACTCACTCATTAATTTGGACTTTTCA 2187
QY 274 -----Arg-----Pro----- 275
Db 2186 GCTGTTGTGCTTCGATCTCAATCTATCTCTCCCGCTGATCCAGACAGAAATAGGAC 2127
QY 276 -----Phe-----LeuSerLysLeu-----Ile-----PhePhe----- 283
Db 2126 TTGAGATACTCAGAACTTTTGGAGATTATCCATGATATCTGTTAGTTTCTTTCATATG 2067
QY 284 -----Asn-----ValSer-----Glu-----His----- 288

Db	2066	TAGCAATAATATAATAGTGTGATCTGAGAAATTATAGGCTCAATTGTCAAATTCGACTTA	2007
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Db	1946	TACTGCATCATATCAGGAGTCGGTTTCTGTTTGATCTTCAAAACCATTCGAGCCATTCG	1887
Qy	291	-----	292
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Qy	293	---TYR---Thr-----Cys-----	295
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Qy	297	-----Ala-----Ser-----	298
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Qy	302	-----	302
Db	1526	TCTGCAACTTCTCGGTTCAAGATCCAGGTGGTTACATCTTCTGTAGACATTCGGTTAAT	1467
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Qy	303	-----HisThr-----Asn-----	305
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Qy	306	AlaSerIle-----Met-----	309
Db	1346	CGGCAAAATTTTGTGTAATTACTGTCTATTTCCCGCACACATCAAAAATGTTCAGACCTCT	1287
Qy	310	-----Leu-----	310
Db	1286	GGCACAAGAGGTTCAAACCTGTCATTGATTCATTTTGCAATGTTGTCAGCCCATCCATG	1227
Qy	311	-----Phe-----	311
Db	1226	AGCTTTTTTCTGTATTCAGGCAATTTGTGTTCTGCCCACTCTGTATAGCCAAAGTAGATAC	1167
Qy	312	---Gly-----Pro---Gly-----	314
Db	1166	AAMGGCAACCATTTGTCATCTGCGCTGGTTCTTGGAAAGCATCCGATATCCATCTCGAAGT	1107
Qy	315	-----Ala-----ValSer-----	317
Db	1106	ACGCGTCCAGGGCTTCAAGGATACAGGTCAAATATTCGGAATGTATCCCTGCTGTTTC	1047
Qy	317	-----	317
Db	1046	CCGATGTTTATTCGAAACTTGGACCAATCTTTATCCAACCTTACCCCGGATGTCTTTAAT	987
Qy	317	-----	317

D	b		986	GCTCCATACAAGTAGCTGTGACATGATGATTGATACATTTCCGGATTTGAGCGCCTTGG	927
Q	y		317	-----	317
D	b		926	TAGACATATCCTCTTAGATCTGCACAACTTTTGTAGTATTGATGTAAGAAGGAATCTCC	867
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D	b		866	TTTGATTTTCTGAAGTAATCTGCCGGTATTCCACTGGATCCTCATTTGCAGGAAGTTTT	807
Q	y		317	-----	317
D	b		806	GGAACTATGACTGTGTGTCAATGATTCCTTGTGACTGTAAACAGACATTTTGATTACTGTT	747
Q	y		318	GluValSer-----AsnGly-----	322
D	b		746	AAAAGTTTCTCTGACGCTTTTAAATGATAATAATGCTTTGTCTCTCGTCCCTATAGTG	687
Q	y		323	-----ThrSerArg-----Arg-----	326
D	b		686	AGTCGTATTACACTCGAGGGGGGGCCCCGGTACCCAATTCGCCCTATAGTGAGTCGTATT	627
Q	y		326	-----	326
D	b		626	ACAATTCACTGGCGTCGTTTTACAACGTCGTGACTGGGAAAA CCTGGCGCTTACCCAAC	567
Q	y		327	-----AlaGly-----	328
D	b		566	TTAATTCGCTTGCAGCACATCCCCTTTTCGCAGCTGGCGTAATAGCAGAGGCCCGCA	507
Q	y		329	-----Cys-----	329
D	b		506	CCGATCGCCTTCCCAACAGTTGGCGAGCCTGAATGGGAATGGGACGCGCCTGTAGCG	447
Q	y		330	-----ValTrp-----	331
D	b		446	GCGATTAAAGCGCGCGGTGTGTGGTTTACGCGCAGCGTGACCGTACACTTGCACGC	387
Q	y		332	-----LeuLeu-----	333
D	b		386	CCCTAGCGCCGCTCCCTTCGCTTTCCTCCCTTCCTGTCGCAACGTTGCGCGCTTC	327
Q	y		334	Pro-----Leu-----LeuValLeu-----	338
D	b		325	CCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCCTTACGGCACC	267
Q	y		333	-----	338
D	b		265	TCGACCCCAAAAACCTTGATTAGGGTGATGGTTCA CGTAGTGGGCCATCGCCTGATAGA	207
Q	y		333	-----	338
D	b		206	CGGTTTTTCGCCCTTTGACGCTTGAGTCCACGTTCTTTAATAGTGGNACTCTGTTC AAA	147
Q	y		339	-----His-----LeuLeu-----LeuLys---Phe	344
D	b		146	CTGGAACAACACTAACCCCTPATCTCGTCTCATTTCTTTTGATTTATAGGANIT	93

RESULT 30
US-08-646-695-7
; Sequence 7, Application US/08646695
; Patent No. 6158943
; GENERAL INFORMATION:
; APPLICANT: Rose, John K.
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

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; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,695
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-646-695-7

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Alignment Scores:
Pred. No.: 1,51e-24 Length: 14311
Score: 1712.20 Matches: 293
Percent Similarity: 10.13% Conservative: 43
Best Local Similarity: 8.83% Mismatches: 4
Query Match: 71.10% Indels: 2978
DB: 3 Gaps: 253

US-10-017-084a-523 (1-344) x US-08-646-695-7 (1-14311)

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QY 3-----Thrile-----4
DB 4338 TGGATAAGACATCTGAGATAACCATATTTGTAATAATGTGATCTGTATTTCCCTTTT 4397
QY 5-----Gln-----Pro-----6
DB 4398 CAATTAGACGGCATTTGATTTGAAGTAATTTCTGACCAATCACCCCATATCACGGTTGC 4457
QY 6-----Lys-----Met-----HisSerile-----12
DB 4458 TTGTCGGATAGAGGTTGGGATCTTGTGGGATCGTTTCTAATTCGTCTCTAATAGGTC 4517
QY 7-----Lys-----Met-----HisSerile-----12
DB 4518 CTGATCTAGTAAGAAAGGAATGAGGTGATACAC---TCAATTATCAATCAAGTAAA 4574
QY 13 Ser-----Trp-----Ala-----Ile-----PheThrGly-----19
DB 4575 TCAACCTCCGTACACTCGTTGGCGCCCTCTTCAATAGAGCCAGACTTCTCGGGTGA 4634
QY 20-----LeuAlaAlaLeu-----23
DB 4635 TTACTTGGCAGCAACTTCTCTATTATTCGTCTAGCAACCTTTTAAAGAACTCGAC 4694
QY 24-----Cys-----Leu 25
DB 4695 CTCTAATACGACCTTGTATAGATAGAGGAATAGAGAACTGTCTCGGCATGATGATT 4754
QY 26 Phe-----26
DB 4755 TTCTATAGCCCAAGTCTCCATATAGAAAACCTATACATCTGCCGACTTGTAGGATTGCT 4814

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QY 34 -----Gly-----Asp-----35
DB 5055 GAGCATAGAGCAACGTTGCTTGGATAAAAGTCGAAATTTCTGATCTCCAGATCCCTCA 5114
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QY 38 -----PheProlys-----40
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QY 45 -----Val-----45
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QY 49 ---Gln-----49
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QY 49 -----49
DB 5775 GAGAAATTTGAAATAGACTGATGAGCCCGTCTCGGACTCCCAAAAAAGTGCCTGATTTGA 5834
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QY 53 -----53

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QY 61 ----- 61
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QY 72 ----- 72
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QY 73 -----ThrIle----- 74
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QY 74 ----- 74
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QY 74 ----- 74
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QY 75 Leu-----Tyr----- 76
Db 6735 CTTGATTATCACTTTGTGCCAAGACTTTGACAGCAGTGTTCCTGATTTTAGCCTCTCTTT 6794
QY 76 ----- 76
Db 6795 GAATAACCAAGTAGATTGAGGATAGTCCATCTTTTGGCGTAGACCTTCCAGTCCACCT 6854
QY 77 -----Ala-----Gly-----Asn----- 79
Db 6855 CTTGTCTTGCACAAACTCGTTGGGAGGTGGAATTTGATGATGATGATGTGTGTGTGAACAC 6914
QY 80 ----- 81
Db 6915 GCATCAAGTCTGCTCTCCATTTGATGATATAGACTTTTCTCAAAATATTCATGAGTTC 6974
QY 81 ----- 81

Db 6975 TCTCGATTAAAGATGGATAACCTAAGAACTGGCCCAATACTCGGAACACTGGGCGGTTG 7034
QY 82 -----Tip-----Cys----- 83
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QY 83 ----- 83
Db 7095 CCTCATATGATCTCAATCCTTGGCCGGATGAGGAATCTAAATCTTTTAAATGACTGAG 7154
QY 84 LeuAsp-----Pro----- 86
Db 7155 TTAGATCGTCGGCAATCTGTTCAGGCCITTAACATAGAGCAAAATGAGTCTTTATCAAAT 7214
QY 87 -----Val-----Arg-----Val----- 88
Db 7215 ATTGGTAATTAACAAAGTATTTCTCGCAATTTCCAAGACATTAGGGAGAAAAATCTACCTG 7274
QY 89 -----Val----- 89
Db 7275 CCAACTTCAGTTCCTCTCTCTTTTAAAGCAATTAATTAGATCATCATCATCTAAGC 7334
QY 90 -----Leu-----LeuSerAsn----- 93
Db 7335 CTTCTCATCAATCTCTTTAAAGAAATCTTTCCAATTTGGTAGCTTTGTGTCACAAATG 7394
QY 93 ----- 93
Db 7395 TCTGCAACACTTTTACTAGGATAGGAGTGTTCGGAATTCATTCGACATGTTTCAACA 7454
QY 94 -----Thr-----GlnThr----- 96
Db 7455 CCTCTGACCTATTCATTTGAATGACCTTTTGTGAGAGTATATTATCGATGGGTCTAGTAAGT 7514
QY 96 ----- 96
Db 7515 CGGGTATTTCAAAACATTTAATCAGCGGAAGTTTCAGCCATTTATCTCCAAATCTTGAA 7574
QY 97 -----Gln-----Tyr----- 98
Db 7575 CTTGACAGCTGTGGCCATGTATTTCTTTAAACATGACTTTTAAAGGATGATCATGAG 7634
QY 99 -----Ser-----IleGlu----- 101
Db 7635 GGAGCAAGTCTCCATTCACGACCACTTTTATGATCATTTGAACCTTTGAAATAGAACAA 7694
QY 101 ----- 101
Db 7695 TCCGAGCTAAATCACTTGCAGTGTCTTTTGCATATGACATCAATATCTTTCTTCATGG 7754
QY 103 -----Ile-----Gln-----Asn 104
Db 7755 TTACTTGGGAATGTAAATTTTCTAGTCCAGTGAATAATCTATAAAGGATGACCCCAAT 7814
QY 105 Val----- 106
Db 7815 GTCTGAACGATCCATATACACAGTGTGAGATCCACTGTTTTCACACTCATTTCTGAT 7874
QY 107 -----Val-----Tyr----- 108
Db 7875 CATGGAGGAATCTTATACCTCGGTCAATTTTGGCCCTTCATCAACAGAAGTCTTTGATAT 7934
QY 109 Asp-----Glutly----- 111
Db 7935 GATTTTCAAAATGAGGAATTTGGGACTAAAGCCCTTGATTTCTTCTAATTTTCA 7994
QY 111 ----- 111
Db 7995 GCATCAAGTTGCATATCGGTTCCACCAATTTTAAATCAAGTATAAGAAAAATTTCCCTGCC 8054
QY 112 ---Pro-----Tyr----- 113
Db 8055 TCTCCACAATTTTATCTCCAATTTCTAGATATTTTAGAAGGAGAGATGCTTTGCTCTG 8114

[illegible]

Qy	151	----	-----	151	
Db	9195	TTTGATAGCCAGTATCACC	AAAAATAAACTCTCATCATCAGGAAGTTCGGAAGCAGC	9254	
Qy	152	-----	Asn	-----	153
Db	9255	GTCTTGAATGTGAGGATGTT	CGAACACCTGAGCCTTTTGAGCTAAGATGAAGATCGGATC	9314	
Qy	154	-----	Ser	-----	156
Db	9315	CAACATACCATGTCCAATCAT	GTATAAAGAAACATATATCTCTGAAGTGGTCTCTCAGAAC	9374	
Qy	157	-----	Cys	-----	158
Db	9375	TCCATTGGGTCCAAATTTCC	AGCTCTTCATATGTTGCCAGTCATCCACAGTTCCCTTTC	9434	
Qy	158	-----	-----	-----	158
Db	9435	TGTGTAGTTCACATGATCAT	TTCGACCAATCTTGAGAGGATTGGAGCACAATATCGAC	9494	
Qy	159	-----	-----	-----	160
Db	9495	TCGTATGTATCTGGTCTCAA	AGTATTTTGGGTACCATTTAGTTATGGTGAAGCAGCAGC	9554	
Qy	161	Gly	-----	-----	162
Db	9555	GGTCTCTGGGTTTTTAGG	AGCAAGATGAGATCCACTGGAGAGATTGGAAAGACCCGC	9614	
Qy	163	-----	Pro	-----	165
Db	9615	TCTGATTTGCTCCAGGTTCT	TGGCAGAGGAATAATCCAAGATCCTCTCAAGTCTCG	9674	
Qy	165	-----	Thr	-----	169
Db	9675	AATTAGACTTACATCCACT	GAGTCTGAGATGGAGCAGAGATCTTGACCTTCTGGCA	9734	
Qy	170	---Arg	-----	-----	172
Db	9735	TTCAGGGAATCTGGCTCG	ACAAAGAGATCCTTATCAGCCACTCGAACCCAGACCTGA	9794	
Qy	173	-----	SerProLys	-----	179
Db	9795	TGGAGTCTGACTCCCAAT	GCTTGCAGTATTGCATTTTGCAGGCGCTTCCCTCCAGTTTC	9854	
Qy	180	ValSer	-----	-----	181
Db	9855	ATAAGCAAAGTAGTTACT	TCTGAAACCTGTGCCCTCTTCCAGGGATGATAGCTCTCC	9914	
Qy	182	-----	Glu	-----	184
Db	9915	GTCTCTGAGAGAGAGGT	GTATGTCATGGAATGAGTTAGAAATCAGATGCCCTTTGAC	9974	
Qy	185	-----	-----	-----	185
Db	9975	CTTATAGTCAGATGCCAG	GTGTAGATTGAGACAGTGGGGCATATGTAATTGCTGCA	10034	
Qy	186	Leu	-----	-----	189
Db	10035	TTTTCGGTTGATGAAC	TGTGATCAACCATCTCTCTGTGTATTCATCAACAGCAATG	10094	
Qy	190	-----	-----	-----	192
Db	10095	GTGAGAGTACCTGGCAAT	CACTGTCTTCGGCATCCGTCACAGTTGCATATCCACAAT	10154	
Qy	193	-----	ArgGlu	-----	195
Db	10155	TTGAGGAGGAGCCTGGAT	TACGCCAAGTTCCTGTGTTTGGTTTCAATGCTTTCCTT	10214	
Qy	196	-----	Ser	-----	202
Db	10215	GCATTGTTCTACAGAT	GAGTGAAGGATCGATGGATCTG---TGTTATATACTTCGGTCC	10271	
Qy	203	-----	Ala	-----	204

Db 10272 ATACGAGCGGAATCACAAGTAGTAGACCCATTTGGAGCATGACATCCAACCGTCTGC 10331
QY 205 ---Asn---
Db 10332 TTGAATAGCCTTGTGACTCTTGGGCATTTTGACTTGTATGGCTGTGCTATTAAAGTCATT 10391
QY 209 AlaPro---ValValArgArg---Val---Lys 216
Db 10392 ATGCCAATTTAAATCTGAGCTTGACGGGCAATAATGGTAATTAGAAGCAACATTTTCCA 10451
QY 217 ValThr---Val---AsnTyr--- 221
Db 10452 GTTTCCTTTTGTGTGGGAAACTATGGTGAACCTTGCATTCACCCCAATGAATAA 10511
QY 221 --- 221
Db 10512 AAAGCTAAGTACAAAAGGCACTTCATAGTACGCGTAAACACATCGATCTCTGTAGTT 10571
QY 221 --- 221
Db 10572 TTTTTCATAGGATAGAAAAGACAGATATTAGTTGTTCCGAGGCTGGAATTAAGAGAG 10631
QY 221 --- 221
Db 10632 ACTGAGTAAACCGGGGATGTTTCAGAAGCTAGAAGTTAGACTAGCTCATTTGAGTGGCT 10691
QY 222 ---Pro--- 222
Db 10692 GATAGAAATCCAGGACCCAGCTCCAGATGCTTTTCTCGCAATCAGGCCAAACATTAA 10751
QY 223 --- 223
Db 10752 GGCCTTCTCTGAAATCAGAAAATTTGGAAGATTGAAATGATCCAGATCATAGGAGC 10811
QY 223 --- 223
Db 10812 TGCCTCCAGTGAATCATCGTAGATGGTCAATCTGTGAGCTCAATCGTTCCCTGTGAAG 10871
QY 224 ---TyrIle---SerGluAla---Lys---GlyThrGly--- 232
Db 10872 ACCTAATATGAATGCTCTCTGAGTGTCTGTGTATGATGAGCATGGGAGGGTCTTCCC 10931
QY 233 ---Val---Pro---Val--- 235
Db 10932 CATCTATGTGCAATAAGCCCTGCTTCGCAGTGAAGTGAATCTGTTGACTTG 10991
QY 236 ---GlyThr---GlnLys--- 238
Db 10992 ATCTGCCAATACCGTGGAGTGGCTTTAGATTAGAAGAACCCAAAGCCAAAGATTTT 11051
QY 239 ---GlyThr---Gln---Leu--- 241
Db 11052 GTAGAGGGACGTTTCCCTGCCATTCGATGTACATGTGATCCCAATGGGATACAGCGG 11111
QY 242 --- 242
Db 11112 TGCCACATCTGAGTATGTTCTGAACGGAGGATTAGATCTAACCGTCATTTTCACITGTAAA 11171
QY 244 ---Glu--- 244
Db 11172 GAAGAAATTTCTCATATCTTAATTGATTGGGATCATAGTGTCATCTCGTCACTCCAAA 11231
QY 245 ---Ala---Ser---Ala---Val--- 248
Db 11232 ATAGGATTTGTCAATTTGAGCGCTCGGAGCATATCCATGCTAGTGTCTCTTCATAAGG 11291
QY 249 ---Pro---SerAlaGluPhe---Gln--- 254
Db 11292 GGGTGGTGGATCCCTAATTTCTTAGATTCTTACC---TTTCCCTTCAGACCGAG 11345
QY 255 ---Tyr--- 255

Db 11346 AATCTTCTTTAAAGRACTCATGATGAATGGATTGGGATAAACAATTAGATCGTGTATCTG 11405
QY 255 --- 255
Db 11406 TTACTTTTTTTTCTATAGTCTACAGAGAAATATTGACTCTCGCCTGATTTGACAACTTTTGG 11465
QY 256 Tyr--- 256
Db 11466 TATCTCAGGCCGAGCAGGATGSCCTCTTTATGAGACATTCGTCCGTCACTCGGACAGAG 11525
QY 257 ---LysAsp--- 258
Db 11525 ATGAATCTCTCTCTAGATGAGAAACAATTCATCCAAGGATATGTTGAGAGGCTGAAGACTT 11585
QY 259 ---Asp---LysArg--- 261
Db 11585 GCTTTCCTGGGTTGGAAAGTCAATGGATGTCTTTGAGAGAGACCAAAACATCTGATACTGCT 11645
QY 261 --- 261
Db 11646 TCTGATTGGGACCGATGTGTTCATCACTGAGTGACCTTATATACATCCGGAGTTATC 11705
QY 261 --- 261
Db 11706 TGGCGCTCTTTCATAATGACCCCTTCTCCGATGCTTCAAAATGTGCATCTGCCAGATTC 11765
QY 263 ---LeuIle---Glu--- 264
Db 11766 CAGTATTTGGCACITTTGCACGACTGCTTTAATCGTGAAGCCACTGGGATTTCTGCTCT 11825
QY 265 ---Gly---Lys--- 266
Db 11826 CCATTTAAACCTCTGCGGATGTCAACGTAAGTCTTTTCCATGCTCTGCAGATTCAGC 11885
QY 266 --- 266
Db 11886 TCAGGCTGTTTCCAGTCGAAGTAAATAACAATCCACTTCTCTCATCTGCATAGTCACT 11945
QY 267 LysGly---ValLys--- 270
Db 11946 AAAGSCCTCTGTATAAGCCTTCAACTTGTGCAGCTTCTGATCTGCTGCTGAAATAA 12005
QY 271 ---Val--- 271
Db 12006 TGATGTCTTCAATTTCTGGTTTCAGATTCGTGTGTCAGAAATCATCTGCTGCTGAAATAA 12065
QY 272 Glu---Asn--- 273
Db 12066 GAGGCTTAGTATGCTCTTCCATCCATCCCTTTGGAAACAACATCAATTTGGACTTTTCA 12125
QY 274 ---Arg---Pro--- 275
Db 12126 GCTGTTGTGCTTGAATCTCATCTATCTCTTACCGCTGATCCAGAGAAATAGGAC 12185
QY 276 ---Phe---LeuSerLysLeu---Ile---PhePhe--- 283
Db 12186 TTGAGTACTCAGCAACTTTTGTGAGATTTATCATGATATCTGTAGTCTTTTTCATATG 12245
QY 284 ---Asn---ValSer---Glu---His--- 288
Db 12246 TAGCATATATATANTAGTGTGATCTGAGAATTTATAGGTCATTTGTCAAATTTCTGACTTA 12305
QY 289 ---Asp--- 289
Db 12306 GCATCTTGCAATTTGCTTCTCTCTTAGCCCTTGCAGTGACATGACTGCTCTTTTTCGCA 12365
QY 290 Tyr--- 290
Db 12366 TACTGCATCATATCAGGAGTCGGTCTTCTGTGTTTGTATCTTCAAACCATCCGAGCCATTG 12425
QY 291 ---Gly---Asn--- 292
Db 12426 ACCACATCTCTGCTTGTGGCGTGCATTAGTGTGTCATCAATCTCCGGTACTATCATCTGGA 12485


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QY 293 ---Tyr---Thr---Cys--- 295
Db 12486 GTGTAATTGTTATCTCAACACAAACTGTGTGCCAAGTCGCAGAGGATCCTACTGCA 12545
QY 296 ---Val--- 296
Db 12546 TAAGCGTACAAACAACTGCTGTAGTAAGAGATGTATCTCAATGTCATCAGGCTGTGCG 12605
QY 297 ---Ala---Ser--- 298
Db 12606 GCATTCCTTGTCTGTGTGATCTGACGACAGAGAGCTGTCAATTGCCCCCAGAGTGAAG 12665
QY 299 ---Asn---Lys--- 300
Db 12666 GCAGGTTTTTGACGGAAGAAATGAGAGACTTAGAAGACAATCCAAAGTCGATCAATAA 12725
QY 301 ---Leu---Gly--- 302
Db 12726 GGCATGTATGAATCGGCCTTGTCAATTTCTTGGCCTGGAGCATCATTTGGACCATTTCA 12785
QY 302 --- 302
Db 12786 TCTGCAACTTCTCGGTTCAGATCCAGTCTGTATCATCTTCTGTAGACATTCGGGTATT 12845
QY 302 --- 302
Db 12846 TTGCAGAGTGTCCAAATGTTGCCAATGACAGACAAATCTTTGAATCTGGAACAATAGTT 12905
QY 303 ---HisThr---Asn--- 305
Db 12906 CGGTATCTGAACGAGGCATTCATGTTTGTGAACATGTGGAAGAACATGTCCTACTGCA 12965
QY 306 AlaSerIle---Met--- 309
Db 12966 GGCACATTTTGTGTAAATTAATGTCATTTCCACACATCAAAAATGTCAGACCTTCT 13025
QY 310 ---Leu--- 310
Db 13026 GGCACAAGAGTTCAAACTGTTTCATGTATGATTTTGCAATTTGTCAGCCCATCCATG 13085
QY 311 ---Phe--- 311
Db 13086 AGCTTTTCTGTATTCAGGCAATTTGTCTGCCACTCTGTATAGCCAAAGTAGATAC 13145
QY 312 ---Gly---Pro---Gly--- 314
Db 13146 AAGGCAACCAATTTGTCTATCTGCGTGTCTGGAAGCATCCGATACCTCCATCTGGAAGT 13205
QY 315 ---Ala---ValSer--- 317
Db 13206 ACGCGTCCAGGGCTTTCAAGGATACAAGGTCAATATTCGATTTGATCTCCCTGCTTTC 13265
QY 317 --- 317
Db 13266 CCGANGTTTATCCGAAACTTGACCAATCTTTATCCAATTAACCCCGGATGTCCTTTAAT 13325
QY 317 --- 317
Db 13326 GCTCCATACAAGTAGCTGTGACATGATGATGATACATTTCCGGATTTGAGGCCCTTGG 13385
QY 317 --- 317
Db 13386 TAGACATATCTCTTAGATCTGACAACTTTTCTAGTATTTGATGATGAAGAGAAATCTCC 13445
QY 317 --- 317
Db 13446 TTTGATTTTCTGAAGTAATCTGCGGGTATTCCTGGATCCTCATTTGCGAGGAAGTTT 13505
QY 317 --- 317
Db 13506 GGAACATGACTGTGTGTCATGATCTCTTGACTGTAAACAGACATTTTGATTAATCTGTT 13565
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QY 318 GluValSer---AsnGly--- 322
Db 13566 AAGTTTCTCCTGAGGCTTTTAATGATAATAAGTGTGTTTGTCTCTGCTCCTATAGTG 13625
QY 323 ---ThrSerArg---Arg--- 326
Db 13625 AGTCGTATTACAACTCGAGGGGGGGCCGGTACCCTATTCGCTATAGTAGTGTATT 13685
QY 325 --- 326
Db 13685 ACAATTCACTGGCGCTGCTTTTACAACTGCTGACTGGGAAAACCTTGGCGTTACCCAC 13745
QY 327 ---AlaGly--- 328
Db 13746 TTAATCGCTTGCACACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCGCA 13805
QY 329 ---Cys--- 329
Db 13806 CCGATCGCCCTTCCCAACAGTTTGGCAGCCTGAATGGGAATGGACGGCGCTGTAGCG 13865
QY 330 ---ValTrp--- 331
Db 13866 GCGCATTAAGCGCGCGCGGTGTGTGTGTTACGCGCAGCGTGACCGCTACACTTGCCAGCG 13925
QY 332 ---LeuLeu--- 333
Db 13926 CCCTAGCGCCCGCTCTTTCCTTCTTCCCTTCTCGCCACGTTCCGCGCTTTC 13985
QY 334 Pro---Leu---LeuValLeu--- 338
Db 13986 CCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTTAGTGTCTTACGGCACC 14045
QY 338 --- 338
Db 14046 TCGACCCCAAAAACCTTGATTAAGGTGATGTTACGTAGTGGGCCATCGCCCTGATAGA 14105
QY 338 --- 338
Db 14106 CGGTTTTTCGCCCTTTGACCGTTGGAGTCCAGGTTCTTTAATAGTGGACTCTTGTCCAAA 14165
QY 339 ---His---LeuLeu---LeuIys---Phe 344
Db 14166 CTGGAACAACACTCAACCTTATCTCGGTCTATCTTTTGATTTATAAGGATTT 14219
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Job time : 715 secs